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## (57) Abstract

A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three-dimensional image, the method comprising: (i) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor; (ii) modifying said x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand; (iii) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (iv) if required modifying the homology model for greater consistency with those binding properties.

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## HOMOLOGY MODELS OF THE GLUCOCORTICOID RECEPTOR

### INTRODUCTION

#### Technical Field

This invention relates to combined computational and chemical methods of obtaining improved homology models of the human glucocorticoid receptor and to computational methods using such models for the design of ligands that bind to the glucocorticoid receptor.

### BACKGROUND

#### Nuclear Receptors

The glucocorticoid receptor is a member of a superfamily of soluble proteins, the nuclear receptors. Unlike receptors associated with or integrated in the cell membrane the nuclear receptors reside in the cytoplasm or the cell nucleus. The members of the nuclear receptor superfamily have in common the ability to bind specifically their respective cognate ligands as well as DNA-elements. The ligands include physiologically-relevant ligands that are small molecules such as steroid hormones (androgens, oestrogen, mineralocorticoids, progestagens, and glucocorticoids), vitamins A and D, as well as pharmacologically important synthetic hormone mimetics that can act as agonists and/or antagonists. Upon ligand binding the receptor-ligand complex is able to modulate the transcription of genes that are controlled by that particular receptor's physiologic ligand. Depending on the nature of a specific target gene, it can be either up- or down-regulated via a classical mechanism that involves the interaction of the receptor-ligand complex with specific DNA-sequences upstream of target genes or by non-classical mechanisms such as protein-protein interactions between the receptor-ligand complex and other proteins involved in a signal transduction. The nuclear receptors bind DNA by means of a protein fold that contains cysteine residues coordinated to zinc atoms, the so-called zinc finger.

The zinc-finger motif has been used to identify and to clone members of the nuclear hormone receptor family. The nuclear receptors have 5 regions: the N-terminal A-B domain that contains an activation function; the DNA-binding domain; DBD(C); the hinge D; the ligand binding domain, LBD(E), and the F-domain (that is specific for the estrogen receptor). The 3D structures for the DNA-binding domains of the GR, oestrogen receptor (ER), thyroid hormone receptor (THR) and retinoic acid receptor (RAR), have earlier been determined by X-ray crystallography or NMR spectroscopy.

More recently, the 3D-structures of the ligand-LBD complexes of some nuclear receptors, (THR, RAR, ER and progesterone receptor (PR)) have been published. The overall fold of the LBD of these nuclear receptors is an anti-parallel alpha-helical sandwich. This fold does not occur in any other known protein. Therefore it has previously not been possible to homology-model nuclear receptor LBDs correctly. A prerequisite for homology modelling is that the target and template structures have a similar tertiary structure. The sequence homology between the LBD's of various nuclear hormone receptors is low to moderate (10-50%) which alone does not guarantee that the LBDs of other members of this family will share similar tertiary folds. However, all these nuclear hormone receptors share a common function (transcriptional regulation), ID organisation (vide ante; A-E(f) region organisation), and many but not all are activated by ligand (i.e. endogenous hormones). In addition the structures of the LBDs of all members of the nuclear hormone family that have been solved to date share a common fold (antiparallel alpha-helical sandwich). Taken together, this evidence suggests that other members of this family are also likely to share this fold and therefore it should be possible to create homology models for the LBDs of these nuclear hormone receptors.

The conformation of the C-terminal  $\alpha$ -helix (helix-12) in the X-ray crystallographic structure of ER- $\alpha$  complexed with raloxifene together with the PR-based GR-homology model was used to produce a GR homology model for the study of antagonist binding.

### Glucocorticoids

Glucocorticoids are steroid hormones that mediate some of the body's responses to stress. The primary function of glucocorticoids is to protect the organism from the potentially harmful defence mechanisms induced by different forms of stress. Two such potentially harmful stress reactions are the induction of hypoglycaemia by insulin and the inflammatory response. Increased levels of glucocorticoids will increase the blood levels of glucose as well as exerting and anti-inflammatory action.

The mobilisation of blood glucose by glucocorticoids results from their induction of gluconeogenesis primarily by the induction of key enzymes in intermediary metabolism. For instance tyrosine amino-transferase and other transaminases are induced which results in redirection of energy in the amino acid to carbohydrate metabolism. One of the key regulatory enzymes in the gluconeogenic pathway, phospho-*enol*-pyruvate carboxykinase (PEPCK), is also induced by the glucocorticoids. The mechanism of induction of these enzymes is mediated by the DNA-binding of the steroid-activated glucocorticoid receptor (GR) which results in increased transcription of the genes for these enzymes.

In contrast, the anti-inflammatory effects of glucocorticoids involve the inhibition of the expression of a large number of proteins induced within the inflammatory response cascade. Examples of such proteins are cytokines (e.g. IL-2, IL-8), enzymes (e.g. collagenase I, iNOS, cyclooxygenase-2) and adhesion molecules. The principle mechanism involved is the repression of the transcriptional activation of these genes induced by various intermediary transcriptional factors (e.g. AP-1, NF- $\kappa$ B). Glucocorticoids prevent the induction of these genes by protein-protein interaction between the steroid-activated GR and the intermediary activating transcriptional factors.

The initial step in the mechanism of action of glucocorticoids is their binding to a specific soluble cytoplasmic receptor protein, the glucocorticoid receptor (GR). Thereafter a chaperone protein, HSP 90 is released from the GR, and the hormone receptor complex translocates to the cell nucleus. GR belongs to the superfamily of nuclear receptors that have a zinc-finger DNA-binding motif. This motif enables ligand activated GR to bind to glucocorticoid response elements (GREs) situated on DNA upstream of GR-regulated genes. The transcription of those genes is then up- or down-regulated in response to the hormone. The  $K_d$  for binding of dexamethasone to GR is  $\sim 7$ nM and the natural hormone

cortisol binds with ~ 10% of that affinity. In the PR based GR model an alternative orientation of the side chain of Thr-739 is found which enables it to hydrogen bond to both the C-20 keto group and the C21b hydroxyl group. However, it is not currently known if the C-20 carbonyl contributes to affinity.

### **Homology Modelling**

Homology modelling involves the replacement of the differing amino acids in a related template protein structure in order to produce a model of the target protein structure. The basic assumption and requirement is that the template and target have a similar three-dimensional structure. The usefulness of a homology model is to be judged on the ability of such a model to explain the biochemical data for the target structure. A homology model can never be correct in all details, but it should capture one or more of the essential characteristics of the protein. Before a determination of the three-dimensional structure of the target is available the only way to evaluate a homology model is to assess its explanatory power. That the model is reasonable from a protein structure standpoint of view is not enough, since it can be very different from the target, especially if it was made from an unsuitable template. Therefore we have in the present invention tried to validate our model by checking it and refining it against as much experimentally-derived biochemical data available for the glucocorticoid receptor as possible. For the same purpose we have also docked representative glucocorticoids in the banana shaped cavity of the homology model and minimised the resultant steroid-protein complexes with molecular mechanics. The experimental binding affinities for GR obtained in this invention were correlated with the computed protein interaction energies.

The first homology model in accordance with this invention was based on the thyroid hormone receptor (THR).

TR was initially used for homology modeling of GR. Because of the higher degree of sequence homology of the LBDs of GR vs ER (26%) than with THR (13%), and because of the close similarity of the preferred ligands of ER and GR (i.e. steroids), ER will be a better template than THR and therefore ER was then used as a preferred template for GR homology modelling in the present invention. For similar reasons a progesterone receptor (PR) was also used as a preferred template for GR modelling in the present invention.

## Glucocorticoid Structure - Activity Relationships

Synthetic glucocorticoids were investigated at an early stage for their anti-inflammatory properties. The ranking order of GR binding affinities correlates well with both the metabolic and anti-inflammatory effects of glucocorticoids. A combination of experimental, QSAR and computational chemistry studies have produced the following concept of important features for ligand binding to the glucocorticoid receptor.

The C-3 and C-20 keto groups of glucocorticoids are regarded as important for binding since their reduction to hydroxyl reduces binding affinity. This has been interpreted as suggestive of hydrogen bond donors located at corresponding positions in the receptor structure. Certain pyrazolosteroids, such as deacycortivazol, bind with high affinity although they do not have the C-3 keto group. There are also steroids without the C-20 keto group that have high affinity for GR, so neither the C-3 nor the C-20 keto group appear to be absolute requirements of glucocorticoids for high affinity GR binding.

The C-11 and C-21 hydroxyl groups are likewise as important for binding, and therefore suggest the existence of complementary hydrogen bond acceptors-donors in the receptor.

The replacement of the C-11 $\beta$  hydroxyl with a keto group is detrimental to binding whereas a chlorine substituent at this position does not lead to loss of binding affinity. A C-17  $\alpha$  hydroxyl group increases affinity of glucocorticoids for the human receptor, but decreases the affinity for the rat receptor.

Hydrophobic pockets of limited size appear to exist in GR corresponding to the C-6 $\alpha$  and C-9 $\alpha$  positions of glucocorticoids, since small halogen atoms and methyl substituents here increase binding affinity, whereas bromine or methoxy substituents in the C-0 position decrease ligand binding affinity.

It may be concluded from thermodynamic analysis that the ligand binding cavity of GR is predominantly hydrophobic since the binding enthalpy decreases when the temperature increases, which indicates that the driving force for binding is hydrophobic in nature. Surface area calculations indicate that both faces of the steroid are in contact with the protein, i.e. it is completely enclosed by the binding cavity.

An important feature of GR binding is the presence of the 4,5-diene double bond in the A-ring of the steroid. A second double bond in the A-ring, the 1-2,diene, further enhances the binding affinity. This double bond causes the A-ring to tilt downwards (toward the  $\alpha$ -face of the steroid) from the main plane of the molecule. This downward bend of the A-ring was parameterized as the distance of the C-3 to C-17 carbon atoms (A- to D-ring distance) in the QSAR study of Wolff et al. It was found in that study that the shorter this distance was, the higher the affinity of the glucocorticoid was for the glucocorticoid receptor, i.e. the more bent the steroid is out of its main plane, the higher its affinity is for the glucocorticoid receptor.

Taken together, the structure-activity relationships presented above clearly indicate that the receptor imposes strict steric requirements on ligand binding.

## UTILITY OF THE INVENTION

The glucocorticoid receptor models described in this application can be used to design new glucocorticoid receptor ligand, that can be agonists and/or antagonists. Glucocorticoid receptor agonists are useful for treatment of inflammation and immunosuppressive therapy. Glucocorticoid antagonists are expected to be useful in treatment of hypertension, diabetes, obesity, glaucoma, depression, AIDS and for wound healing.

The glucocorticoid receptor models can be used in design of new glucocorticoids in various ways. De novo drug design can be carried out by identification of features in the binding site that can be important for binding with respect to shape, charge, and hydrogen bonding properties. Ligand fragments with complementary properties to receptor features can be optimised for binding, in the same manner, by replacement of ligand fragments by better ones. Both these processes can be carried out manually or with de novo drug design programs, like LUDI and LEAPFROG given the coordinates of the glucocorticoid receptor models described herein.

The models can also be used with molecular mechanics, or 3D-quantitative structure activity relationship programs to assess the protein binding affinity of virtual glucocorticoid receptor ligands in order to prioritise their synthesis.

In summary, the homology models according to the invention will be useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for glucocorticoid receptor by means of molecular mechanics scoring functions.

## BRIEF DESCRIPTION OF THE DRAWINGS

Fig 1 is a structure of a glucocorticosteroid, dexamethasone, with atom numbering.

Fig 2a is the final alignment used between the rat thyroid hormone receptor  $\alpha_1$  and  $\beta$  sequences and the glucocorticoid receptor.

Fig 2b is the final alignment used between the estrogen receptor and sequence and the glucocorticoid receptor.

Fig 3 is a ribbon drawing of the ligand binding domain of the glucocorticoid receptor with a ligand depicted as a space-filling model.

Fig 4 shows cross-sections of a glucocorticoid receptor ligand within the binding site of the glucocorticoid receptor. The van de Waals radii of the ligand atoms as well as the water-excluded surface of the glucocorticoid receptor-model is shown as dots.

Fig 5 shows a drawing of a glucocorticoid receptor ligand with its interactions, with residues in the binding site that are critical for ligand binding.

Fig 6 sequence alignment used for homology modelling of GR from ER and TR.

Fig 7 structure of eight representative glucocorticoids used for experimental GR-binding assays and correlation with their computed protein interaction energies.

Fig 8 Graphs showing the progression of the improved correlation between calculated protein-interatction energy with the experimental free binding energy; (i) molecular mechanics ligand-protein interaction energy, (ii) inclusion of terms for ligand solvation, (iii) inclusion of terms for ligand solvation and strain energy, (iv) scaling of the individual components with respect to each other by means of PLS. Triamcinolone is not included in (i);  $R^2=0.02$  if it is included.

Fig 9 (a) RasMol representation of the main interactions with dexamethasone in the GR homology model.

(b) Sketch of the main interactions with dexamethasone in the GR homology model.

Figures 10 and 10b Orthographic views of mutations in GR LBD that affect transactivation and/or ligand binding (Table 4) displayed as balls on the  $\alpha$ -carbons. The Figure being produced with RasMol.66.

Figure 11 Sequence alignment used for homology modelling of GR from PR.

Figure 12 The three dimensional coordinates of the GR model produced from ER using its X-ray crystallographic structure as a template.

Figure 13 The three dimensional coordinates of the GR model produced from PR using its X-ray crystallographic structure as a template.

Figure 14 Sequence alignment of ER and GR used for the conformation of the C-terminal-helix (helix 12) in a PR-based GR-model for the study of binding of antagonists. The three dimensional coordinates of the GR homology model using the rat TRa/T3 and human TRb/Triac crystallographic structures.

Figure 15 The three-dimensional coordinates of the GR model produced from PR using the conformation of the C-terminal  $\alpha$ -helix (helix 12) such as is in the X-ray crystallographic structure of ER- a complexed with raloifene. A GR-specific antagonist is docked into the binding site.

## DETAILED DESCRIPTION OF THE INVENTION

### Homology Modelling Based on the Thyroid Receptor

Initial multiple sequence alignments of the ligand binder nuclear receptor sequences were obtained using the Pileup program from the Genetics Computer Group at Univ. of Wisconsin program package. For semi-automated homology modelling Modeler, as supplied with Quanta96 from Molecular Simulations Inc., was used. <sup>8</sup> The homology

modelling that we performed involved the replacement of the differing amino acids in a related protein structure (the template) in order to produce a model of the target protein structure. It is essential that the template and target have a similar three-dimensional structure. In manual homology modelling the side-chain positions of the amino-acids are then refined e.g. using rotamer libraries and energy minimisation. Loops can be copied from libraries of the other protein structures, and/or simulated by molecular dynamics. If the model does not exhibit a reasonable protein structure, or if it fails to account for the available biochemical data, the alignment is revised and the model is rebuilt. This process is preferably repeated until the model cannot be further improved. Serious manual homology modelling is thus a tedious enterprise, since the placing and refinement of the side chain positions has to be redone in each modelling cycle. Semi-automated homology modelling facilitates the interactive process since it automates the manual placement and refinement of the amino-acid side-chains as well as modelling of loops. In the present invention we used the program Modeler for this purpose.<sup>15</sup>

The initial sequence alignments were obtained from multiple sequence alignments of nuclear receptors. These alignments were used for the initial runs but they were adjusted for subsequent runs in order to produce a molecular model with a reasonable protein structure that also accounted for the available scientific data. The ligand was not included in the Modeler runs. Iterative Modeler runs, using sequence alignments taking account of the known scientific data, resulted in the final alignment (Fig. 2). The overall fold of the model is shown in Fig 3. In the water-excluded surface of the model a completely enclosed banana-shaped binding cavity can be observed. This accords with calculations that have shown that glucocorticosteroids should be completely enclosed by glucocorticoid receptor, and because it is known that the glucocorticoids with high affinity for glucocorticoid receptor are more bent out of their main-plane (have a shorter A to D-ring distance) than glucocorticoid receptor-ligands with lower affinities. cortisol was manually docked as a rigid body into the glucocorticoid receptor homology model by the best possible fits of its atomic van der Waals radii to the water-excluded surface of the binding cavity (Fig 4). The amino acid residues in the cavity were mainly hydrophobic, except for two residues namely Arg-611 and Thr-739. These were located within 3Å of the 21-OH and 19-OH of cortisol, and their side chain nitrogen atoms could constitute hydrogen bonding partners.

Furthermore, the backbone carbonyl of Leu-563 was within 3Å of the 11-OH group of cortisol, and could thus be a possible hydrogen bond acceptor (Fig 5.).

A small cavity surrounded by carbonyl oxygen atoms near the C-3 of the ligand was observed. This cavity may contain water molecules. Therefore water-mediated hydrogen bonding may be involved in the binding of the C-3 carbonyl oxygen atom. Possibly cortivazol which does not have a C-3 carbonyl oxygen may displace the water molecules by its pyrazole ring which could fill the cavity, thus explaining its high binding affinity.

That C-11 chloro substituted glucocorticosteroids have similar affinities for glucocorticoid receptor as C-11 hydroxyl substituted glucocorticosteroids has been rationalized by the assumption that there exists an accessory hydrophobic pocket for such halogen substituents.<sup>3</sup> However this assumption may not be necessary, because in our model both the C-11 chloro or hydroxyl substituents may interact with a carbonyl oxygen, and carbonyl oxygens in other X-ray structures are known to interact with halogen atoms at less than the sum of their van der Waals radii. In the THR x-ray structure the ligand iodines thus interact with backbone carbonyl oxygens.<sup>5</sup>

That the binding cavity in this model is more bent than steroid makes sense in view of the classical structure-affinity relationships for glucocorticoid-steroids since it would preserve the rank order of affinities where the most bent glucocorticoid receptor-binding steroids (that have the shortest A-D ring distances) bind with the highest affinities to glucocorticoid receptor and the more planar ligands bind with lower affinities. It is known that the receptor-bound conformations of ligands frequently differ from their minimum energy conformations. It may thus be concluded that ligand binding to a receptor is a complex process where both the ligand and the binding site has to adjust for binding.

Warriar *et al.* have shown by point mutations that M565 and G567 are important for ligand specificity and binding, respectively.<sup>12</sup> In our glucocorticoid receptor model these residues are close to the binding site. Stromstedt *et al.* have covalent affinity labelling with radiolabelled glucocorticoid receptor ligands and protein sequencing studies demonstrated three residues, namely Met-622, Cys-754 and Cys-656, to be in the vicinity of the binding site of the glucocorticoid receptor<sup>13</sup>. In our initial alignment two of these residues were in our glucocorticoid receptor-model in the vicinity of the ligand. We therefore improved the

alignment so that the third residue was nearer the binding site after homology modelling. However, this revision of the models did not affect the binding site. The final alignments are shown in Fig 2A and 2B.

### Homology Modelling Based on the Estrogen and Progesterone Receptors

#### Materials

[<sup>3</sup>H]TA was obtained from NEN-Dupont, unlabelled steroids from Sigma and cell culture media, fetal bovine serum and penicillin-streptomycin from Gibco-BRL.

#### Plasmids

The mammalian vector pCMVhGR, expressing the wild type hGR, was constructed by cutting out a BamHI-XbaI fragment from pUC18/ATG-NX and inserting it into pCMV4. This fragment contains the entire coding region of the human GR gene and about 400 bp of the 3'-untranslated sequence.

#### Mammalian Cell Culture and Transfection

COS-7 cells were grown in Dulbecco's modified Eagle's medium, supplemented with 10% fetal calf serum, penicillin (100 IU/mL) and streptomycin (100 µg/mL), at 37°C in a humidified atmosphere with 5% CO<sub>2</sub>. For ligand binding assays and competition assays 10 cm plates containing cells at 60-80% confluency, plated out 1-3 days before transfection, were transfected with 10-15 µg expression vector using the calcium phosphate method. Cells were incubated 48 hours after transfection before assays were performed.

#### Ligand Binding and Competition Assays

Cells were washed with and scraped in PBS and spun in a microfuge. They were then resuspended in a buffer consisting of 1mM EDTA, 20mM potassium phosphate pH 7.8, 10% glycerol, 20mM sodium molybdate and 1 mM DTT, homogenised with a glass homogenizer and the lysate was spun for 30 min at 100,000 xg at 4°C. For saturation analysis different concentrations of [<sup>3</sup>H]TA(0.2-0.7 nM) were added and for competitive

binding assays 10nM [ $^3\text{H}$ ]TA and increasing concentrations of different non-radiolabelled steroids were added. The extracts were incubated at 4°C overnight. Bound and free [ $^3\text{H}$ ]TA were then separated by gel filtration on a Nick column (Pharmacia) and the amount of [ $^3\text{H}$ ]TA bound was measured in a scintillation counter. Free [ $^3\text{H}$ ]TA was calculated as total minus bound [ $^3\text{H}$ ]TA. The level of unspecific binding was negligible as monitored by adding 200 fold excess non-radiolabelled TA to parallel incubations with the different concentrations of [ $^3\text{H}$ ]TA.

### Homology modelling and molecular dynamics

Initial multiple sequence alignments of the ligand binding nuclear receptor sequences were obtained using the Pileup program from the GCG program package. For semi-automated homology modelling, Modeler, as supplied with Quanta96, was run using the no optimism option, with the ER- $\alpha$  LBD/estradiol complex X-ray crystallographic structure (Brookhaven PDB accession number 1ERE) as the template. Hydrogen atoms were added to the homology model using the HBUILD routine in CHARMM. Sodium and chloride counterions were placed at the maxima and minima of the protein electrostatic potential near charged amino acid residues so as to achieve net neutrality of the system. The C- and N-termini were made neutral. The 3D molecular editor of QUANTA96 was used to build the various glucocorticoids. The constructed glucocorticoids were minimised in vacuo using Gasteiger - Huckel charges and a dielectric constant of 78. Partial atomic charges for the resulting structures were calculated by fitting the water-accessible surfaces of the molecules to their 6-31G\* electrostatic potentials according to Singh and Kollamn, as implemented in Gaussian 94. The 6-31G\* ESP charges were used for the ensuing protein-ligand interaction studies. The fit of dexamethasone in the binding site with the lowest ligand-protein interaction energy after minimization of various explored alternative starting orientations was chosen as an initial conformation for subsequent molecular dynamics. The minimisation was carried out with CHARMM and started with 200 initial cycles of steepest descent and continued by the adopted-basis Newton-Raphson algorithm until the root means square energy gradient was less than 0.01 kcal/Å. The default heuristic non-bonded list-update method and a distance dependent dielectric function (scaled with 1/r) were used. The protein-ligand interaction energies were when required calculated for each resulting minimised conformation. The system was subjected to molecular dynamics

using the Verlet and Shake algorithms using the same conditions as for the minimisation. The protein was surrounded by a 21 Å solvent cap of TIP3 waters centred on the ligand for the dynamics simulation. The initial dynamics simulation was for 10 ps using a step-size of 0.01 followed by 60 ps with a step-size of 0.02. The solvent cap was then removed and the remaining dexamethasone-GR complex structure resulting from the final trajectory after 70 ps of dynamics, was energy-minimised using the same constraints as described above and thereafter used for energy-minimisation with other ligands instead of dexamethasone.

The Modeler program was used, and it has been shown that it produces results as good as manual modelling at different levels of homology.

The initial sequence alignments were obtained from multiple sequence alignments of nuclear receptors. These alignments were used for the initial runs but they were adjusted for subsequent runs in order to produce a molecular model with a reasonable protein structure that also accounted for the available scientific data. The ligand was not included in the Modeler runs. Iterative Modeler runs, using sequence alignments considering the scientific data, resulted in the final alignment (Fig. 6). In the water-excluded surface of the model a completely enclosed banana-shaped binding cavity could be observed. This is reassuring, since it has been calculated that glucocorticoids should be completely enclosed by GR, and because it is known that the glucocorticoids with high affinity for GR are more bent out of their main plane (have a short A- to D-ring distance) than GR ligand with lower affinities. Dexamethasone was manually docked as a rigid body into the GR receptor homology model by the best possible fits of its atomic van der Waals radii to the water-excluded surface of the binding cavity. The initially selected position of dexamethasone within the homology model correspond to that of estradiol in the ER- $\alpha$  crystallographic complex (binding mode 1, Table 1). The dexamethasone molecule was also rotated 180 degrees about its long axis, such that the positions of the A- and D-rings were reversed (binding mode 5, Table 1) and thereafter at each of these two orientations, the molecule was rotated in steps 90 degrees about its short axis (binding modes 2-4 and 6-8, Table 1). An alternative orientation of the C-17-side chain corresponding to binding mode 1 was also investigated (binding mode 9, Table 1). The orientation with the most favourable protein ligand-interaction energy (Table 1) agrees with that of the ligand in the ER and PR X-ray crystallographic structures but not with the orientation of the

glucocorticoid in an earlier published GR model. The fit with the lowest ligand-protein interaction energy was chosen as a starting conformation for subsequent molecular dynamics. A water molecule was placed in the cavity near the C-3 carbonyl oxygen, based on the bridging water between the glutamate, arginine and 3'-OH of estradiol in the ER- $\alpha$  X-ray crystallographic structure. Side-chains of residues or water molecules within 5 Å of the ligand were allowed to move freely, whereas the main chain C, Ca and N atoms within the same zone were restrained with a harmonic potential of 100 kcal/Å. The rest of the protein was kept rigid. These restraints were imposed because too much unrestrained minimisation and molecular dynamics has in blind tests been shown to cause the homology models to be more off the target than the template. The system was equilibrated with molecular dynamics together with the explicit solvent for 70 ps. The potential energy and temperature appeared stable during the last 10 ps of the trajectory. The solvent water was then removed and the remaining dexamethasone-GR complex structure resulting from the final trajectory after 70 ps of dynamics was energy-minimised using the same constraints as described above. The other ligand structures were then fit into the binding site in this same position and orientation as the best fit obtained for dexamethasone, and energy-minimised and used for correlation with the in this study experimentally determined IC<sub>50</sub>s for human GR (Table 2).

Because a crystallographic structure of the progesterone receptor bound to an PR antagonist such as RU-38486 is not currently available, it is not certain how the conformation of PR changes when complexed with an PR antagonist. If RU-486 is docked into the binding cavity of the PR crystallographic structure or the GR homology model in an orientation analogous to progesterone in PR, there is insufficient space to accommodate its bulky 11-N,N-dimethylaniline substituent (i.e., it sterically clashes with helix-12). Therefore it is likely that H12 of GR is displaced by RU-486 in analogy to the displacement of H12 by ER antagonists in estrogen receptor complexes. This displacement of H12 will then allow sufficient space to accommodate the 11-b-substituent of RU-486 and other GR antagonists with bulky 11-b-substituents. Therefore to produce an antagonistic GR homology model, H12 and the loop connect H11 and H12 in the PR based GR homology model was moved to where it is located in the ER -raloxifene complex by superimposition of the C-carbons according to the alignment in Fig 9. This was accomplished by splicing H12 and the loop between H11 and H12 from the ER -raloxifene complex X-ray crystallographic structure

into the GR-model, followed by mutation of the ER amino acid residues to the corresponding GR residues.

Table 1 Molecular Mechanics Interaction Energies For Various Biding Modes of Dexamethasone

Binding Mode *	Molecular Mechanics Interaction Energy (kcal/mol)
1	-82.5
2	-54.4
3	-73.6
4	-57
5	-64.9
6	-73.4
7	-64.2
8	-64.2
9	-79.6

\*Binding mode 1 corresponds to that of estradiol in the ER- $\alpha$  crystallographic complex. Rotating the dexamethasone molecule in this binding mode by 180 degrees about its long axis, such that the positions of the A and D rings are reversed, results in binding mode 5. Binding modes 2-4 and 6-8 respectively, result from the progressive rotation of the molecule in steps of 90 degrees about its short axis at each of these two orientations. Binding modes 1 and 9 have a different orientation of the C-17 side.

#### Calculation of Solvation Energy

6-31G\* electrostatic potential-fit charges and the corresponding CHARMM in vacuo optimised geometries of the steroids were used for calculation of solvent free energies with the GB/SA algorithm as implemented in the solvation module of the pseudoreceptor drug design software package PrGen. All calculations were run on Silicon Graphics R10000 workstations under IRIX 6.2/6.4.

#### Statistical Analysis

The sigmoidal dose-response curves obtained by competitive ligand binding assays were linearized with the log-logit function and the  $IC_{50}$  determined as the intersection with the X-axis (where  $\text{logit}=0$ ) as described by Rodbard. The statistical analyses were performed using Microsoft Excel 5.0 and the partial least squares methodology as implemented in the QSAR module of Sybyl 6.4.

### Molecular Mechanics Interaction Energies

Initially, the last frame of the molecular dynamics simulation performed with dexamethasone was energy minimised as described in Methods. It was noted that Thr-739 could possibly form a hydrogen bond with the steroid's 21-hydroxyl group by simple rotation of the amino acid's side-chain. The complex was then re-minimised following this alteration. As this led to an improvement in the protein-ligand interaction energy, and the 21-hydroxyl is known to contribute to the affinity of glucocorticoid steroids, this complex was then used as a template to investigate the interactions of the other ligands with the protein. A spectrum of ligands was chosen to represent typical glucocorticoids ranging from natural ligand cortisol to potent synthetic ligands such as triamcinolone acetonide. The ligands were selected to include various combinations of common substituents of pharmacologically interesting GR-ligands such as  $\Delta$ -1, 9 $\alpha$ -fluoro and 16 $\alpha$ -, 17 $\alpha$ --substitutions (c.f. Fig 7 for the structures of the ligands used in the present study).

Table 2

Table 2. Relative binding of glucocorticoids to human GR.

Ligand	$IC_{50} \pm SD^a (nM)$
Dessonide	$7.0 \pm 3.4$
9 $\alpha$ -F prednisolone	$7.3 \pm 7.0$
TA	$7.2 \pm 1.8$
Dexamethasone	$12.5 \pm 7.1$
9 $\alpha$ -F cortisol	$18 \pm 1.7$
Prednisolone	$18.4 \pm 8.5$
Cortisol	$68.0 \pm 39.5$
Triamcinolone	$131.0 \pm 7$

<sup>a</sup>n=3 for all compounds except for Ta where n=2

As can be seen from Table 2, the modifications of the cortisol structure employed here lead to quite significant alterations in binding affinity. Thus, this series of steroid ligands was well suited to challenge the explanatory powers of the model. Different orientations of the side chains of both ligands and amino acid residues were investigated and the model yielding the best correlation between molecular mechanics interaction energy and experimental data is analysed below and its interactions discussed with respect to the points described in the introduction.

It was not possible to obtain a useful correlation between the molecular mechanics interaction energy and the experimental free binding energy for all ligands (data now shown;  $R^2=0.10$  vs.  $0.45$  when triamcinolone is excluded). Triamcinolone, which is the outlier, is the only ligand in this investigation having a  $16\alpha$ -hydroxyl substituent. In other studies, it has been shown that in order to reproduce experimental relative free energies of binding, ligand desolvation effects have to be taken into account. The GB/SA algorithm has been validated with a series of small substituted hydrocarbons. We have within the context of another study (Carlsson et al., manuscript in preparation) applied the PrGen solvation module to the Wolfenden data set which consists of the experimentally determined free energies of solvation in water of ten aromatic and cyclic molecules. Due to the greater degree of resemblance of the molecules in the Wolfenden data set to drug molecules, the solvation energies calculated by the solvation module of PrGen are scaled according to the equation resulting from the fit between that data set and the experimental data

$$(\Delta G_{\text{solv}}(\text{GB/SA}) = (\Delta G_{\text{solv}}(\text{PrGen}) + 0.25) / 0.88; R^2 = 0.91$$

with 6-31G\* ESP charges calculated on the CHARMM in vacuo optimised geometries.

When a solvation correlation was included, the correlation between computed and experimental free energies for GR ligand binding was not improved ( $R^2 = 0.01$  for all ligands vs.  $0.45$  when triamcinolone is excluded). The activity of triamcinolone was under-predicted in the correlation, as its  $C-15\alpha$ -hydroxyl group was unable to make any hydrogen bonds with the protein but yet had the largest solvation penalty (Table 3). It was

then noted that Gln-642 could make a hydrogen bond with the C-16a hydroxyl oxygen atom of triamcinolone and the C-16 ether oxygen atoms.

Table 3: Summary of Ligand-Protein Interaction Energies (kcal/mol), Calculated Solvation Energies (kcal/mol), Ligand Strain Energies (kcal/mol) and Experimental Binding Affinities (kcal/mol) of the Glucocorticoids.

Ligand	Molecular Mechanics Interaction Energy (kcal/mol)	Scaled Calculated Solvation Energy (kcal/mol)	Ligand Strain Energy (kcal/mol)	Experimental free binding energy <sup>a</sup> (kcal/mol)
Desonide	-78.0	-26.32	5.66	11.55
9 $\alpha$ -F prednisolone	-72.4	-23.33	3.08	11.53
TA	-78.7	-25.88	5.96	11.47
Dexamethasone	-74.3	-21.13	4.71	11.24
9 $\alpha$ -F cortisol	-72.1	-20.35	3.42	11.04
Prednisolone	-73.9	-21.81	2.90	11.03
Cortisol	-70.6	-17.99	2.93	10.32
Triamcinolone	-82.9	-27.78	5.69	9.96

<sup>a</sup>  $\Delta G_{\text{bind (exptl.)}} = RT \ln K^*$ ,  $K^* = (1/K_d \text{ for } [^3\text{H}]\text{TA}) / (IC_{50} \text{ for tested ligand} / IC_{50} \text{ unlabeled TA})$ ,  $K_d$  for TA = 0.66 nM.

of triamcinolone acetonide and desonide. Thus, the side chain of Gln-642 was rotated so as to achieve a hydrogen bond with the C16-oxygen substituent of these ligands and the complexes minimized. Although the other steroids do not possess a C16-substituent capable of acting as either a hydrogen bond donor or acceptor, Gln-642 in these complexes was also rotated to the same position as that in triamcinolone and the resulting complexes minimised. The amide nitrogen of Gln-642 formed hydrogen bonds ( $\sim 3.1\text{\AA}$ ) with the S of Met-639 and also with the 16 $\alpha$  oxygen atoms of triamcinolone, desonide and triamcinolone acetonide. A good correlation between the molecular mechanics interaction energy for all the ligands could then be achieved with this model if solvation and ligand strain energy (ligand strain energy is the difference in energy between the ligand conformation in the protein and when minimised in vacuo) corrections were included. Figure 8 shows the progressive improvement of the correlation with the addition of these corrections. the  $R^2$  increases from 0.04 (0.49 without triamcinolone; Fig 8A) to 0.48 with the solvation penalty (Fig 8B) and further to 0.69 if the ligand strain energy penalty is also included (Fig 8C). When considering only molecular mechanics interaction energy together with ligand strain energy, the correlation coefficient is 0.1 (0.49 without triamcinolone). Thus it is the combination of the solvation and strain terms that results in good correlation with the experimental free energy binding data. A partial least squares analysis using the molecular mechanics interaction energy together with the solvation (not scaled according to Wolfenden data set) and strain energies was then performed, increasing the  $R^2$  from 0.04 (molecular mechanics term only) to 0.80 (inclusion of solvation and strain energies, Fig. 3(iv)). The resulting equation was:

$$\Delta G_{\text{bind}}(\text{calc}) = 0.384 - \Delta G_{\text{inter}}(\text{MM})0.343 - \Delta G_{\text{solv}}(\text{PrGen}) - 0.466 - \Delta G_{\text{strain}}(\text{MM}) - 31.058.$$

The main interactions of dexamethasone with the protein are shown schematically in Fig. 4. In another model the C-17-side-chain of the ligands was rotated so as to enable the C20-keto group to form a hydrogen bond with the CD2 hydrogen of Tyr-735, but at the same time maintaining the hydrogen bond interaction between the C21-hydroxyl and Thr-739. Such hydrogen bond interactions have been reported in the literature and interestingly, Tyr-735 corresponds to His-524 in hER $\alpha$ , the residue which forms a hydrogen bond with the C-17-OH group of estradiol. The corresponding residue for the other members of the steroid hormone superfamily is either a phenylalanine or a tyrosine.

However, this model yielded a poor correlation ( $R^2 < 0.5$ ) and was therefore discarded from further analysis.

It will be noted that whilst the description refers to a method of designing a GR homology model from rat thyroid hormone receptors and a Human Progesterone Receptor, the same process may be used to design a GR model from a Human Progesterone Receptor. Figure 11 shows the sequence alignment which would be used to design a GR from PR.

### **Explanation of the Glucocorticoids Structure-Activity Relationships**

#### Reduction of the C-3 keto to a hydroxyl group reduces binding affinity

Tanenbaum et al have contrasted the hydrogen bonding interactions of the phenolic group of estradiol and the C-3 keto group of progesterone complexed with their respective receptors. Steroid receptors which bind 3-keto groups have a conserved glutamine corresponding to the sequence position of Gln-725 in hPR, but the equivalent residue in hER $\alpha$  is a glutamate residue (Glu-353). Hence, these residues are responsible for the discrimination by the steroid receptors of keto and hydroxy moieties as the arginine residues which form either direct (hPR) or direct and water mediated interactions (hER $\alpha$ ) with the keto and hydroxyl functions are conserved throughout the steroid receptor family. Additionally, there is a conformational change (atomic displacement) associated with a change in hybridization from a  $sp^2$  C-3 keto to a  $sp^3$  hydroxyl. Thus, as the ligand makes several hydrogen bonds with the receptor, a protein with functional groups at an optimum separation for simultaneous binding to the O-3 and O-20 keto oxygen atoms, and O-11, O-17 and O-21 hydroxyl oxygen atoms may bind less to a ligand which has a 3-hydroxyl group instead of a 3-keto group.

In our homology model, the C-3 keto groups of the glucocorticoid ligands form direct hydrogen bonds with Gln-570 and Arg-611. In contrast, in hPR Arg-766 directly contacts progesterone's C-3-keto group, and in hER $\alpha$  the equivalent interaction (Arg-394) with the phenolic oxygen of estradiol is also direct.

#### Reduction of the C-20 keto group reduces binding affinity

In the homology model, the C-20 keto group does not engage in hydrogen bonding, but does have a favourable electrostatic interaction with the sulfur of Met-560. For the eight glucocorticoids, the O-A distance is  $\sim 3\text{\AA}$ . (Many examples of both intermolecular and intramolecular nonbonded sulfur-nucleophile close contacts in which the sulfur-nucleophile distance is less than the sum of the sulfur and nucleophile van de Waals radii have been reported in the crystallographic literature).

The C-11 $\beta$ - and C-21 $\beta$ - hydroxyl groups are important for binding

The main weakness of the present model is its inability to explain the importance of the C-11 $\beta$ -hydroxyl as the nearest potential hydrogen bond partner is the backbone carbonyl of Leu-563, with a distance of  $\sim 4\text{\AA}$ . That C-11 $\beta$ -chloro substituted glucocorticoids have similar affinities for Gr as C-11 $\beta$ -hydroxyl substituted glucocorticoids has been rationalised by the assumption that there exists an accessory hydrophobic pocket for such halogen substituents. However this assumption may not be necessary, because in our model both the C-11 chloro or hydroxyl substituents may interact with the Leu-563 carbonyl oxygen, and carbonyl oxygens in other X-ray structures are known to interact with halogen atoms at less than the sum of their van de Waals radii. In the thyroid hormone receptor X-ray structure the ligand iodines interact thus with backbone carbonyl oxygens.

The C-21 hydroxyl forms a hydrogen bond ( $2.6\text{\AA}$ ) with Try-739 and also with the backbone carbonyl of Tyr-735 ( $2.9\text{\AA}$ ). Thr-730 corresponds to Thr-894 in hPR, but in the complex with progesterone (which lacks the C-21 hydroxyl group) no hydrogen bond could be made by this residue with the ligand.

A C-17 $\alpha$  hydroxyl group increases affinity for the hGR, but decreases it for rat GR

The C-17 $\alpha$  hydroxyl group in both cortisol and 9 $\alpha$ -F cortisol forms a good hydrogen bond with Met-639 (oxygen-sulfur distance =  $\sim 3.2\text{\AA}$ ). However, from our model it appears that compounds possessing a 16-methyl substituent are unable to form a short hydrogen bond with this residue due to a steric repulsion between Met-639 and 16-Me. By comparing the sequences of rat and human GR, there were no species differences in the vicinity of Met-639. Thus the model is unable to explain the intolerance of the rat GR for a C17 $\alpha$ -OH group.

Bromine or methoxy substituents in the C-9 position decrease ligand binding affinity

The C-9 $\alpha$  fluorine of the ligands is in close contact with the CE2 carbon atom of Phe-623 (3.4Å). Thus, introducing a more bulky substituent would presumably result in the displacement of Phe-623 from a position in which it can form a "pi-teeing" interaction with the ligand's A-ring and/or displacement of the ligand from its preferred position, causing a disruption of its interactions with the receptor.

The ligand is completely enclosed by the hydrophobic binding cavity

In the model the ligand is completely enclosed by predominantly hydrophobic residues: Leu-563, Leu-566, Trp-600, Met-601, Met-604, Phe-623, Leu-723 and Leu-753. The ligands make many favourable hydrophobic contacts with the receptor, in particular the C18- and C19- methyl groups with Met-601 and Leu-732 respectively. Significantly, these residues are preserved in the hPR, human androgen receptor and human mineralocorticoid receptor, whose ligands also have C18- and C19- methyl groups, but not in hER whose natural ligands 17  $\beta$ -estradiol lacks the C19-methyl group. Additionally, hydrophobic contact exist between the C16-methyl group of dexamethasone and the acetonide functions of desonide and triamcinolone acetonide with Tyr-735.

In order to assess the utility of the PR-based GR homology model modified to accommodate GR antagonists for the design of such drugs the compound 10e described Gebhard et al. Biorg. Med. Chem. Lett. 7(17) 2229, 1997 was used. The ligand was placed in the receptor with its steroid core in the same orientation as progesterone in PR and the complex minimized to gradient norm of 0.05 with the residues within 7 Å of the ligand treated as flexible while the remainder of the protein was held rigid. After minimization the carbonyl oxygen atom of the 2-oxo-1-pyrrolidinyl group was within hydrogen bonding distance (2.7 Å) to the hydroxyl oxygen atom of Thr-556, which corresponds to Ser-711 in PR. The distance from the steroid C-3 carbonyl oxygen atom to Arg-611 was 2.6 Å. Thus the model may be used to interpret and improve the binding of GR antagonists to GR.

A second double bond in the A-ring improves binding affinity

The fact that the binding cavity in this GR homology model is more bent than the steroid ligand is consistent with the classical structure-affinity relationship for glucocorticoids, since it would preserve the rank order of affinities where the most bent GR-binding steroids (those that have the shortest A- to D- ring distances) bind with the highest affinities to GR and the more planar ligands bind with lower affinities. It is known that the receptor bound conformation of ligands frequently differs from the minimum energy conformation of ligands. In the liganded RAR structure the 9-cis retinoic acid is more bent than the binding cavity whereas the all-trans retinoic acid is flatter than the binding cavity. It was thus concluded that ligand binding to a nuclear receptor is a complex process where both the ligand and the binding site have to adjust for binding. If our modelling has produced a correct impression of the ligand binding cavity, the above statement will be valid for GR as well.

Each of the pair cortisol and prednisolone, 9 $\alpha$ -F, prednisolone represent ligands which differ only in whether they have a 1,2-diene double bond or not (Fig 7). In our model, the A-ring of the 1,2-unsaturated ligands adopt a 1 $\alpha$ , 2 $\beta$ -half chair conformation which represents one of the ideal forms. Relative to the docked 9 $\alpha$ -F prednisolone, the 3-C keto oxygen of the docked 9 $\alpha$ -F cortisol is displaced by 0.2Å. This leads to minor adjustments in its interactions with the protein so that the coordinates of the water oxygen atom and nitrogen of the Gln-570 side-chain differ by 0.1 Å as compared to those in the 9 $\alpha$ -F prednisolone protein binding site. Additionally, displacements of the 11-O, 17-O, 20-O and 21-O oxygen atoms and 9 $\alpha$ -F atom of between 0.1 to 0.2Å occur. Atomic movements of the same magnitude also occur for cortisol with respect to prednisolone, with the exception of the 17-O and 20-O atoms which are displaced to a lesser extent, (0.04 Å vs. 0.1Å respectively). Prednisolone has a distinctly superior molecular mechanics interaction energy as compared to cortisol (~3 kcal/mol), but 9 $\alpha$ -F cortisol has only a marginally better molecular mechanics interaction energy than 9 $\alpha$ -F prednisolone (Table 3). These differences are attenuated (9 $\alpha$ -F cortisol vs 9 $\alpha$ -F prednisolone) or at least maintained (cortisol vs prednisolone) when ligand strain energy is added to the molecular mechanics

term (Table 3). Thus, the model does reflect the preference of GR for ligands with a 1,2-diene double bond relative to those that lack this feature.

The shorter the C-3 to C-17 distance the higher the affinity of a Glucocorticoid is for the Glucocorticoid Receptor

Although there is not a direct relationship between the C-3 to C-17 distance of the ligand in the homology model and ligand binding affinity (Table 4), it is notable that this distance is greatest for cortisol and its 9-fluorinated analog. When compared to the other ligands, both lack a 1,2-diene double bond in the A-ring and with the exception of triamcinolone, they have the highest free binding energies (together with prednisolone).

Explanation of Mutational Data

The HSP90 heat-shock protein is required for GR ligand binding, but as a part of activation of GR which is conceived as a steroid-induced conformation change of Gr necessary for DNA-binding and glucocorticoid dependent transcriptional regulation) it dissociates from the receptor. The HSP90 interaction sites on the GR surface have been mapped with peptide competition studies. It was found that the critical contact site is located in the region between residues 632-659 of mouse GR. In our model this region (626-653) in hGR) corresponds to S1-S2 hairpin  $\beta$ -sheets and H6-H7  $\alpha$ -helices which constitute a part of the protein surface and which also line the binding cavity. Thus, our GR model is consistent with what is known about the GR-HSP90 interactions.

A number of mutations of GR in various species have been described. Most of the mutations in the GR LBD completely disrupt the function of the receptor, presumably by perturbation of the fold of the LBD. Those detrimental mutations are not useful for validation of a GR homology mode. On the other hand, mutations in the LBD that affect ligand binding specificity and/or GR ligand-dependent activation/repression of transcription without totally activating the protein are of the greatest interest for our invention, validation of a GR homology model, since they ought to be located near the binding site. Such residues whose mutations modulate the function of GR are (in terms of the human GR sequence): P541, M565, G567, A573, M601, C638, D641, C643, M646, L653, C665, E668, V729, C736, T774, 764, F774, and these are shown as purple balls in

the receptor model in Fig. 10a and 10b. It can be seen that they seem to cluster around the ligand site and/or on H12 or its vicinity. Most of the mutations which are non-detrimental to protein activation are within 7Å of the ligand, i.e. on the parts closest to the binding site of the helices that line the binding cavity (Table 5). Most of the mutated side-chains had direct ligand contact before the mutation (c.f. the inventory of the residues lining the binding cavity). That those mutations affect ligand binding affinity and/or ligand-dependent transactivation is thus consistent with our mode.

Table 4

Summary of Ligand Binding Affinities and C-3/C-17 Distances (Å) within Homology Model

Ligand	-ΔGbind(exptl.) (kcal/mol)	C-3/C-17 (Å)
Desonide	11.55	8.21
9αF prednisolone	11.53	8.3
TA	11.47	8.24
Dexamethasone	11.24	8.28
9αF cortisol	11.04	8.45
Prednisolone	11.03	8.23
Cortisol	10.32	8.47
Triamcinolone	9.96	8.17

Table 5. Mutations affecting GR transactivation/ligand affinity within GR.

Mutation	Decreased affinity for DEX	Decreased transactivation with DEX
P541A	<i>nt</i>	> 100-fold
L563F	6-fold	15 – 60-fold
M601L	3-fold	<i>nt</i>
C638Y	Normal	Normal
C638G	10-fold INCREASED	10-fold INCREASED
C638W	Normal	Normal
D641G	Normal	no activity
D641V	Normal	no activity
C643R	<i>nt</i>	Slightly reduced
C643G	<i>nt</i>	2 – 3-fold
C643S	4-fold	<i>nt</i>
M646T	<i>nt</i>	Slightly reduced
L653S	Reduced	Reduced
C665A	<i>nt</i>	> 100-fold
C665S	<i>nt</i>	4-fold
M666I	4-fold	10 – 25-fold
E688K	Normal	no activity
V729I	2-fold	4-fold
C736S	2-fold	10-fold
C736G	<i>nt</i>	no activity
T744I	<i>nt</i>	Reduced
I747T	2-fold	50-fold
L753F	Normal	no activity
Y764N	2-fold	3 – 4-fold
F774A	6-fold	20-fold

DEX = dexamethasone

*nt* = not tested

Some mutated residues were remote from the ligand, or did not have direct ligand contact. These mutations were further scrutinised, in order to confirm that they do not invalidate our GR homology model. Mutations in residues <523 and residues >761 are in the hinge or on the C-terminal part of H12 that is not included in the template X-ray structure and outside our GR model so they cannot be used for model validation.

The P541A mutation in Gr results in that more than 100-fold increase in steroid concentration is needed to preserve biological activity, presumably due to decreased steroid affinity. Although this mutation is remove from the binding site it is at the very beginning of the strand between H1 and H3 (at the end of H1) and it may therefore be critical for its conformation. This strand (consisting of residues 540-560) delimits the binding site with residues 542-544. Therefore, a conformational change in this strand brought about by the P541A mutation could affect ligand binding from a distance.

The patient mutation V762I which reduces affinity for dexamethasone 2-fold and the C643S mutation, which reduces affinity 4-fold, are located in proximity of the ligand binding site but the side chains of the residues are not directed towards the steroid. Thus, these residues do not appear to be in direct contact with the steroid and secondary effects of these mutations would be required to explain the difference in ligand affinity. The L653S and F744A mutants that were reported by Garabedian and Yamamoto were tested in a yeast expression system, in which binding receptor binding assays were not performed so their effect may be exerted on transcription only, and need not necessarily directly affect ligand binding.

The I747T mutation reported by Roux is 9-10Å from the ligand, so it is difficult to explain why it decreases binding affinity with our model. The E688K mutation has been reported by Garabedian and Yamamoto to abolish transcriptional activity of Gr expressed in yeast and COS cells and to decrease the affinity for dexamethasone. This residue is located on H9, as far from the binding site as you can get in the GR LBD, located near H1 and facing outwards. It is here H1 connects to the hinge region to the DBD and thus it is plausible that the effect of this mutation is caused by disturbances of the interaction with DBD, rather than an direct effect on the binding site.

The C655A/S mutants required a 100-fold higher steroid concentration for biological activity of the mouse GR, but C665S in human GR has no effect on binding affinity. This residue in our model is located in H8, remove from the ligand, but since it does not affect binding affinity it does not have to be located near the binding site to validate our model. Hence, the inhibition of binding observed by Lee et al, by the mutation of the neighbouring residue, M666I, is then difficult to rationalise. However, their other mutation affecting binding affinity, L563F is near the C-ring of the steroid's  $\alpha$ -face, and thus consistent with the model.

Warriar et al, have described that the point mutations M565R and A573Q greatly enhance the affinity of Gr for dexamethasone, whereas the G567A mutant fails to bind ligands efficiently. In our GR model these residues are relatively close to the binding site. The C $\alpha$ 's of M565, G567 and A573 are  $\sim 7\text{\AA}$  from C1,  $3\text{\AA}$  from C2 to  $11\text{\AA}$  from the C3-carbonyl of dexamethasone, respectively. IN our model G567 and A574 are facing the binding cavity, in contrast to M565, which is directed from it( and constitutes part of the protein surface). Thus the M565R mutation should not affect the ligand affinity of GR to a great extent if our model is correct. In the context of another study (Lind. U., Wright, A.P.H. and Carlstedt-Duke, J., ms. in preparation) a random combination of GR to mineralocorticoid receptor mutations (between residues 565-574) was created and screened for activity with glucocorticoids and mineralocorticoids. We found in agreement with Warriar et a., that the A573Q mutant had increased activity with dexamethasone, and that the G567A mutation inactivated GR. Finally, in contrast to Warriar et al, it was also found that the M565R mutant had no effect on the activity of dexamethasone which is in better agreement with the GR model proposed.

Thus, of the mutations described in the literature affecting ligand affinity, only two (M666I, 1747T) cannot easily be accounted for by the present GR-model.

Carlstedt-Duke et al have demonstrated three residues to be in the vicinity of the binding site of GR by covalent affinity labelling with radiolabelled Gr ligands with protein sequencing studies, Cys-638 is affinity-labelled through an electrophilic group of the 21-position in dexamethasone 21-mesylate reacting with a thiol. There is an absolute requirement for the C-20 carbonyl group for this labelling reaction. In our model the sulfur

of Cys-638 is located 7Å from the hydroxyl oxygen on C-21 of dexamethasone. The Cys-736 sulfur is even closer, which may explain why this residue is preferentially labelled.

Regarding the other two affinity labels, the chemistry is not known following the photoactivation of UV-light of the bound TA ligand. IN our GR-model the C-18 and C-19 methyl groups of Ta are located within 4 Å of Cys-736S, and 5.6 Å of Met-604S, respectively. If the reaction mechanism involves direct binding to the A- or B-ring, the affinity labelling of Cys-736 would require that the ligand be flipped with respect to A- and B-ring location at the time of the reaction. These two support the orientation of the steroid. In an earlier GR model the orientation of the dexamethasone is reversed with respect to the location of the A- and D-rings. With that orientation the Cys-736 is closer to the A-ring, but the other two residues (Met-604 and Cys-638) involved in the covalent affinity labelling are much further away, as compared to our orientation of the steroid. Thus, the orientation of the steroid in our model is more congruent with the affinity labelling data previously known.

Figures 12 and 13 show the -ray crystallography data obtained from the GR models produced using the X-ray crystallographic structures of TR, ER and PR as templates.

### References

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CLAIMS

1. A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three-dimensional image, the method comprising:
  - (i) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor,
  - (ii) modifying said x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand,
  - (iii) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor, and
  - (iv) if required modifying the homology model for greater consistency with those binding properties.
2. A method according to claim 1, wherein amino acids lining the binding cavity of the glucocorticoid receptor are identified chemically and the information thus gained used to verify and if appropriate modify the homology model.
3. A method according to claim 2, wherein (v) amino acids lining the binding cavity of the glucocorticoid receptor are identified by chemically mutating the glucocorticoid receptor so as to change one amino acid thereof, and experimentally determining how the

mutation affects the binding properties of the receptor to one or more ligands known to bind to the unmutated receptor.

4. A method according to claim 3, wherein step (v) is repeated one or more times, each time changing a different amino acid of the glucocorticoid receptor.
5. A method according to claim 2, including: (vi) introducing a photolabile group into a ligand having affinity for the glucocorticoid receptor, and forming a complex of the modified ligand with the receptor, expose the resulting complex to light to cause it to decompose to form reactive groups which bind to adjacent amino acids of the receptor, break up the complex into peptide fragments, analysing fragments to identify those bound to reactive groups from the modified ligand and thus the amino acids lining the binding cavity of the receptor.
6. A method according to any preceding claim, wherein the homology model is compared with the structures of other, similar, proteins.
7. A method according to any preceding claim, wherein the homology model is checked and if necessary modified to ensure that it shows predominantly hydrophobic amino acids lining the binding cavity and predominantly hydrophilic amino acids exposed to the outside.
8. A method according to any preceding claim, wherein the thyroid, estrogen or progesterone receptor is a human receptor.

9. A homology model of the ligand binding domain of a glucocorticoid receptor designed in accordance with any preceding claim and having hydrogen bonding partners for the C-16 and C-21 OH groups of a glucocorticosteroid.
10. A homology model according to claim 9, showing a hydrophilic cavity positioned to interact with the C-3 carbonyl group of a glucocorticosteroid.
11. A homology model according to claims 8, 9 or 10, showing at least one small hydrophobic pocket capable of interacting with a methyl or halogen substituent at the C-6 and/or C-9 position of a glucocorticosteroid.
12. Use of a homology model according to any of claims 9 to 11 to identify or design ligands capable of binding to the ligand binding domain of a glucocorticoid receptor.
13. Use of a homology model according to any of claims 9 to 11 to identify or design glucocorticoid receptor antagonists or agonists.
14. A glucocorticoid receptor antagonist or agonist identified by use of a homology model according to any of claims 9 to 11.
15. A medicinal product comprising a glucocorticoid agonist according to claim 14 for treatment of inflammation or for use in immunosuppressive therapy.

16. A medicinal product comprising a glucocorticoid antagonist according to claim 14 for use in the treatment of hypertension, diabetes, obesity, glaucoma, depression, AIDS, and wounds.
17. A computer programmed with a homology model of the ligand binding domain of a glucocorticoid receptor according to any of claims 9 to 11.
18. A machine-readable data-storage medium on which has been stored in machine-readable form a homology model of the ligand binding domain of a glucocorticoid receptor according to any of claims 9 to 11.
19. The use of a homology model according to any of claims 9 to 11 as input to a computer programmed for drug design and/or database searching and/or molecular graphic imaging in order to identify new ligands for the glucocorticoid receptor.
20. A computational and chemical method of iteratively generating a homology model of the ligand binding domain of a glucocorticoid receptor, which homology model is capable of being displayed as a three-dimensional image, the method comprising:
  - (i) entering into a computer an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor;
  - (ii) modifying under computer control said x-ray crystallographic structure to take account of known differences between the amino acid configuration of the ligand

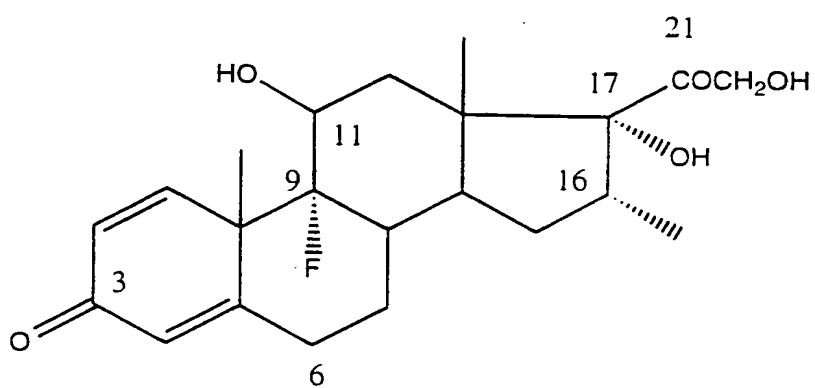
binding domains of the glucocorticoid receptor on the one hand and at least one of the thyroid, estrogen, or progesterone receptors on the other hand,

(iii) reconciling under computer control the resulting modified crystallographic structure with the chemically-determined binding properties of a number of ligands for the glucocorticoid receptor;

(iv) identifying by chemical means the amino acids that line the binding cavity of the ligand binding domain and reconciling under computer control the modified crystallographic structure with these;

(v) repeating steps (ii) and (iii).

Fig. 1



Dexamethasone

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FIGURE 2A

TR_t3cyatocys	RPEPTPEEWDLIHVATEAHRSTNAQGSAAWKORRAFLPDDIGASPIVSMPDGDAVDLEAFS
TRb_triac2	KPEPTDEEWELIKTVTEAHVATNAQGSAAWKOKR-KFLPEDIG-----QVDLEAFS
erhum7	----SLALSLTADQMVSALLDAEPPI-LYSEYDPTRP-----FSE-----ASMMG
grmodel	----PATLPQLTPTLVSLLEVIEPEV-LYAGYDSSVP-----DST-----WRIMT
TR_t3cyatocys	EFTAIITPAITRVVDFAKKLPMFAELPCEDQIILLKGCCMEIMSLRAAVRYDPASD---TL
TRb_triac2	HFTAIITPAITRVVDFAKKLPMFCELPCEQIILLKGCCMEIMSLRAAVRYDPESE---TL
erhum7	LLTNLADRELVHMINWAKRVPGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPG---KL
grmodel	TLNMLGGROVIAAVKWAKAIPGFRNLHLDQMTLLQYSWMFLMAFALGWRSYRQSSANLL
TR_t3cyatocys	TLSGEMAVKREQLKN-GGLGVVSDAIFALGKSLSAFALDDTEVALLQAVLLMST-----D
TRb_triac2	TLNGEMAVTRGQLKN-GGLGVVSDAIFDLGMSLSSFNLDDTEVALLQAVLLMSS-----D
erhum7	LFAPNLLDRNQGKCVGEMVEIFDMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTF
grmodel	CFAPDLIINEQRMFL-PCMYDQCKHMLYVSSSELHRLQVSYEEYLCMKTLTLLLS---SVP
TR_t3cyatocys	RAGLLCVDAIAASQAAYLLAFEHYVNHVK-----HAIPHFWPKLLMKVTDLRMIGACHA
TRb_triac2	RPGLACVERIEKYQDSFLLAFEHYINYRK-----HHVTHFWPKLLMKVTDLRMIGACHA
erhum7	SSTLKSLEEKDHIHRVLDKITDTLIHLMKAGLTLOQQHQRLAQLLLILSHIRHMSNKG
grmodel	KDGLKSQELFDEIRMTYIKELGKAIVKREGN---SSQNWRQFYQLTKLLDSMHEVENLL
TR_t3cyatocys	SRFAHMKVECPTA---LFPPLFLEV
TRb_triac2	SRFLHMKVACPTA---LFPPLFLAVFED
erhum7	EHLYSMKCKN---VVP-LYDLLLEMLDAHR
grmodel	NYCFQTFLD-K-TMSIEFFPEMLAEIITNQI

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FIGURE 2B

ere\_ref4\_a SLALSLTADQMVSALLDAEPPI-LYSEYDPTRP-----FSE-----ASMMGLLTN  
lere-kb SLALSLTADQMVSALLDAEPPI-LYSE-----FSE-----ASMMGLLTN  
erhum7 SLALSLTADQMVSALLDAEPPI-LYSEYDPTRP-----FSE-----ASMMGLLTN  
grmodelfrer PATLPQLTPTLVSLLEVIEPEV-LYAGYDSSVP-----DST-----WRIMTTLNM

ere\_ref4\_a LADRELVHMINWAKRVPGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPG--KLLFAP  
lere-kb LADRELVHMINWAKRVPGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPG--KLLFAP  
erhum7 LADRELVHMINWAKRVPGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPG--KLLFAP  
grmodelfrer LGGRQVIAAVKWAIPAIFGRNLHLDQMTLLQYSWMFLMAFALGWRSYQSSANLLCFAP

ere\_ref4\_a NLLLDNRNQGKCEGMVEIFDMLLATSSRFRMMNLOGEEFVCLKSIILLNSGVYTF---TL  
lere-kb NLLLDNRNQGKCEGMVEIFDMLLATSSRFRMMNLOGEEFVCLKSIILLNSGVYTF---TL  
erhum7 NLLLDNRNQGKCEGMVEIFDMLLATSSRFRMMNLOGEEFVCLKSIILLNSGVYTF---TL  
grmodelfrer DLIINEQRMTL-PCMYDQCKHMLYVSSSELHRLQVSYEEYLCMKTLTLLLS----SVPKDGL

ere\_ref4\_a KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLOQQQHORLAQLLLLILSHIRHMSNKGMEHLY  
lere-kb KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLOQQQHORLAQLLLLILSHIRHMSNKGMEHLY  
erhum7 KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLOQQQHORLAQLLLLILSHIRHMSNKGMEHLY  
grmodelfrer KSQELFDEIRMTYIKELGKAIVKREGN---SSQNWQRFYQLTKLLDSMHEVVENLLNYCF

ere\_ref4\_a SMKCKN---VVP-LYDLLLEMLDAHR  
lere-kb SMKCKN---VVP-LYDLLLEMLDAHR  
erhum7 SMKCKN---VVP-LYDLLLEMLDAHR  
grmodelfrer QTFLD-K-TMSIEFPEMLAEIITNQI

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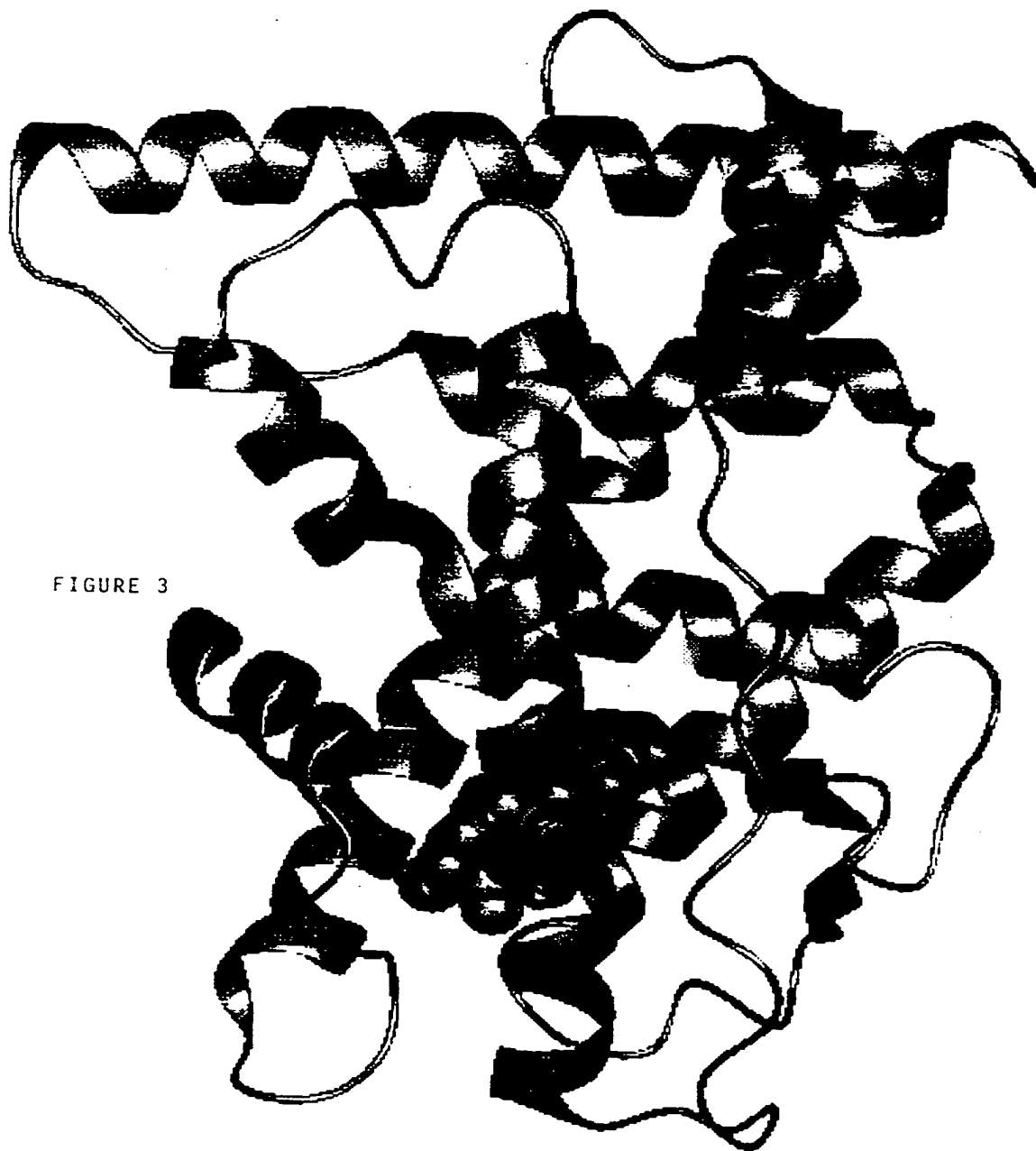
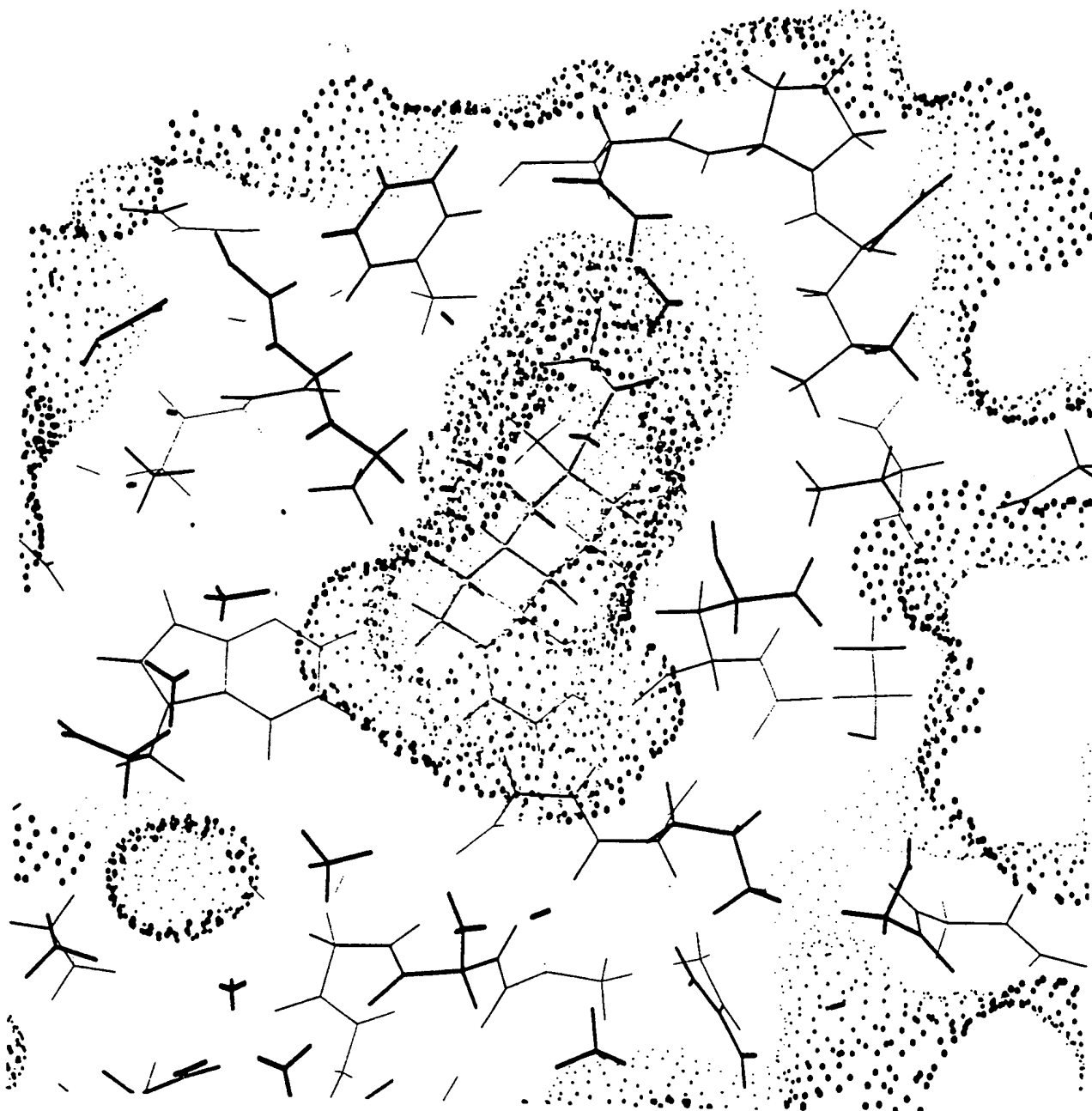
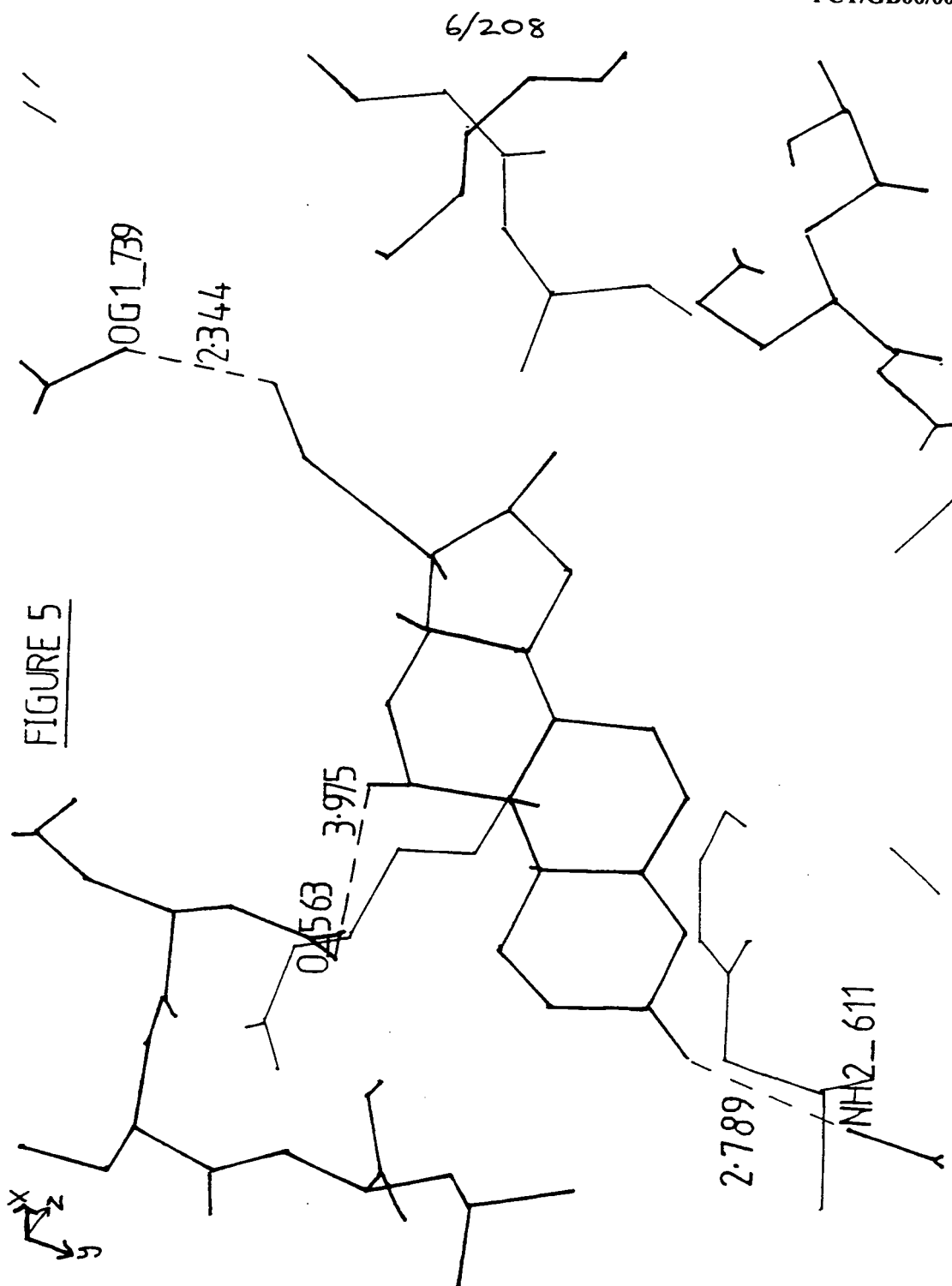


FIGURE 3

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FIGURE 4





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ER 305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV  
GR 522 PATLPQLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAI

ER 365 PGFVDLTLHDQVHLLCAWLEILMIGLVWRSMEHPG--KLLFAPNLLDRNOGKCVEGMV  
GR 582 PGFRNLHLLDDQMTLLQYSWMFLMAFALGWRSYROSSANLLCFAPDLIINEQRM TL-PCMY

ER 423 EIFDMLLATSSRFRMMNLOGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKI  
GR 643 DQCKHMLYVSSSELHRLQVSYEEYLCMKTTTTLLSSVPKDG----LKSQELFDEIRMTYIKE

ER 483 TDTLIHLMAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKN--VVP-LYDL  
GR 697 LGKATVKREGN---SSQNWQRFYQLTKLLDSMHEVVENLLNYCFQTF LD-KTMSIEFP EM

ER 540 LLEMLDAHR  
GR 753 LAEIIITNQI

FIG. 6

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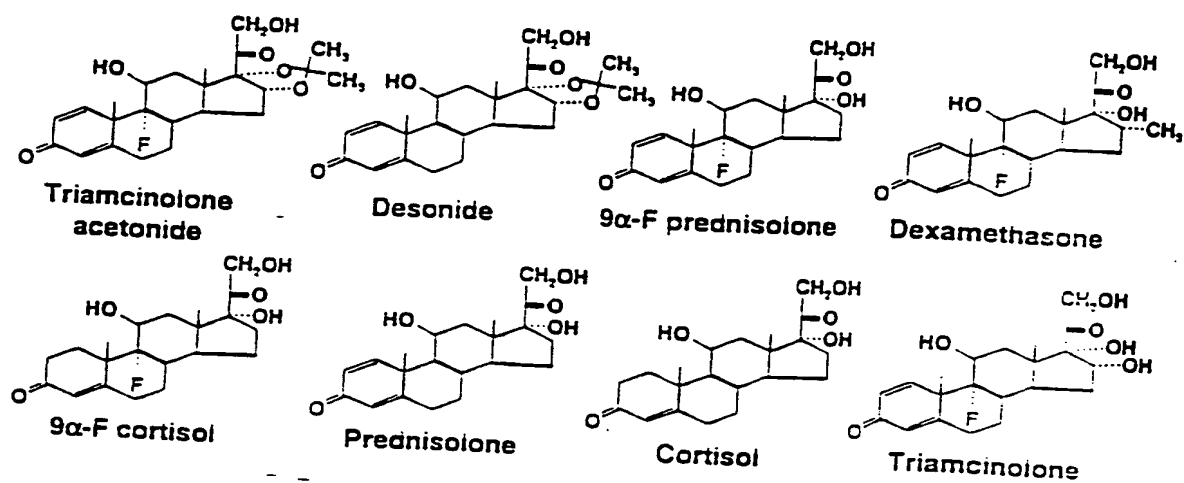


FIG. 7

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Fig 8(i).

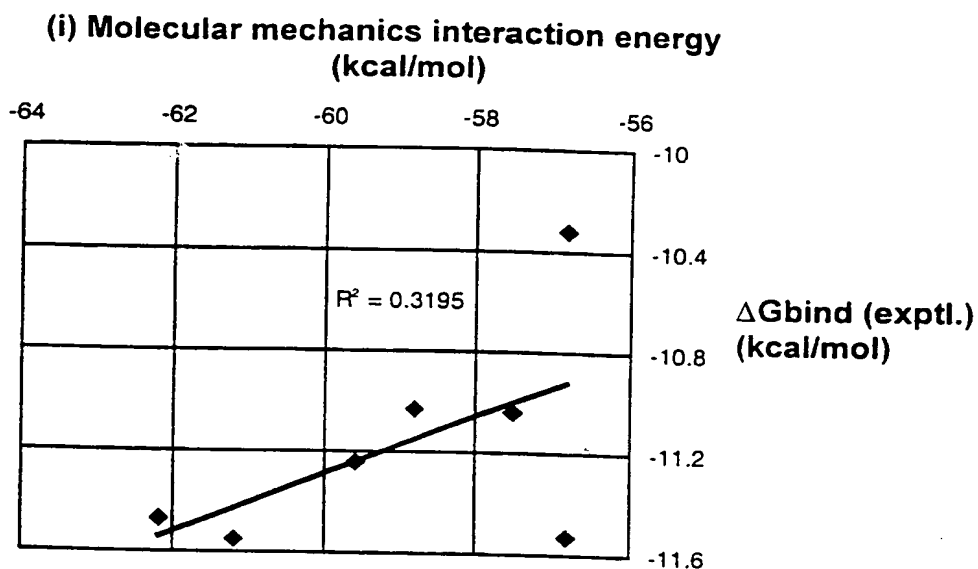
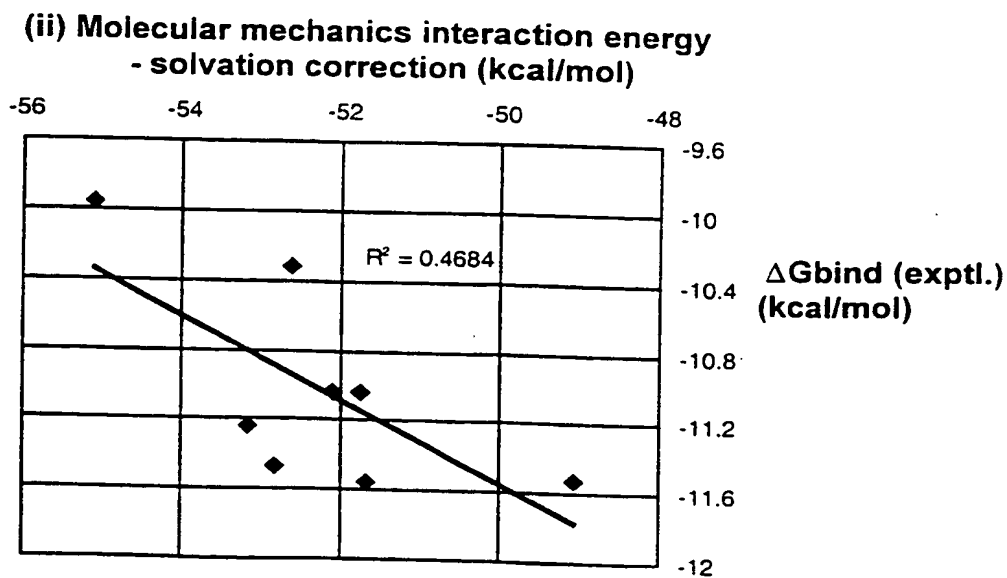


Fig 8(ii).



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Fig 8(iii).

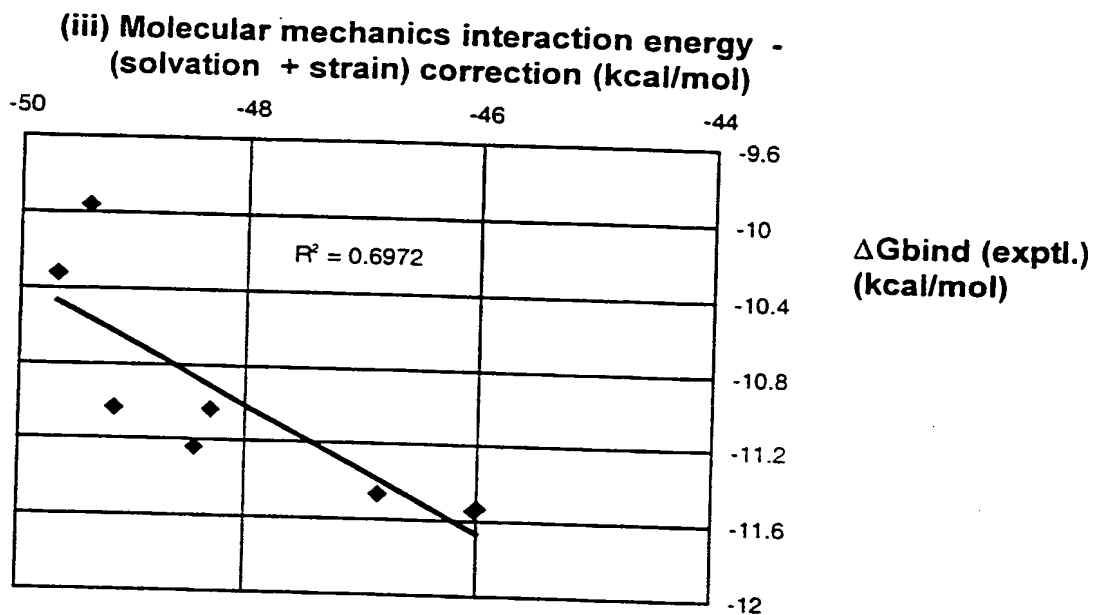
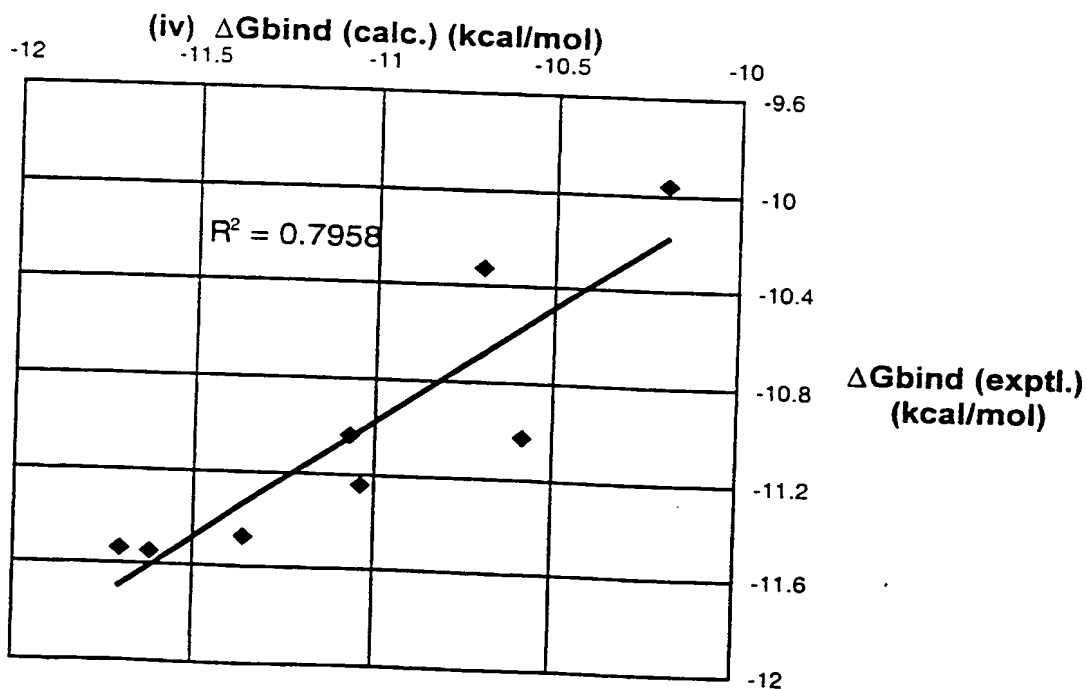
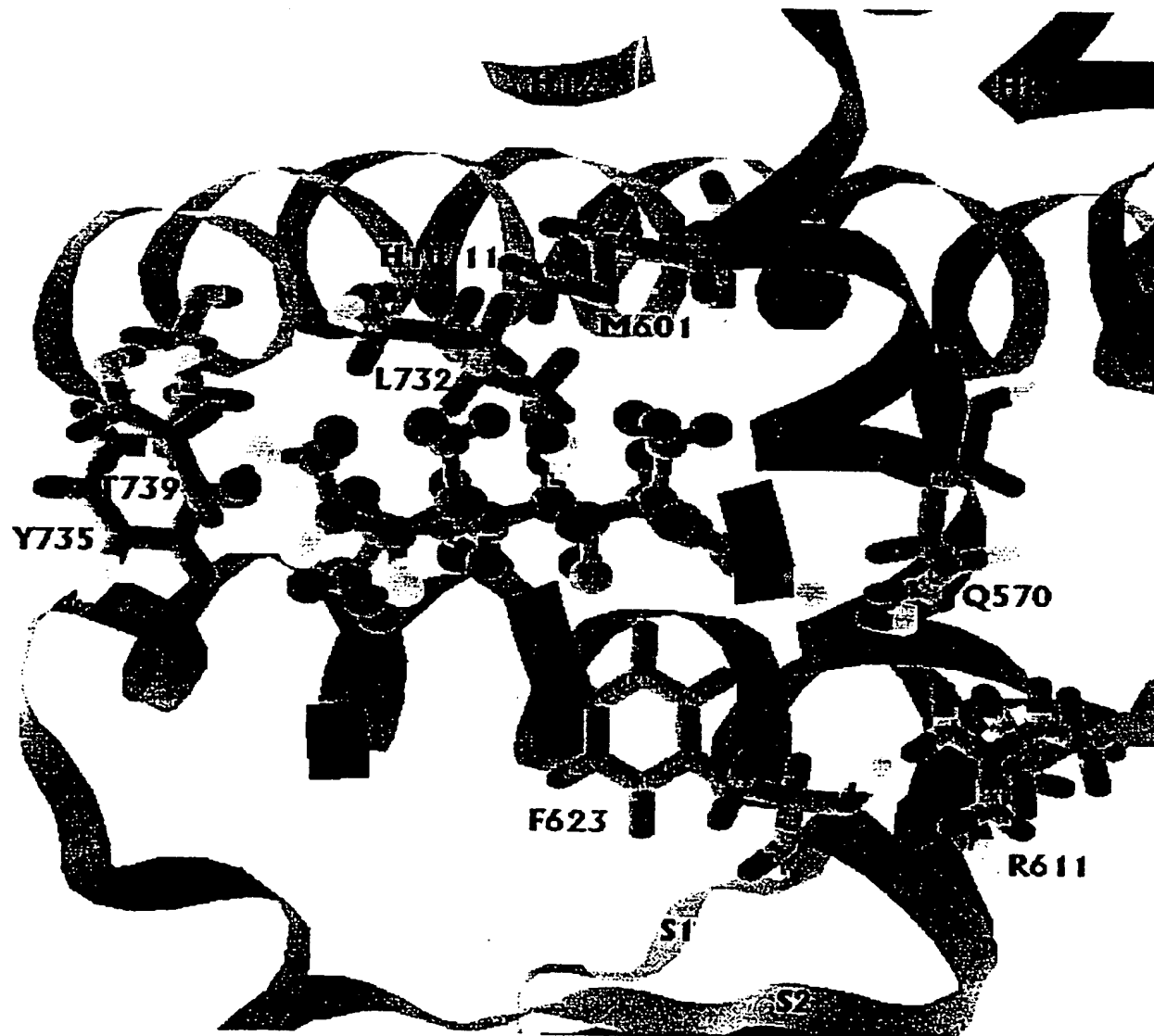


Fig 8(iv).



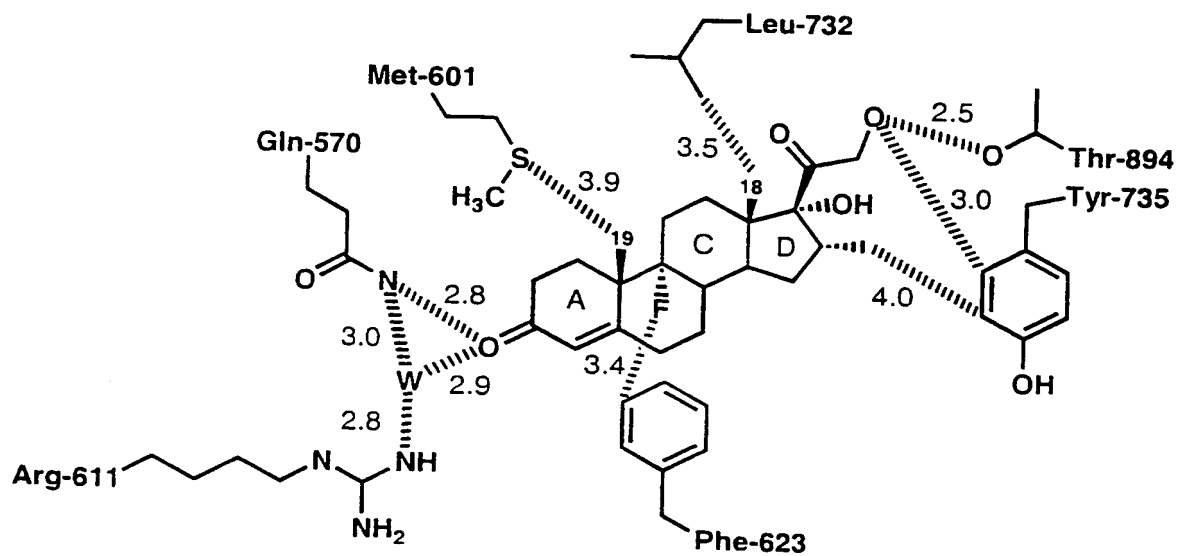
**Figure 9:** (a) RasMol representation of the main interactions with dexamethasone in the GR homology model.  
(b) Sketch of the main interactions with dexamethasone in the GR homology model.

**Figure 9a:**



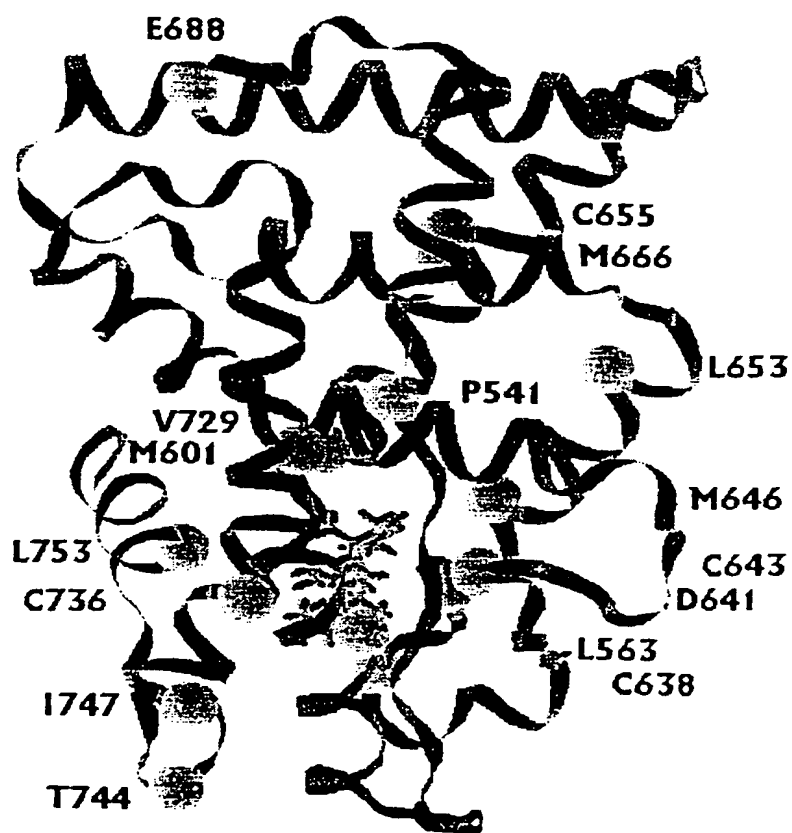
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Figure 9b:



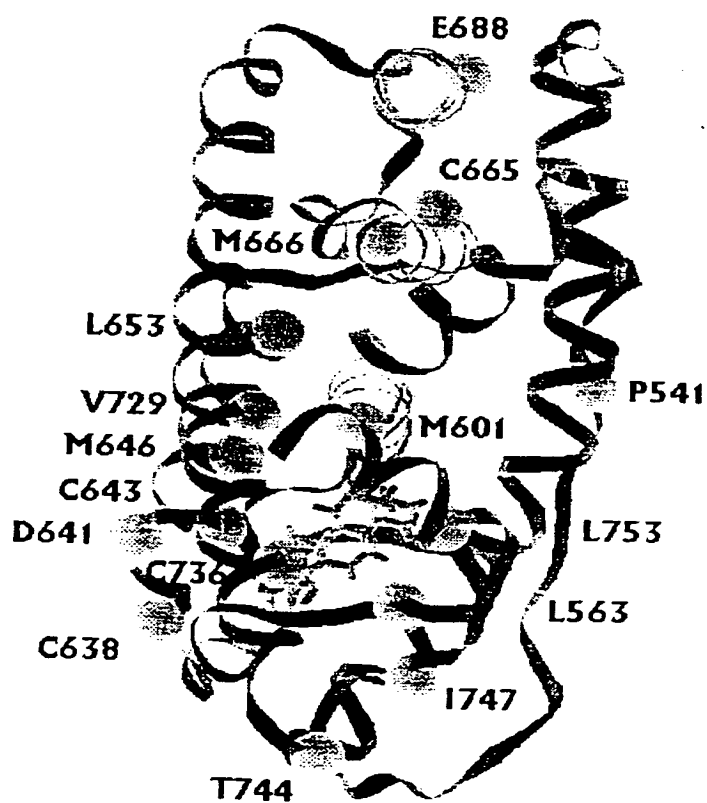
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Figure 10a



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Figure 10b



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progA

QLIPPLINLLMSIEPDVYAGHDNTKPDTSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWM  
GRmodel

QLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFRNLHLLDDQMTLLQYSWM

progA

SLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIP  
GRmodel

FLMAFALGWRSYRQSSANLLCFAPDLIINEQRMTLPCMYDQCKHMLYVSSSELHRLQVSYEEYLCMKTTTTLLSSVP

progA

LEGLRSQTQFEEMRSSYTRELKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFP  
GRmodel

KDGLKSQELFDEIRMTYIKELGKAIVKREGNSSQNWRQFYQLTKLLDSMHEVVENLLNYCFQTFDKT-MSIEFP

progA

EMMSEVIAAQLPKLAGMVKPLLCHK\*

GRmodel

EMLAEITNQIPKYSNGNIKKLLFHQK\*

Figure 11

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Fig 12

REMARK 1 grfromer							
ATOM	1	C25	CORTC	1	-6.118	0.501	0.557 1.00 0.00
ATOM	2	C26	CORTC	1	-5.161	1.475	0.031 1.00 0.00
ATOM	3	C27	CORTC	1	-4.017	1.077	-0.556 1.00 0.00
ATOM	4	C28	CORTC	1	-3.103	2.102	-1.174 1.00 0.00
ATOM	5	C29	CORTC	1	-1.725	2.081	-0.520 1.00 0.00
ATOM	6	C30	CORTC	1	-1.098	0.688	-0.620 1.00 0.00
ATOM	7	C31	CORTC	1	-2.015	-0.396	-0.015 1.00 0.00
ATOM	8	C32	CORTC	1	-3.481	-0.348	-0.549 1.00 0.00
ATOM	9	C33	CORTC	1	-1.345	-1.804	-0.010 1.00 0.00
ATOM	10	C34	CORTC	1	0.095	-1.803	0.562 1.00 0.00
ATOM	11	C35	CORTC	1	0.975	-0.693	-0.029 1.00 0.00
ATOM	12	C36	CORTC	1	0.223	0.626	0.150 1.00 0.00
ATOM	13	C37	CORTC	1	1.250	1.733	-0.047 1.00 0.00
ATOM	14	C38	CORTC	1	2.589	1.090	0.347 1.00 0.00
ATOM	15	C39	CORTC	1	2.249	-0.345	0.791 1.00 0.00
ATOM	16	C40	CORTC	1	1.281	-0.984	-1.518 1.00 0.00
ATOM	17	C41	CORTC	1	-3.619	-0.828	-2.006 1.00 0.00
ATOM	18	C42	CORTC	1	3.489	-1.254	0.722 1.00 0.00
ATOM	19	C43	CORTC	1	3.976	-1.849	-0.588 1.00 0.00
ATOM	20	O6	CORTC	1	-7.096	0.859	1.135 1.00 0.00
ATOM	21	O7	CORTC	1	-1.342	-2.343	-1.318 1.00 0.00
ATOM	22	O8	CORTC	1	1.923	-0.291	2.164 1.00 0.00
ATOM	23	O9	CORTC	1	4.130	-1.424	1.716 1.00 0.00
ATOM	24	O10	CORTC	1	5.346	-2.133	-0.475 1.00 0.00
ATOM	25	C1	CORTC	1	-4.352	-1.232	0.378 1.00 0.00
ATOM	26	C2	CORTC	1	-5.853	-0.959	0.270 1.00 0.00
ATOM	27	H1	CORTC	1	-5.413	2.513	0.111 1.00 0.00
ATOM	28	2H	CORTC	1	-3.538	3.095	-1.080 1.00 0.00
ATOM	29	3H	CORTC	1	-3.020	1.915	-2.245 1.00 0.00
ATOM	30	4H	CORTC	1	-1.800	2.387	0.522 1.00 0.00
ATOM	31	5H	CORTC	1	-1.082	2.820	-0.997 1.00 0.00
ATOM	32	H6	CORTC	1	-0.941	0.487	-1.676 1.00 0.00
ATOM	33	H7	CORTC	1	-2.102	-0.127	1.040 1.00 0.00
ATOM	34	H8	CORTC	1	-1.953	-2.446	0.630 1.00 0.00
ATOM	35	9H	CORTC	1	0.583	-2.771	0.467 1.00 0.00
ATOM	36	0H1	CORTC	1	0.039	-1.632	1.634 1.00 0.00
ATOM	37	H11	CORTC	1	-0.041	0.700	1.208 1.00 0.00
ATOM	38	2H1	CORTC	1	1.001	2.576	0.593 1.00 0.00
ATOM	39	3H1	CORTC	1	1.263	2.094	-1.070 1.00 0.00
ATOM	40	4H1	CORTC	1	3.089	1.642	1.136 1.00 0.00
ATOM	41	5H1	CORTC	1	3.255	1.090	-0.518 1.00 0.00
ATOM	42	6H1	CORTC	1	1.927	-0.232	-1.968 1.00 0.00
ATOM	43	7H1	CORTC	1	0.373	-1.012	-2.114 1.00 0.00
ATOM	44	8H1	CORTC	1	1.701	-1.973	-1.671 1.00 0.00
ATOM	45	9H1	CORTC	1	-3.452	-1.901	-2.089 1.00 0.00
ATOM	46	0H2	CORTC	1	-2.887	-0.350	-2.656 1.00 0.00
ATOM	47	1H2	CORTC	1	-4.607	-0.626	-2.414 1.00 0.00
ATOM	48	2H2	CORTC	1	3.848	-1.145	-1.410 1.00 0.00

SUBSTITUTE SHEET (RULE 26)

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ATOM	49	3H2	CORTC	1	3.440	-2.777	-0.796	1.00	0.00
ATOM	50	H24	CORTC	1	-1.053	-3.251	-1.314	1.00	0.00
ATOM	51	H25	CORTC	1	2.683	-0.664	2.614	1.00	0.00
ATOM	52	H26	CORTC	1	5.547	-2.208	0.462	1.00	0.00
ATOM	53	7H2	CORTC	1	-4.156	-2.281	0.172	1.00	0.00
ATOM	54	8H2	CORTC	1	-4.062	-1.081	1.420	1.00	0.00
ATOM	55	9H2	CORTC	1	-6.416	-1.567	0.975	1.00	0.00
ATOM	56	0H3	CORTC	1	-6.218	-1.167	-0.729	1.00	0.00
ATOM	57	N	ALA A 523		-25.079	3.809	-23.074	1.00	0.00
ATOM	58	CA	ALA A 523		-25.892	4.487	-22.104	1.00	0.00
ATOM	59	C	ALA A 523		-25.170	5.680	-21.569	1.00	0.00
ATOM	60	O	ALA A 523		-25.779	6.716	-21.305	1.00	0.00
ATOM	61	CB	ALA A 523		-26.253	3.589	-20.908	1.00	0.00
ATOM	62	1HT	ALA A 523		-24.576	4.510	-23.655	1.00	0.00
ATOM	63	2HT	ALA A 523		-25.684	3.224	-23.685	1.00	0.00
ATOM	64	HA	ALA A 523		-26.802	4.813	-22.608	1.00	0.00
ATOM	65	1HB	ALA A 523		-25.353	3.249	-20.396	1.00	0.00
ATOM	66	2HB	ALA A 523		-26.799	2.709	-21.249	1.00	0.00
ATOM	67	3HB	ALA A 523		-26.860	4.142	-20.192	1.00	0.00
ATOM	68	N	THR A 524		-23.837	5.574	-21.425	1.00	0.00
ATOM	69	CA	THR A 524		-23.081	6.641	-20.839	1.00	0.00
ATOM	70	C	THR A 524		-23.327	7.904	-21.606	1.00	0.00
ATOM	71	O	THR A 524		-23.479	8.972	-21.015	1.00	0.00
ATOM	72	CB	THR A 524		-21.605	6.372	-20.834	1.00	0.00
ATOM	73	OG1	THR A 524		-20.927	7.391	-20.114	1.00	0.00
ATOM	74	CG2	THR A 524		-21.100	6.307	-22.283	1.00	0.00
ATOM	75	HN	THR A 524		-23.370	4.744	-21.729	1.00	0.00
ATOM	76	HA	THR A 524		-23.444	6.758	-19.818	1.00	0.00
ATOM	77	HB	THR A 524		-21.396	5.417	-20.352	1.00	0.00
ATOM	78	HG1	THR A 524		-20.005	7.175	-20.141	1.00	0.00
ATOM	79	1HG2	THR A 524		-20.958	7.310	-22.687	1.00	0.00
ATOM	80	2HG2	THR A 524		-21.825	5.791	-22.912	1.00	0.00
ATOM	81	3HG2	THR A 524		-20.142	5.788	-22.325	1.00	0.00
ATOM	82	N	LEU A 525		-23.397	7.817	-22.944	1.00	0.00
ATOM	83	CA	LEU A 525		-23.570	8.996	-23.745	1.00	0.00
ATOM	84	C	LEU A 525		-24.870	9.732	-23.529	1.00	0.00
ATOM	85	O	LEU A 525		-24.865	10.960	-23.499	1.00	0.00
ATOM	86	CB	LEU A 525		-23.420	8.705	-25.245	1.00	0.00
ATOM	87	CG	LEU A 525		-21.995	8.237	-25.583	1.00	0.00
ATOM	88	CD1	LEU A 525		-21.773	8.118	-27.099	1.00	0.00
ATOM	89	CD2	LEU A 525		-20.953	9.122	-24.879	1.00	0.00
ATOM	90	HN	LEU A 525		-23.329	6.923	-23.385	1.00	0.00
ATOM	91	HA	LEU A 525		-22.812	9.710	-23.422	1.00	0.00
ATOM	92	1HB	LEU A 525		-23.647	9.608	-25.812	1.00	0.00
ATOM	93	2HB	LEU A 525		-24.132	7.932	-25.535	1.00	0.00
ATOM	94	HG	LEU A 525		-21.818	7.266	-25.119	1.00	0.00
ATOM	95	1HD1	LEU A 525		-21.928	9.081	-27.587	1.00	0.00
ATOM	96	2HD1	LEU A 525		-22.478	7.406	-27.528	1.00	0.00
ATOM	97	3HD1	LEU A 525		-20.753	7.795	-27.307	1.00	0.00

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ATOM	98	1HD2 LEU A 525	-21.080	9.079	-23.798	1.00	0.00
ATOM	99	2HD2 LEU A 525	-21.069	10.159	-25.192	1.00	0.00
ATOM	100	3HD2 LEU A 525	-19.946	8.778	-25.115	1.00	0.00
ATOM	101	N PRO A 526	-25.994	9.073	-23.434	1.00	0.00
ATOM	102	CA PRO A 526	-27.215	9.811	-23.205	1.00	0.00
ATOM	103	C PRO A 526	-27.475	10.277	-21.807	1.00	0.00
ATOM	104	O PRO A 526	-28.343	11.129	-21.629	1.00	0.00
ATOM	105	CB PRO A 526	-28.359	8.964	-23.770	1.00	0.00
ATOM	106	CG PRO A 526	-27.711	7.626	-24.150	1.00	0.00
ATOM	107	CD PRO A 526	-26.240	7.996	-24.368	1.00	0.00
ATOM	108	1HD PRO A 526	-25.584	7.152	-24.155	1.00	0.00
ATOM	109	2HD PRO A 526	-26.063	8.330	-25.390	1.00	0.00
ATOM	110	HA PRO A 526	-27.163	10.776	-23.710	1.00	0.00
ATOM	111	1HB PRO A 526	-28.804	9.443	-24.642	1.00	0.00
ATOM	112	2HB PRO A 526	-29.142	8.821	-23.024	1.00	0.00
ATOM	113	1HG PRO A 526	-27.821	6.892	-23.352	1.00	0.00
ATOM	114	2HG PRO A 526	-28.155	7.214	-25.056	1.00	0.00
ATOM	115	N GLN A 527	-26.761	9.739	-20.807	1.00	0.00
ATOM	116	CA GLN A 527	-26.993	10.096	-19.439	1.00	0.00
ATOM	117	C GLN A 527	-26.834	11.582	-19.328	1.00	0.00
ATOM	118	O GLN A 527	-26.010	12.175	-20.021	1.00	0.00
ATOM	119	CB GLN A 527	-25.919	9.467	-18.537	1.00	0.00
ATOM	120	CG GLN A 527	-26.244	9.400	-17.051	1.00	0.00
ATOM	121	CD GLN A 527	-26.605	7.951	-16.765	1.00	0.00
ATOM	122	OE1 GLN A 527	-27.358	7.323	-17.507	1.00	0.00
ATOM	123	NE2 GLN A 527	-26.039	7.397	-15.658	1.00	0.00
ATOM	124	HN GLN A 527	-26.049	9.072	-21.023	1.00	0.00
ATOM	125	HA GLN A 527	-27.984	9.731	-19.171	1.00	0.00
ATOM	126	1HB GLN A 527	-25.002	10.042	-18.655	1.00	0.00
ATOM	127	2HB GLN A 527	-25.737	8.453	-18.888	1.00	0.00
ATOM	128	1HG GLN A 527	-27.087	10.046	-16.805	1.00	0.00
ATOM	129	2HG GLN A 527	-25.384	9.692	-16.449	1.00	0.00
ATOM	130	1HE2 GLN A 527	-25.549	7.978	-15.009	1.00	0.00
ATOM	131	2HE2 GLN A 527	-26.104	6.416	-15.480	1.00	0.00
ATOM	132	N LEU A 528	-27.646	12.238	-18.474	1.00	0.00
ATOM	133	CA LEU A 528	-27.439	13.647	-18.292	1.00	0.00
ATOM	134	C LEU A 528	-26.548	13.763	-17.108	1.00	0.00
ATOM	135	O LEU A 528	-26.401	12.807	-16.350	1.00	0.00
ATOM	136	CB LEU A 528	-28.701	14.500	-18.039	1.00	0.00
ATOM	137	CG LEU A 528	-29.630	14.017	-16.911	1.00	0.00
ATOM	138	CD1 LEU A 528	-30.808	14.986	-16.720	1.00	0.00
ATOM	139	CD2 LEU A 528	-30.129	12.591	-17.179	1.00	0.00
ATOM	140	HN LEU A 528	-28.370	11.756	-17.981	1.00	0.00
ATOM	141	HA LEU A 528	-26.948	13.992	-19.201	1.00	0.00
ATOM	142	1HB LEU A 528	-29.278	14.529	-18.962	1.00	0.00
ATOM	143	2HB LEU A 528	-28.381	15.512	-17.802	1.00	0.00
ATOM	144	HG LEU A 528	-29.065	13.946	-15.982	1.00	0.00
ATOM	145	1HD1 LEU A 528	-31.397	15.063	-17.634	1.00	0.00
ATOM	146	2HD1 LEU A 528	-30.440	15.981	-16.471	1.00	0.00

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ATOM	147	3HD1 LEU A 528	-31.464	14.629	-15.926	1.00	0.00
ATOM	148	1HD2 LEU A 528	-29.370	11.859	-16.903	1.00	0.00
ATOM	149	2HD2 LEU A 528	-30.352	12.463	-18.238	1.00	0.00
ATOM	150	3HD2 LEU A 528	-31.023	12.388	-16.590	1.00	0.00
ATOM	151	N THR A 529	-25.953	14.955	-16.901	1.00	0.00
ATOM	152	CA THR A 529	-25.011	15.088	-15.833	1.00	0.00
ATOM	153	C THR A 529	-25.630	14.696	-14.530	1.00	0.00
ATOM	154	O THR A 529	-24.911	14.143	-13.703	1.00	0.00
ATOM	155	CB THR A 529	-24.318	16.430	-15.759	1.00	0.00
ATOM	156	OG1 THR A 529	-23.408	16.443	-14.668	1.00	0.00
ATOM	157	CG2 THR A 529	-25.318	17.588	-15.674	1.00	0.00
ATOM	158	HN THR A 529	-26.168	15.736	-17.487	1.00	0.00
ATOM	159	HA THR A 529	-24.272	14.301	-15.982	1.00	0.00
ATOM	160	HB THR A 529	-23.757	16.618	-16.675	1.00	0.00
ATOM	161	HG1 THR A 529	-23.922	16.603	-13.887	1.00	0.00
ATOM	162	1HG2 THR A 529	-25.690	17.702	-14.656	1.00	0.00
ATOM	163	2HG2 THR A 529	-26.171	17.398	-16.325	1.00	0.00
ATOM	164	3HG2 THR A 529	-24.837	18.523	-15.963	1.00	0.00
ATOM	165	N PRO A 530	-26.897	14.913	-14.259	1.00	0.00
ATOM	166	CA PRO A 530	-27.417	14.458	-13.003	1.00	0.00
ATOM	167	C PRO A 530	-27.432	12.964	-12.906	1.00	0.00
ATOM	168	O PRO A 530	-27.159	12.442	-11.828	1.00	0.00
ATOM	169	CB PRO A 530	-28.805	15.078	-12.859	1.00	0.00
ATOM	170	CG PRO A 530	-28.734	16.338	-13.737	1.00	0.00
ATOM	171	CD PRO A 530	-27.709	15.980	-14.825	1.00	0.00
ATOM	172	1HD PRO A 530	-28.205	15.633	-15.732	1.00	0.00
ATOM	173	2HD PRO A 530	-27.083	16.837	-15.072	1.00	0.00
ATOM	174	HA PRO A 530	-26.763	14.779	-12.192	1.00	0.00
ATOM	175	1HB PRO A 530	-29.018	15.333	-11.820	1.00	0.00
ATOM	176	2HB PRO A 530	-29.580	14.397	-13.208	1.00	0.00
ATOM	177	1HG PRO A 530	-29.706	16.569	-14.173	1.00	0.00
ATOM	178	2HG PRO A 530	-28.407	17.203	-13.159	1.00	0.00
ATOM	179	N THR A 531	-27.761	12.252	-14.004	1.00	0.00
ATOM	180	CA THR A 531	-27.830	10.823	-13.907	1.00	0.00
ATOM	181	C THR A 531	-26.461	10.248	-13.760	1.00	0.00
ATOM	182	O THR A 531	-26.269	9.282	-13.024	1.00	0.00
ATOM	183	CB THR A 531	-28.499	10.141	-15.059	1.00	0.00
ATOM	184	OG1 THR A 531	-29.816	10.643	-15.223	1.00	0.00
ATOM	185	CG2 THR A 531	-28.587	8.645	-14.709	1.00	0.00
ATOM	186	HN THR A 531	-27.953	12.714	-14.870	1.00	0.00
ATOM	187	HA THR A 531	-28.377	10.609	-12.989	1.00	0.00
ATOM	188	HB THR A 531	-27.947	10.324	-15.981	1.00	0.00
ATOM	189	HG1 THR A 531	-30.229	10.607	-14.371	1.00	0.00
ATOM	190	1HG2 THR A 531	-29.305	8.479	-13.906	1.00	0.00
ATOM	191	2HG2 THR A 531	-27.616	8.280	-14.373	1.00	0.00
ATOM	192	3HG2 THR A 531	-28.913	8.073	-15.577	1.00	0.00
ATOM	193	N LEU A 532	-25.463	10.834	-14.449	1.00	0.00
ATOM	194	CA LEU A 532	-24.140	10.293	-14.341	1.00	0.00
ATOM	195	C LEU A 532	-23.728	10.336	-12.904	1.00	0.00

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ATOM	196	O	LEU A 532	-23.216	9.356	-12.375	1.00	0.00
ATOM	197	CB	LEU A 532	-23.037	11.072	-15.092	1.00	0.00
ATOM	198	CG	LEU A 532	-22.979	10.907	-16.625	1.00	0.00
ATOM	199	CD1	LEU A 532	-24.194	11.521	-17.322	1.00	0.00
ATOM	200	CD2	LEU A 532	-21.656	11.457	-17.184	1.00	0.00
ATOM	201	HN	LEU A 532	-25.643	11.632	-15.025	1.00	0.00
ATOM	202	HA	LEU A 532	-24.200	9.278	-14.735	1.00	0.00
ATOM	203	1HB	LEU A 532	-22.076	10.760	-14.688	1.00	0.00
ATOM	204	2HB	LEU A 532	-23.173	12.130	-14.877	1.00	0.00
ATOM	205	HG	LEU A 532	-22.929	9.846	-16.866	1.00	0.00
ATOM	206	1HD1	LEU A 532	-24.165	12.609	-17.261	1.00	0.00
ATOM	207	2HD1	LEU A 532	-25.113	11.182	-16.844	1.00	0.00
ATOM	208	3HD1	LEU A 532	-24.204	11.243	-18.376	1.00	0.00
ATOM	209	1HD2	LEU A 532	-20.824	11.200	-16.528	1.00	0.00
ATOM	210	2HD2	LEU A 532	-21.702	12.543	-17.261	1.00	0.00
ATOM	211	3HD2	LEU A 532	-21.455	11.028	-18.166	1.00	0.00
ATOM	212	N	VAL A 533	-23.988	11.475	-12.229	1.00	0.00
ATOM	213	CA	VAL A 533	-23.557	11.670	-10.872	1.00	0.00
ATOM	214	C	VAL A 533	-24.106	10.569	-10.040	1.00	0.00
ATOM	215	O	VAL A 533	-23.395	9.938	-9.260	1.00	0.00
ATOM	216	CB	VAL A 533	-24.181	12.876	-10.230	1.00	0.00
ATOM	217	CG1	VAL A 533	-23.646	13.000	-8.794	1.00	0.00
ATOM	218	CG2	VAL A 533	-23.999	14.111	-11.119	1.00	0.00
ATOM	219	HN	VAL A 533	-24.495	12.205	-12.688	1.00	0.00
ATOM	220	HA	VAL A 533	-22.473	11.779	-10.901	1.00	0.00
ATOM	221	HB	VAL A 533	-25.266	12.772	-10.216	1.00	0.00
ATOM	222	1HG1	VAL A 533	-22.558	12.936	-8.781	1.00	0.00
ATOM	223	2HG1	VAL A 533	-24.039	12.193	-8.175	1.00	0.00
ATOM	224	3HG1	VAL A 533	-23.932	13.961	-8.368	1.00	0.00
ATOM	225	1HG2	VAL A 533	-24.952	14.421	-11.548	1.00	0.00
ATOM	226	2HG2	VAL A 533	-23.317	13.886	-11.940	1.00	0.00
ATOM	227	3HG2	VAL A 533	-23.606	14.942	-10.533	1.00	0.00
ATOM	228	N	SER A 534	-25.416	10.334	-10.198	1.00	0.00
ATOM	229	CA	SER A 534	-26.127	9.359	-9.430	1.00	0.00
ATOM	230	C	SER A 534	-25.601	8.002	-9.723	1.00	0.00
ATOM	231	O	SER A 534	-25.351	7.212	-8.813	1.00	0.00
ATOM	232	CB	SER A 534	-27.617	9.334	-9.788	1.00	0.00
ATOM	233	OG	SER A 534	-28.224	8.203	-9.192	1.00	0.00
ATOM	234	HN	SER A 534	-25.918	10.863	-10.882	1.00	0.00
ATOM	235	HA	SER A 534	-25.993	9.621	-8.381	1.00	0.00
ATOM	236	1HB	SER A 534	-27.748	9.267	-10.868	1.00	0.00
ATOM	237	2HB	SER A 534	-28.113	10.229	-9.415	1.00	0.00
ATOM	238	HG	SER A 534	-27.556	7.532	-9.137	1.00	0.00
ATOM	239	N	LEU A 535	-25.397	7.716	-11.018	1.00	0.00
ATOM	240	CA	LEU A 535	-24.957	6.413	-11.399	1.00	0.00
ATOM	241	C	LEU A 535	-23.671	6.165	-10.706	1.00	0.00
ATOM	242	O	LEU A 535	-23.473	5.109	-10.102	1.00	0.00
ATOM	243	CB	LEU A 535	-24.674	6.303	-12.907	1.00	0.00
ATOM	244	CG	LEU A 535	-24.196	4.904	-13.334	1.00	0.00

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ATOM	245	CD1 LEU A 535	-25.299	3.852	-13.143	1.00	0.00
ATOM	246	CD2 LEU A 535	-23.613	4.922	-14.757	1.00	0.00
ATOM	247	HN LEU A 535	-25.552	8.416	-11.715	1.00	0.00
ATOM	248	HA LEU A 535	-25.748	5.719	-11.114	1.00	0.00
ATOM	249	1HB LEU A 535	-23.909	7.031	-13.174	1.00	0.00
ATOM	250	2HB LEU A 535	-25.584	6.545	-13.454	1.00	0.00
ATOM	251	HG LEU A 535	-23.326	4.625	-12.741	1.00	0.00
ATOM	252	1HD1 LEU A 535	-26.177	4.101	-13.739	1.00	0.00
ATOM	253	2HD1 LEU A 535	-25.602	3.810	-12.097	1.00	0.00
ATOM	254	3HD1 LEU A 535	-24.943	2.872	-13.461	1.00	0.00
ATOM	255	1HD2 LEU A 535	-23.017	5.821	-14.917	1.00	0.00
ATOM	256	2HD2 LEU A 535	-24.416	4.915	-15.493	1.00	0.00
ATOM	257	3HD2 LEU A 535	-22.967	4.058	-14.910	1.00	0.00
ATOM	258	N LEU A 536	-22.765	7.147	-10.741	1.00	0.00
ATOM	259	CA LEU A 536	-21.475	6.943	-10.168	1.00	0.00
ATOM	260	C LEU A 536	-21.618	6.859	-8.676	1.00	0.00
ATOM	261	O LEU A 536	-20.951	6.066	-8.012	1.00	0.00
ATOM	262	CB LEU A 536	-20.499	8.054	-10.577	1.00	0.00
ATOM	263	CG LEU A 536	-19.042	7.574	-10.561	1.00	0.00
ATOM	264	CD1 LEU A 536	-18.532	7.270	-9.152	1.00	0.00
ATOM	265	CD2 LEU A 536	-18.892	6.367	-11.503	1.00	0.00
ATOM	266	HN LEU A 536	-22.991	8.022	-11.168	1.00	0.00
ATOM	267	HA LEU A 536	-21.118	5.975	-10.521	1.00	0.00
ATOM	268	1HB LEU A 536	-20.606	8.893	-9.889	1.00	0.00
ATOM	269	2HB LEU A 536	-20.751	8.399	-11.579	1.00	0.00
ATOM	270	HG LEU A 536	-18.412	8.343	-11.006	1.00	0.00
ATOM	271	1HD1 LEU A 536	-18.391	6.197	-9.016	1.00	0.00
ATOM	272	2HD1 LEU A 536	-19.253	7.612	-8.409	1.00	0.00
ATOM	273	3HD1 LEU A 536	-17.573	7.760	-8.985	1.00	0.00
ATOM	274	1HD2 LEU A 536	-19.327	6.584	-12.479	1.00	0.00
ATOM	275	2HD2 LEU A 536	-19.408	5.501	-11.089	1.00	0.00
ATOM	276	3HD2 LEU A 536	-17.838	6.132	-11.648	1.00	0.00
ATOM	277	N GLU A 537	-22.536	7.666	-8.113	1.00	0.00
ATOM	278	CA GLU A 537	-22.768	7.706	-6.696	1.00	0.00
ATOM	279	C GLU A 537	-23.166	6.342	-6.225	1.00	0.00
ATOM	280	O GLU A 537	-22.698	5.872	-5.189	1.00	0.00
ATOM	281	CB GLU A 537	-23.943	8.637	-6.345	1.00	0.00
ATOM	282	CG GLU A 537	-24.259	8.742	-4.852	1.00	0.00
ATOM	283	CD GLU A 537	-23.474	9.909	-4.274	1.00	0.00
ATOM	284	OE1 GLU A 537	-23.662	10.204	-3.064	1.00	0.00
ATOM	285	OE2 GLU A 537	-22.684	10.526	-5.036	1.00	0.00
ATOM	286	HN GLU A 537	-23.079	8.261	-8.706	1.00	0.00
ATOM	287	HA GLU A 537	-21.848	8.061	-6.233	1.00	0.00
ATOM	288	1HB GLU A 537	-24.832	8.274	-6.858	1.00	0.00
ATOM	289	2HB GLU A 537	-23.713	9.633	-6.717	1.00	0.00
ATOM	290	1HG GLU A 537	-23.970	7.826	-4.336	1.00	0.00
ATOM	291	2HG GLU A 537	-25.324	8.916	-4.699	1.00	0.00
ATOM	292	N VAL A 538	-24.056	5.672	-6.979	1.00	0.00
ATOM	293	CA VAL A 538	-24.556	4.390	-6.568	1.00	0.00

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ATOM	294	C	VAL A 538	-23.516	3.314	-6.628	1.00	0.00
ATOM	295	O	VAL A 538	-23.511	2.405	-5.803	1.00	0.00
ATOM	296	CB	VAL A 538	-25.740	3.907	-7.362	1.00	0.00
ATOM	297	CG1	VAL A 538	-26.863	4.951	-7.249	1.00	0.00
ATOM	298	CG2	VAL A 538	-25.309	3.563	-8.796	1.00	0.00
ATOM	299	HN	VAL A 538	-24.374	6.073	-7.838	1.00	0.00
ATOM	300	HA	VAL A 538	-24.831	4.491	-5.519	1.00	0.00
ATOM	301	HB	VAL A 538	-26.082	2.947	-6.975	1.00	0.00
ATOM	302	IHG1	VAL A 538	-26.456	5.961	-7.298	1.00	0.00
ATOM	303	2HG1	VAL A 538	-27.383	4.843	-6.297	1.00	0.00
ATOM	304	3HG1	VAL A 538	-27.571	4.833	-8.069	1.00	0.00
ATOM	305	IHG2	VAL A 538	-24.340	3.064	-8.798	1.00	0.00
ATOM	306	2HG2	VAL A 538	-25.221	4.472	-9.391	1.00	0.00
ATOM	307	3HG2	VAL A 538	-26.035	2.893	-9.256	1.00	0.00
ATOM	308	N	ILE A 539	-22.595	3.403	-7.604	1.00	0.00
ATOM	309	CA	ILE A 539	-21.645	2.358	-7.858	1.00	0.00
ATOM	310	C	ILE A 539	-20.761	2.121	-6.681	1.00	0.00
ATOM	311	O	ILE A 539	-20.295	1.000	-6.483	1.00	0.00
ATOM	312	CB	ILE A 539	-20.732	2.669	-8.999	1.00	0.00
ATOM	313	CG1	ILE A 539	-21.553	3.171	-10.195	1.00	0.00
ATOM	314	CG2	ILE A 539	-19.883	1.418	-9.276	1.00	0.00
ATOM	315	CD1	ILE A 539	-22.880	2.440	-10.388	1.00	0.00
ATOM	316	HN	ILE A 539	-22.572	4.225	-8.171	1.00	0.00
ATOM	317	HA	ILE A 539	-22.221	1.458	-8.073	1.00	0.00
ATOM	318	HB	ILE A 539	-20.088	3.512	-8.747	1.00	0.00
ATOM	319	IHG2	ILE A 539	-20.519	0.571	-9.534	1.00	0.00
ATOM	320	2HG2	ILE A 539	-19.307	1.150	-8.391	1.00	0.00
ATOM	321	3HG2	ILE A 539	-19.207	1.600	-10.112	1.00	0.00
ATOM	322	IHG1	ILE A 539	-20.957	3.053	-11.099	1.00	0.00
ATOM	323	2HG1	ILE A 539	-21.757	4.231	-10.055	1.00	0.00
ATOM	324	IHD1	ILE A 539	-23.096	1.801	-9.532	1.00	0.00
ATOM	325	2HD1	ILE A 539	-22.838	1.811	-11.276	1.00	0.00
ATOM	326	3HD1	ILE A 539	-23.694	3.158	-10.486	1.00	0.00
ATOM	327	N	GLU A 540	-20.503	3.188	-5.897	1.00	0.00
ATOM	328	CA	GLU A 540	-19.615	3.196	-4.766	1.00	0.00
ATOM	329	C	GLU A 540	-19.648	1.908	-3.999	1.00	0.00
ATOM	330	O	GLU A 540	-20.702	1.356	-3.687	1.00	0.00
ATOM	331	CB	GLU A 540	-19.933	4.348	-3.798	1.00	0.00
ATOM	332	CG	GLU A 540	-18.850	4.602	-2.757	1.00	0.00
ATOM	333	CD	GLU A 540	-17.667	5.258	-3.455	1.00	0.00
ATOM	334	OE1	GLU A 540	-16.780	5.783	-2.731	1.00	0.00
ATOM	335	OE2	GLU A 540	-17.633	5.248	-4.715	1.00	0.00
ATOM	336	HN	GLU A 540	-20.968	4.044	-6.122	1.00	0.00
ATOM	337	HA	GLU A 540	-18.603	3.298	-5.158	1.00	0.00
ATOM	338	IHB	GLU A 540	-20.864	4.119	-3.282	1.00	0.00
ATOM	339	2HB	GLU A 540	-20.076	5.258	-4.378	1.00	0.00
ATOM	340	IHG	GLU A 540	-18.526	3.664	-2.305	1.00	0.00
ATOM	341	2HG	GLU A 540	-19.219	5.265	-1.975	1.00	0.00
ATOM	342	N	PRO A 541	-18.462	1.416	-3.745	1.00	0.00

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ATOM	343	CA	PRO A 541	-18.293	0.176	-3.033	1.00	0.00
ATOM	344	C	PRO A 541	-18.481	0.367	-1.567	1.00	0.00
ATOM	345	O	PRO A 541	-18.484	1.503	-1.097	1.00	0.00
ATOM	346	CB	PRO A 541	-16.882	-0.311	-3.354	1.00	0.00
ATOM	347	CG	PRO A 541	-16.552	0.357	-4.695	1.00	0.00
ATOM	348	CD	PRO A 541	-17.375	1.652	-4.680	1.00	0.00
ATOM	349	IHD	PRO A 541	-16.771	2.496	-4.348	1.00	0.00
ATOM	350	2HD	PRO A 541	-17.774	1.874	-5.670	1.00	0.00
ATOM	351	HA	PRO A 541	-19.038	-0.548	-3.364	1.00	0.00
ATOM	352	IHB	PRO A 541	-16.851	-1.398	-3.438	1.00	0.00
ATOM	353	2HB	PRO A 541	-16.177	-0.009	-2.580	1.00	0.00
ATOM	354	IHG	PRO A 541	-15.486	0.569	-4.776	1.00	0.00
ATOM	355	2HG	PRO A 541	-16.837	-0.280	-5.532	1.00	0.00
ATOM	356	N	GLU A 542	-18.639	-0.749	-0.833	1.00	0.00
ATOM	357	CA	GLU A 542	-18.786	-0.718	0.588	1.00	0.00
ATOM	358	C	GLU A 542	-17.432	-0.466	1.160	1.00	0.00
ATOM	359	O	GLU A 542	-16.420	-0.621	0.479	1.00	0.00
ATOM	360	CB	GLU A 542	-19.285	-2.049	1.175	1.00	0.00
ATOM	361	CG	GLU A 542	-18.347	-3.227	0.897	1.00	0.00
ATOM	362	CD	GLU A 542	-18.417	-3.551	-0.591	1.00	0.00
ATOM	363	OE1	GLU A 542	-19.469	-3.240	-1.210	1.00	0.00
ATOM	364	OE2	GLU A 542	-17.422	-4.104	-1.128	1.00	0.00
ATOM	365	HN	GLU A 542	-18.654	-1.633	-1.300	1.00	0.00
ATOM	366	HA	GLU A 542	-19.496	0.078	0.809	1.00	0.00
ATOM	367	IHB	GLU A 542	-20.264	-2.273	0.751	1.00	0.00
ATOM	368	2HB	GLU A 542	-19.396	-1.937	2.253	1.00	0.00
ATOM	369	IHG	GLU A 542	-18.653	-4.102	1.470	1.00	0.00
ATOM	370	2HG	GLU A 542	-17.321	-2.969	1.160	1.00	0.00
ATOM	371	N	VAL A 543	-17.388	-0.040	2.437	1.00	0.00
ATOM	372	CA	VAL A 543	-16.125	0.195	3.068	1.00	0.00
ATOM	373	C	VAL A 543	-15.795	-1.069	3.786	1.00	0.00
ATOM	374	O	VAL A 543	-16.621	-1.625	4.509	1.00	0.00
ATOM	375	CB	VAL A 543	-16.144	1.314	4.072	1.00	0.00
ATOM	376	CG1	VAL A 543	-16.445	2.627	3.331	1.00	0.00
ATOM	377	CG2	VAL A 543	-17.163	0.980	5.175	1.00	0.00
ATOM	378	HN	VAL A 543	-18.237	0.111	2.944	1.00	0.00
ATOM	379	HA	VAL A 543	-15.421	0.427	2.269	1.00	0.00
ATOM	380	HB	VAL A 543	-15.179	1.381	4.574	1.00	0.00
ATOM	381	IHG1	VAL A 543	-17.412	2.575	2.831	1.00	0.00
ATOM	382	2HG1	VAL A 543	-15.684	2.816	2.575	1.00	0.00
ATOM	383	3HG1	VAL A 543	-16.475	3.458	4.036	1.00	0.00
ATOM	384	IHG2	VAL A 543	-16.736	0.284	5.896	1.00	0.00
ATOM	385	2HG2	VAL A 543	-18.048	0.516	4.741	1.00	0.00
ATOM	386	3HG2	VAL A 543	-17.449	1.886	5.709	1.00	0.00
ATOM	387	N	LEU A 544	-14.569	-1.575	3.578	1.00	0.00
ATOM	388	CA	LEU A 544	-14.209	-2.815	4.187	1.00	0.00
ATOM	389	C	LEU A 544	-13.656	-2.531	5.543	1.00	0.00
ATOM	390	O	LEU A 544	-13.348	-1.387	5.870	1.00	0.00
ATOM	391	CB	LEU A 544	-13.131	-3.564	3.395	1.00	0.00

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ATOM	392	CG	LEU	A	544	-13.493	-3.682	1.906	1.00	0.00
ATOM	393	CD1	LEU	A	544	-13.254	-2.350	1.187	1.00	0.00
ATOM	394	CD2	LEU	A	544	-12.800	-4.861	1.224	1.00	0.00
ATOM	395	HN	LEU	A	544	-13.915	-1.086	3.001	1.00	0.00
ATOM	396	HA	LEU	A	544	-15.118	-3.413	4.244	1.00	0.00
ATOM	397	1HB	LEU	A	544	-13.010	-4.562	3.814	1.00	0.00
ATOM	398	2HB	LEU	A	544	-12.184	-3.035	3.493	1.00	0.00
ATOM	399	HG	LEU	A	544	-14.541	-3.965	1.807	1.00	0.00
ATOM	400	1HD1	LEU	A	544	-12.442	-1.797	1.660	1.00	0.00
ATOM	401	2HD1	LEU	A	544	-14.151	-1.732	1.230	1.00	0.00
ATOM	402	3HD1	LEU	A	544	-12.980	-2.527	0.147	1.00	0.00
ATOM	403	1HD2	LEU	A	544	-12.938	-5.775	1.802	1.00	0.00
ATOM	404	2HD2	LEU	A	544	-11.729	-4.672	1.142	1.00	0.00
ATOM	405	3HD2	LEU	A	544	-13.220	-5.022	0.232	1.00	0.00
ATOM	406	N	TYR	A	545	-13.553	-3.581	6.380	1.00	0.00
ATOM	407	CA	TYR	A	545	-12.972	-3.450	7.684	1.00	0.00
ATOM	408	C	TYR	A	545	-11.713	-4.251	7.646	1.00	0.00
ATOM	409	O	TYR	A	545	-11.640	-5.275	6.970	1.00	0.00
ATOM	410	CB	TYR	A	545	-13.835	-4.014	8.827	1.00	0.00
ATOM	411	CG	TYR	A	545	-14.981	-3.088	9.051	1.00	0.00
ATOM	412	CD1	TYR	A	545	-14.854	-2.036	9.929	1.00	0.00
ATOM	413	CD2	TYR	A	545	-16.172	-3.259	8.384	1.00	0.00
ATOM	414	CE1	TYR	A	545	-15.902	-1.174	10.148	1.00	0.00
ATOM	415	CE2	TYR	A	545	-17.220	-2.390	8.588	1.00	0.00
ATOM	416	CZ	TYR	A	545	-17.085	-1.346	9.471	1.00	0.00
ATOM	417	OH	TYR	A	545	-18.154	-0.448	9.677	1.00	0.00
ATOM	418	HN	TYR	A	545	-13.890	-4.474	6.084	1.00	0.00
ATOM	419	HA	TYR	A	545	-12.808	-2.384	7.838	1.00	0.00
ATOM	420	1HB	TYR	A	545	-13.248	-4.092	9.742	1.00	0.00
ATOM	421	2HB	TYR	A	545	-14.213	-5.002	8.566	1.00	0.00
ATOM	422	HD1	TYR	A	545	-13.921	-1.887	10.453	1.00	0.00
ATOM	423	HE1	TYR	A	545	-15.795	-0.361	10.851	1.00	0.00
ATOM	424	HD2	TYR	A	545	-16.286	-4.081	7.693	1.00	0.00
ATOM	425	HE2	TYR	A	545	-18.149	-2.530	8.055	1.00	0.00
ATOM	426	HH	TYR	A	545	-17.937	0.394	9.299	1.00	0.00
ATOM	427	N	ALA	A	546	-10.676	-3.791	8.370	1.00	0.00
ATOM	428	CA	ALA	A	546	-9.426	-4.489	8.363	1.00	0.00
ATOM	429	C	ALA	A	546	-9.603	-5.756	9.130	1.00	0.00
ATOM	430	O	ALA	A	546	-10.566	-5.900	9.884	1.00	0.00
ATOM	431	CB	ALA	A	546	-8.282	-3.699	9.022	1.00	0.00
ATOM	432	HN	ALA	A	546	-10.780	-2.958	8.915	1.00	0.00
ATOM	433	HA	ALA	A	546	-9.188	-4.688	7.318	1.00	0.00
ATOM	434	1HB	ALA	A	546	-8.514	-3.481	10.064	1.00	0.00
ATOM	435	2HB	ALA	A	546	-8.131	-2.752	8.505	1.00	0.00
ATOM	436	3HB	ALA	A	546	-7.360	-4.281	8.998	1.00	0.00
ATOM	437	N	GLY	A	547	-8.672	-6.714	8.923	1.00	0.00
ATOM	438	CA	GLY	A	547	-8.686	-7.983	9.595	1.00	0.00
ATOM	439	C	GLY	A	547	-8.822	-7.661	11.039	1.00	0.00
ATOM	440	O	GLY	A	547	-8.298	-6.649	11.499	1.00	0.00

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ATOM	441	HN	GLY A 547	-7.938	-6.529	8.269	1.00	0.00
ATOM	442	IHA	GLY A 547	-7.748	-8.499	9.398	1.00	0.00
ATOM	443	2HA	GLY A 547	-9.540	-8.560	9.243	1.00	0.00
ATOM	444	N	TYR A 548	-9.453	-8.584	11.790	1.00	0.00
ATOM	445	CA	TYR A 548	-9.937	-8.318	13.111	1.00	0.00
ATOM	446	C	TYR A 548	-8.940	-7.624	13.981	1.00	0.00
ATOM	447	O	TYR A 548	-9.107	-6.440	14.269	1.00	0.00
ATOM	448	CB	TYR A 548	-10.356	-9.629	13.804	1.00	0.00
ATOM	449	CG	TYR A 548	-11.182	-9.322	15.003	1.00	0.00
ATOM	450	CD1	TYR A 548	-12.506	-8.985	14.848	1.00	0.00
ATOM	451	CD2	TYR A 548	-10.694	-9.538	16.272	1.00	0.00
ATOM	452	CE1	TYR A 548	-13.324	-8.828	15.942	1.00	0.00
ATOM	453	CE2	TYR A 548	-11.507	-9.384	17.370	1.00	0.00
ATOM	454	CZ	TYR A 548	-12.825	-9.031	17.205	1.00	0.00
ATOM	455	OH	TYR A 548	-13.666	-8.889	18.330	1.00	0.00
ATOM	456	HN	TYR A 548	-9.589	-9.497	11.406	1.00	0.00
ATOM	457	HA	TYR A 548	-10.789	-7.645	13.015	1.00	0.00
ATOM	458	IHB	TYR A 548	-9.472	-10.187	14.114	1.00	0.00
ATOM	459	2HB	TYR A 548	-10.938	-10.245	13.118	1.00	0.00
ATOM	460	HD1	TYR A 548	-12.908	-8.841	13.856	1.00	0.00
ATOM	461	HE1	TYR A 548	-14.358	-8.545	15.808	1.00	0.00
ATOM	462	HD2	TYR A 548	-9.663	-9.831	16.406	1.00	0.00
ATOM	463	HE2	TYR A 548	-11.110	-9.540	18.362	1.00	0.00
ATOM	464	HH	TYR A 548	-13.522	-8.040	18.727	1.00	0.00
ATOM	465	N	ASP A 549	-7.850	-8.294	14.395	1.00	0.00
ATOM	466	CA	ASP A 549	-6.948	-7.558	15.232	1.00	0.00
ATOM	467	C	ASP A 549	-5.683	-8.324	15.365	1.00	0.00
ATOM	468	O	ASP A 549	-5.629	-9.359	16.027	1.00	0.00
ATOM	469	CB	ASP A 549	-7.494	-7.335	16.654	1.00	0.00
ATOM	470	CG	ASP A 549	-6.584	-6.355	17.379	1.00	0.00
ATOM	471	OD1	ASP A 549	-5.576	-5.914	16.766	1.00	0.00
ATOM	472	OD2	ASP A 549	-6.885	-6.035	18.561	1.00	0.00
ATOM	473	HN	ASP A 549	-7.680	-9.244	14.136	1.00	0.00
ATOM	474	HA	ASP A 549	-6.780	-6.599	14.742	1.00	0.00
ATOM	475	IHB	ASP A 549	-7.515	-8.276	17.204	1.00	0.00
ATOM	476	2HB	ASP A 549	-8.502	-6.924	16.613	1.00	0.00
ATOM	477	N	SER A 550	-4.609	-7.821	14.744	1.00	0.00
ATOM	478	CA	SER A 550	-3.373	-8.521	14.881	1.00	0.00
ATOM	479	C	SER A 550	-2.645	-7.794	15.955	1.00	0.00
ATOM	480	O	SER A 550	-3.151	-6.823	16.517	1.00	0.00
ATOM	481	CB	SER A 550	-2.526	-8.504	13.598	1.00	0.00
ATOM	482	OG	SER A 550	-1.473	-9.449	13.698	1.00	0.00
ATOM	483	HN	SER A 550	-4.671	-6.983	14.202	1.00	0.00
ATOM	484	HA	SER A 550	-3.625	-9.547	15.149	1.00	0.00
ATOM	485	IHB	SER A 550	-2.088	-7.518	13.447	1.00	0.00
ATOM	486	2HB	SER A 550	-3.140	-8.766	12.736	1.00	0.00
ATOM	487	HG	SER A 550	-0.895	-9.291	12.962	1.00	0.00
ATOM	488	N	SER A 551	-1.439	-8.267	16.297	1.00	0.00
ATOM	489	CA	SER A 551	-0.702	-7.585	17.309	1.00	0.00

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ATOM	490	C	SER A 551	-0.469	-6.217	16.768	1.00	0.00
ATOM	491	O	SER A 551	0.342	-6.026	15.864	1.00	0.00
ATOM	492	CB	SER A 551	0.641	-8.274	17.608	1.00	0.00
ATOM	493	OG	SER A 551	1.360	-7.589	18.614	1.00	0.00
ATOM	494	HN	SER A 551	-1.064	-9.080	15.851	1.00	0.00
ATOM	495	HA	SER A 551	-1.328	-7.572	18.202	1.00	0.00
ATOM	496	1HB	SER A 551	1.258	-8.293	16.710	1.00	0.00
ATOM	497	2HB	SER A 551	0.469	-9.293	17.954	1.00	0.00
ATOM	498	HG	SER A 551	2.271	-7.596	18.352	1.00	0.00
ATOM	499	N	VAL A 552	-1.170	-5.219	17.339	1.00	0.00
ATOM	500	CA	VAL A 552	-1.031	-3.881	16.855	1.00	0.00
ATOM	501	C	VAL A 552	0.410	-3.529	16.975	1.00	0.00
ATOM	502	O	VAL A 552	0.852	-2.649	16.236	1.00	0.00
ATOM	503	CB	VAL A 552	-1.932	-2.839	17.492	1.00	0.00
ATOM	504	CG1	VAL A 552	-1.754	-2.760	19.016	1.00	0.00
ATOM	505	CG2	VAL A 552	-1.651	-1.508	16.776	1.00	0.00
ATOM	506	HN	VAL A 552	-1.786	-5.414	18.102	1.00	0.00
ATOM	507	HA	VAL A 552	-1.238	-3.931	15.787	1.00	0.00
ATOM	508	HB	VAL A 552	-2.970	-3.084	17.269	1.00	0.00
ATOM	509	1HG1	VAL A 552	-0.784	-2.330	19.269	1.00	0.00
ATOM	510	2HG1	VAL A 552	-1.805	-3.757	19.454	1.00	0.00
ATOM	511	3HG1	VAL A 552	-2.526	-2.127	19.453	1.00	0.00
ATOM	512	1HG2	VAL A 552	-1.522	-1.666	15.705	1.00	0.00
ATOM	513	2HG2	VAL A 552	-0.738	-1.057	17.163	1.00	0.00
ATOM	514	3HG2	VAL A 552	-2.487	-0.821	16.916	1.00	0.00
ATOM	515	N	PRO A 553	1.160	-4.153	17.874	1.00	0.00
ATOM	516	CA	PRO A 553	2.572	-3.997	17.780	1.00	0.00
ATOM	517	C	PRO A 553	2.839	-4.634	16.475	1.00	0.00
ATOM	518	O	PRO A 553	2.831	-5.855	16.329	1.00	0.00
ATOM	519	CB	PRO A 553	3.197	-4.627	19.024	1.00	0.00
ATOM	520	CG	PRO A 553	1.990	-5.107	19.854	1.00	0.00
ATOM	521	CD	PRO A 553	0.789	-4.348	19.267	1.00	0.00
ATOM	522	1HD	PRO A 553	-0.128	-4.931	19.343	1.00	0.00
ATOM	523	2HD	PRO A 553	0.641	-3.389	19.764	1.00	0.00
ATOM	524	HA	PRO A 553	2.820	-2.936	17.724	1.00	0.00
ATOM	525	1HB	PRO A 553	3.789	-3.899	19.578	1.00	0.00
ATOM	526	2HB	PRO A 553	3.846	-5.461	18.758	1.00	0.00
ATOM	527	1HG	PRO A 553	1.855	-6.185	19.760	1.00	0.00
ATOM	528	2HG	PRO A 553	2.123	-4.872	20.910	1.00	0.00
ATOM	529	N	ASP A 554	3.070	-3.759	15.508	1.00	0.00
ATOM	530	CA	ASP A 554	3.109	-4.093	14.145	1.00	0.00
ATOM	531	C	ASP A 554	4.536	-4.346	13.841	1.00	0.00
ATOM	532	O	ASP A 554	5.427	-3.941	14.583	1.00	0.00
ATOM	533	CB	ASP A 554	2.635	-2.882	13.334	1.00	0.00
ATOM	534	CG	ASP A 554	1.951	-3.364	12.080	1.00	0.00
ATOM	535	OD1	ASP A 554	1.372	-2.506	11.363	1.00	0.00
ATOM	536	OD2	ASP A 554	1.967	-4.600	11.845	1.00	0.00
ATOM	537	HN	ASP A 554	3.225	-2.805	15.764	1.00	0.00
ATOM	538	HA	ASP A 554	2.451	-4.948	13.993	1.00	0.00

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ATOM	539	IHB	ASP A 554	3.485	-2.257	13.058	1.00	0.00
ATOM	540	2HB	ASP A 554	1.931	-2.288	13.917	1.00	0.00
ATOM	541	N	SER A 555	4.776	-5.073	12.743	1.00	0.00
ATOM	542	CA	SER A 555	6.104	-5.349	12.312	1.00	0.00
ATOM	543	C	SER A 555	6.030	-5.073	10.856	1.00	0.00
ATOM	544	O	SER A 555	4.938	-4.848	10.338	1.00	0.00
ATOM	545	CB	SER A 555	6.514	-6.816	12.521	1.00	0.00
ATOM	546	OG	SER A 555	5.603	-7.675	11.852	1.00	0.00
ATOM	547	HN	SER A 555	4.005	-5.430	12.216	1.00	0.00
ATOM	548	HA	SER A 555	6.759	-4.692	12.884	1.00	0.00
ATOM	549	IHB	SER A 555	6.503	-7.065	13.582	1.00	0.00
ATOM	550	2HB	SER A 555	7.511	-6.991	12.116	1.00	0.00
ATOM	551	HG	SER A 555	5.751	-7.557	10.923	1.00	0.00
ATOM	552	N	THR A 556	7.183	-5.076	10.161	1.00	0.00
ATOM	553	CA	THR A 556	7.172	-4.781	8.758	1.00	0.00
ATOM	554	C	THR A 556	6.244	-5.759	8.124	1.00	0.00
ATOM	555	O	THR A 556	5.354	-5.390	7.362	1.00	0.00
ATOM	556	CB	THR A 556	8.511	-4.981	8.118	1.00	0.00
ATOM	557	OG1	THR A 556	9.474	-4.118	8.704	1.00	0.00
ATOM	558	CG2	THR A 556	8.382	-4.706	6.612	1.00	0.00
ATOM	559	HN	THR A 556	8.045	-5.284	10.623	1.00	0.00
ATOM	560	HA	THR A 556	6.860	-3.741	8.659	1.00	0.00
ATOM	561	HB	THR A 556	8.845	-6.009	8.258	1.00	0.00
ATOM	562	HG1	THR A 556	9.460	-3.314	8.202	1.00	0.00
ATOM	563	IHG2	THR A 556	7.884	-3.753	6.435	1.00	0.00
ATOM	564	2HG2	THR A 556	7.791	-5.488	6.135	1.00	0.00
ATOM	565	3HG2	THR A 556	9.369	-4.661	6.152	1.00	0.00
ATOM	566	N	TRP A 557	6.412	-7.044	8.467	1.00	0.00
ATOM	567	CA	TRP A 557	5.573	-8.072	7.932	1.00	0.00
ATOM	568	C	TRP A 557	4.169	-7.891	8.395	1.00	0.00
ATOM	569	O	TRP A 557	3.224	-7.991	7.617	1.00	0.00
ATOM	570	CB	TRP A 557	5.970	-9.465	8.426	1.00	0.00
ATOM	571	CG	TRP A 557	7.251	-9.979	7.837	1.00	0.00
ATOM	572	CD1	TRP A 557	7.419	-10.886	6.838	1.00	0.00
ATOM	573	CD2	TRP A 557	8.561	-9.507	8.186	1.00	0.00
ATOM	574	NE1	TRP A 557	8.755	-11.037	6.572	1.00	0.00
ATOM	575	CE2	TRP A 557	9.468	-10.184	7.380	1.00	0.00
ATOM	576	CE3	TRP A 557	8.975	-8.580	9.100	1.00	0.00
ATOM	577	CZ2	TRP A 557	10.812	-9.953	7.466	1.00	0.00
ATOM	578	CZ3	TRP A 557	10.331	-8.349	9.190	1.00	0.00
ATOM	579	CH2	TRP A 557	11.232	-9.022	8.391	1.00	0.00
ATOM	580	HN	TRP A 557	7.138	-7.288	9.111	1.00	0.00
ATOM	581	HA	TRP A 557	5.663	-8.018	6.847	1.00	0.00
ATOM	582	IHB	TRP A 557	5.178	-10.169	8.173	1.00	0.00
ATOM	583	2HB	TRP A 557	6.086	-9.437	9.509	1.00	0.00
ATOM	584	HE3	TRP A 557	8.270	-8.051	9.724	1.00	0.00
ATOM	585	HD1	TRP A 557	6.621	-11.408	6.331	1.00	0.00
ATOM	586	HE1	TRP A 557	9.139	-11.653	5.914	1.00	0.00
ATOM	587	HZ2	TRP A 557	11.514	-10.477	6.836	1.00	0.00

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ATOM	588	HZ3 TRP A 557	10.696	-7.625	9.903	1.00	0.00
ATOM	589	HH2 TRP A 557	12.287	-8.814	8.492	1.00	0.00
ATOM	590	N ARG A 558	4.005	-7.601	9.693	1.00	0.00
ATOM	591	CA ARG A 558	2.695	-7.561	10.258	1.00	0.00
ATOM	592	C ARG A 558	1.909	-6.485	9.583	1.00	0.00
ATOM	593	O ARG A 558	0.749	-6.681	9.224	1.00	0.00
ATOM	594	CB ARG A 558	2.762	-7.263	11.763	1.00	0.00
ATOM	595	CG ARG A 558	1.578	-7.783	12.573	1.00	0.00
ATOM	596	CD ARG A 558	1.839	-7.698	14.077	1.00	0.00
ATOM	597	NE ARG A 558	0.831	-8.545	14.771	1.00	0.00
ATOM	598	CZ ARG A 558	1.075	-9.869	14.997	1.00	0.00
ATOM	599	NH1 ARG A 558	2.205	-10.454	14.502	1.00	0.00
ATOM	600	NH2 ARG A 558	0.195	-10.607	15.736	1.00	0.00
ATOM	601	HN ARG A 558	4.803	-7.413	10.266	1.00	0.00
ATOM	602	HA ARG A 558	2.236	-8.533	10.079	1.00	0.00
ATOM	603	IHB ARG A 558	2.822	-6.184	11.897	1.00	0.00
ATOM	604	2HB ARG A 558	3.672	-7.710	12.161	1.00	0.00
ATOM	605	IHG ARG A 558	1.386	-8.820	12.301	1.00	0.00
ATOM	606	2HG ARG A 558	0.693	-7.196	12.330	1.00	0.00
ATOM	607	IHD ARG A 558	1.725	-6.677	14.440	1.00	0.00
ATOM	608	2HD ARG A 558	2.827	-8.082	14.328	1.00	0.00
ATOM	609	HE ARG A 558	-0.032	-8.142	15.074	1.00	0.00
ATOM	610	IHH1 ARG A 558	2.857	-9.913	13.970	1.00	0.00
ATOM	611	2HH1 ARG A 558	2.379	-11.425	14.670	1.00	0.00
ATOM	612	IHH2 ARG A 558	-0.745	-10.289	15.857	1.00	0.00
ATOM	613	2HH2 ARG A 558	0.491	-11.465	16.155	1.00	0.00
ATOM	614	N ILE A 559	2.516	-5.305	9.292	1.00	0.00
ATOM	615	CA ILE A 559	1.827	-4.119	8.731	1.00	0.00
ATOM	616	C ILE A 559	1.497	-4.396	7.283	1.00	0.00
ATOM	617	O ILE A 559	0.366	-4.265	6.822	1.00	0.00
ATOM	618	CB ILE A 559	2.656	-2.787	8.783	1.00	0.00
ATOM	619	CG1 ILE A 559	1.967	-1.560	8.132	1.00	0.00
ATOM	620	CG2 ILE A 559	4.060	-2.914	8.240	1.00	0.00
ATOM	621	CD1 ILE A 559	0.721	-1.051	8.861	1.00	0.00
ATOM	622	HN ILE A 559	3.453	-5.200	9.578	1.00	0.00
ATOM	623	HA ILE A 559	0.895	-4.007	9.286	1.00	0.00
ATOM	624	HB ILE A 559	2.893	-2.543	9.804	1.00	0.00
ATOM	625	IHG2 ILE A 559	4.120	-2.765	7.164	1.00	0.00
ATOM	626	2HG2 ILE A 559	4.412	-3.883	8.472	1.00	0.00
ATOM	627	3HG2 ILE A 559	4.748	-2.270	8.777	1.00	0.00
ATOM	628	IHG1 ILE A 559	1.714	-1.773	7.093	1.00	0.00
ATOM	629	2HG1 ILE A 559	2.672	-0.731	8.090	1.00	0.00
ATOM	630	IHD1 ILE A 559	-0.007	-1.846	9.020	1.00	0.00
ATOM	631	2HD1 ILE A 559	0.242	-0.254	8.293	1.00	0.00
ATOM	632	3HD1 ILE A 559	0.983	-0.634	9.833	1.00	0.00
ATOM	633	N MET A 560	2.586	-4.806	6.598	1.00	0.00
ATOM	634	CA MET A 560	2.513	-5.064	5.177	1.00	0.00
ATOM	635	C MET A 560	1.384	-6.043	4.913	1.00	0.00
ATOM	636	O MET A 560	0.660	-5.940	3.937	1.00	0.00

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ATOM	637	CB	MET A 560	3.840	-5.628	4.656	1.00	0.00
ATOM	638	CG	MET A 560	3.772	-5.929	3.156	1.00	0.00
ATOM	639	SD	MET A 560	3.305	-4.449	2.226	1.00	0.00
ATOM	640	CE	MET A 560	2.780	-5.201	0.678	1.00	0.00
ATOM	641	HN	MET A 560	3.463	-4.907	7.078	1.00	0.00
ATOM	642	HA	MET A 560	2.274	-4.111	4.702	1.00	0.00
ATOM	643	1HB	MET A 560	4.106	-6.536	5.201	1.00	0.00
ATOM	644	2HB	MET A 560	4.639	-4.912	4.848	1.00	0.00
ATOM	645	1HG	MET A 560	3.035	-6.709	2.967	1.00	0.00
ATOM	646	2HG	MET A 560	4.718	-6.332	2.808	1.00	0.00
ATOM	647	1HE	MET A 560	3.583	-5.175	-0.059	1.00	0.00
ATOM	648	2HE	MET A 560	1.926	-4.659	0.276	1.00	0.00
ATOM	649	3HE	MET A 560	2.462	-6.227	0.842	1.00	0.00
ATOM	650	N	THR A 561	1.254	-6.972	5.877	1.00	0.00
ATOM	651	CA	THR A 561	0.230	-7.957	5.717	1.00	0.00
ATOM	652	C	THR A 561	-1.132	-7.338	5.753	1.00	0.00
ATOM	653	O	THR A 561	-1.942	-7.591	4.863	1.00	0.00
ATOM	654	CB	THR A 561	0.253	-9.015	6.778	1.00	0.00
ATOM	655	OG1	THR A 561	1.491	-9.710	6.754	1.00	0.00
ATOM	656	CG2	THR A 561	-0.907	-9.991	6.513	1.00	0.00
ATOM	657	HN	THR A 561	1.885	-7.023	6.651	1.00	0.00
ATOM	658	HA	THR A 561	0.384	-8.408	4.737	1.00	0.00
ATOM	659	HB	THR A 561	0.134	-8.564	7.763	1.00	0.00
ATOM	660	HG1	THR A 561	2.165	-9.061	6.598	1.00	0.00
ATOM	661	1HG2	THR A 561	-1.011	-10.185	5.445	1.00	0.00
ATOM	662	2HG2	THR A 561	-1.845	-9.567	6.872	1.00	0.00
ATOM	663	3HG2	THR A 561	-0.720	-10.942	7.012	1.00	0.00
ATOM	664	N	THR A 562	-1.371	-6.504	6.773	1.00	0.00
ATOM	665	CA	THR A 562	-2.671	-5.876	6.947	1.00	0.00
ATOM	666	C	THR A 562	-3.073	-5.043	5.712	1.00	0.00
ATOM	667	O	THR A 562	-4.151	-5.207	5.157	1.00	0.00
ATOM	668	CB	THR A 562	-2.575	-5.035	8.237	1.00	0.00
ATOM	669	OG1	THR A 562	-2.067	-5.838	9.297	1.00	0.00
ATOM	670	CG2	THR A 562	-3.945	-4.514	8.686	1.00	0.00
ATOM	671	HN	THR A 562	-0.606	-6.273	7.377	1.00	0.00
ATOM	672	HA	THR A 562	-3.391	-6.686	7.073	1.00	0.00
ATOM	673	HB	THR A 562	-1.920	-4.166	8.084	1.00	0.00
ATOM	674	HG1	THR A 562	-1.128	-6.023	9.203	1.00	0.00
ATOM	675	1HG2	THR A 562	-4.389	-3.856	7.939	1.00	0.00
ATOM	676	2HG2	THR A 562	-3.856	-3.947	9.613	1.00	0.00
ATOM	677	3HG2	THR A 562	-4.638	-5.336	8.866	1.00	0.00
ATOM	678	N	LEU A 563	-2.142	-4.157	5.310	1.00	0.00
ATOM	679	CA	LEU A 563	-2.440	-3.258	4.196	1.00	0.00
ATOM	680	C	LEU A 563	-2.561	-4.047	2.878	1.00	0.00
ATOM	681	O	LEU A 563	-3.452	-3.801	2.073	1.00	0.00
ATOM	682	CB	LEU A 563	-1.381	-2.149	4.098	1.00	0.00
ATOM	683	CG	LEU A 563	-1.569	-0.984	5.091	1.00	0.00
ATOM	684	CD1	LEU A 563	-1.720	-1.439	6.549	1.00	0.00
ATOM	685	CD2	LEU A 563	-0.413	0.017	4.954	1.00	0.00

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ATOM	686	HN	LEU A 563	-1.264	-4.106	5.796	1.00	0.00
ATOM	687	HA	LEU A 563	-3.410	-2.801	4.390	1.00	0.00
ATOM	688	1HB	LEU A 563	-1.439	-1.707	3.105	1.00	0.00
ATOM	689	2HB	LEU A 563	-0.382	-2.579	4.191	1.00	0.00
ATOM	690	HG	LEU A 563	-2.487	-0.461	4.821	1.00	0.00
ATOM	691	1HD1	LEU A 563	-0.876	-2.055	6.857	1.00	0.00
ATOM	692	2HD1	LEU A 563	-2.635	-2.010	6.700	1.00	0.00
ATOM	693	3HD1	LEU A 563	-1.775	-0.581	7.219	1.00	0.00
ATOM	694	1HD2	LEU A 563	-0.560	0.881	5.602	1.00	0.00
ATOM	695	2HD2	LEU A 563	-0.326	0.384	3.930	1.00	0.00
ATOM	696	3HD2	LEU A 563	0.540	-0.440	5.222	1.00	0.00
ATOM	697	N	ASN A 564	-1.646	-5.027	2.717	1.00	0.00
ATOM	698	CA	ASN A 564	-1.710	-5.941	1.569	1.00	0.00
ATOM	699	C	ASN A 564	-3.102	-6.582	1.520	1.00	0.00
ATOM	700	O	ASN A 564	-3.801	-6.536	0.512	1.00	0.00
ATOM	701	CB	ASN A 564	-0.592	-7.011	1.653	1.00	0.00
ATOM	702	CG	ASN A 564	-0.641	-8.077	0.538	1.00	0.00
ATOM	703	OD1	ASN A 564	-1.700	-8.457	0.065	1.00	0.00
ATOM	704	ND2	ASN A 564	0.545	-8.582	0.169	1.00	0.00
ATOM	705	HN	ASN A 564	-0.928	-5.159	3.402	1.00	0.00
ATOM	706	HA	ASN A 564	-1.582	-5.330	0.675	1.00	0.00
ATOM	707	1HB	ASN A 564	-0.651	-7.542	2.602	1.00	0.00
ATOM	708	2HB	ASN A 564	0.379	-6.522	1.619	1.00	0.00
ATOM	709	1HD2	ASN A 564	0.559	-9.377	-0.441	1.00	0.00
ATOM	710	2HD2	ASN A 564	1.444	-8.223	0.435	1.00	0.00
ATOM	711	N	MET A 565	-3.472	-7.139	2.692	1.00	0.00
ATOM	712	CA	MET A 565	-4.686	-7.899	2.761	1.00	0.00
ATOM	713	C	MET A 565	-5.855	-7.025	2.425	1.00	0.00
ATOM	714	O	MET A 565	-6.733	-7.428	1.664	1.00	0.00
ATOM	715	CB	MET A 565	-4.937	-8.481	4.163	1.00	0.00
ATOM	716	CG	MET A 565	-3.928	-9.557	4.569	1.00	0.00
ATOM	717	SD	MET A 565	-4.074	-11.110	3.635	1.00	0.00
ATOM	718	CE	MET A 565	-5.609	-11.633	4.455	1.00	0.00
ATOM	719	HN	MET A 565	-2.938	-6.992	3.525	1.00	0.00
ATOM	720	HA	MET A 565	-4.595	-8.703	2.030	1.00	0.00
ATOM	721	1HB	MET A 565	-5.937	-8.912	4.188	1.00	0.00
ATOM	722	2HB	MET A 565	-4.895	-7.671	4.890	1.00	0.00
ATOM	723	1HG	MET A 565	-4.066	-9.787	5.625	1.00	0.00
ATOM	724	2HG	MET A 565	-2.921	-9.170	4.419	1.00	0.00
ATOM	725	1HE	MET A 565	-6.429	-10.989	4.136	1.00	0.00
ATOM	726	2HE	MET A 565	-5.500	-11.548	5.536	1.00	0.00
ATOM	727	3HE	MET A 565	-5.845	-12.660	4.178	1.00	0.00
ATOM	728	N	LEU A 566	-5.845	-5.812	3.021	1.00	0.00
ATOM	729	CA	LEU A 566	-6.856	-4.788	2.773	1.00	0.00
ATOM	730	C	LEU A 566	-7.043	-4.576	1.264	1.00	0.00
ATOM	731	O	LEU A 566	-8.154	-4.613	0.750	1.00	0.00
ATOM	732	CB	LEU A 566	-6.464	-3.475	3.487	1.00	0.00
ATOM	733	CG	LEU A 566	-6.893	-3.414	4.968	1.00	0.00
ATOM	734	CD1	LEU A 566	-5.988	-2.478	5.781	1.00	0.00

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ATOM	735	CD2 LEU A 566	-8.353	-2.956	5.095	1.00	0.00
ATOM	736	HN LEU A 566	-5.087	-5.613	3.643	1.00	0.00
ATOM	737	HA LEU A 566	-7.791	-5.160	3.176	1.00	0.00
ATOM	738	1HB LEU A 566	-6.893	-2.613	2.973	1.00	0.00
ATOM	739	2HB LEU A 566	-5.388	-3.342	3.410	1.00	0.00
ATOM	740	HG LEU A 566	-6.798	-4.408	5.407	1.00	0.00
ATOM	741	1HD1 LEU A 566	-4.981	-2.879	5.866	1.00	0.00
ATOM	742	2HD1 LEU A 566	-6.363	-2.343	6.796	1.00	0.00
ATOM	743	3HD1 LEU A 566	-5.914	-1.497	5.316	1.00	0.00
ATOM	744	1HD2 LEU A 566	-8.650	-2.858	6.138	1.00	0.00
ATOM	745	2HD2 LEU A 566	-9.029	-3.662	4.622	1.00	0.00
ATOM	746	3HD2 LEU A 566	-8.503	-1.982	4.627	1.00	0.00
ATOM	747	N GLY A 567	-5.891	-4.374	0.598	1.00	0.00
ATOM	748	CA GLY A 567	-5.899	-4.129	-0.841	1.00	0.00
ATOM	749	C GLY A 567	-6.516	-5.286	-1.627	1.00	0.00
ATOM	750	O GLY A 567	-7.377	-5.103	-2.480	1.00	0.00
ATOM	751	HN GLY A 567	-5.023	-4.395	1.103	1.00	0.00
ATOM	752	1HA GLY A 567	-4.867	-3.974	-1.156	1.00	0.00
ATOM	753	2HA GLY A 567	-6.481	-3.231	-1.031	1.00	0.00
ATOM	754	N GLY A 568	-6.043	-6.488	-1.267	1.00	0.00
ATOM	755	CA GLY A 568	-6.495	-7.693	-1.948	1.00	0.00
ATOM	756	C GLY A 568	-8.001	-7.959	-1.776	1.00	0.00
ATOM	757	O GLY A 568	-8.615	-8.640	-2.582	1.00	0.00
ATOM	758	HN GLY A 568	-5.345	-6.546	-0.547	1.00	0.00
ATOM	759	1HA GLY A 568	-5.925	-8.524	-1.533	1.00	0.00
ATOM	760	2HA GLY A 568	-6.253	-7.593	-3.007	1.00	0.00
ATOM	761	N ARG A 569	-8.568	-7.380	-0.701	1.00	0.00
ATOM	762	CA ARG A 569	-9.988	-7.439	-0.493	1.00	0.00
ATOM	763	C ARG A 569	-10.710	-6.424	-1.328	1.00	0.00
ATOM	764	O ARG A 569	-11.707	-6.727	-1.980	1.00	0.00
ATOM	765	CB ARG A 569	-10.338	-7.144	0.977	1.00	0.00
ATOM	766	CG ARG A 569	-9.768	-8.193	1.934	1.00	0.00
ATOM	767	CD ARG A 569	-9.594	-7.720	3.379	1.00	0.00
ATOM	768	NE ARG A 569	-10.941	-7.532	3.984	1.00	0.00
ATOM	769	CZ ARG A 569	-11.478	-6.280	4.060	1.00	0.00
ATOM	770	NH1 ARG A 569	-10.793	-5.217	3.548	1.00	0.00
ATOM	771	NH2 ARG A 569	-12.689	-6.097	4.662	1.00	0.00
ATOM	772	HN ARG A 569	-7.980	-7.066	0.045	1.00	0.00
ATOM	773	HA ARG A 569	-10.314	-8.441	-0.770	1.00	0.00
ATOM	774	1HB ARG A 569	-11.422	-7.116	1.085	1.00	0.00
ATOM	775	2HB ARG A 569	-9.943	-6.165	1.246	1.00	0.00
ATOM	776	1HG ARG A 569	-8.796	-8.508	1.557	1.00	0.00
ATOM	777	2HG ARG A 569	-10.432	-9.055	1.932	1.00	0.00
ATOM	778	1HD ARG A 569	-9.077	-6.762	3.419	1.00	0.00
ATOM	779	2HD ARG A 569	-9.064	-8.463	3.974	1.00	0.00
ATOM	780	HE ARG A 569	-11.450	-8.319	4.333	1.00	0.00
ATOM	781	1HH1 ARG A 569	-9.901	-5.357	3.119	1.00	0.00
ATOM	782	2HH1 ARG A 569	-11.184	-4.298	3.602	1.00	0.00
ATOM	783	1HH2 ARG A 569	-12.893	-5.232	5.122	1.00	0.00

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ATOM	784	2HH2 ARG A 569	-13.372	-6.827	4.644	1.00	0.00
ATOM	785	N GLN A 570	-10.148	-5.202	-1.264	1.00	0.00
ATOM	786	CA GLN A 570	-10.705	-4.047	-1.949	1.00	0.00
ATOM	787	C GLN A 570	-10.795	-4.290	-3.471	1.00	0.00
ATOM	788	O GLN A 570	-11.690	-3.789	-4.138	1.00	0.00
ATOM	789	CB GLN A 570	-9.800	-2.832	-1.665	1.00	0.00
ATOM	790	CG GLN A 570	-9.791	-2.333	-0.204	1.00	0.00
ATOM	791	CD GLN A 570	-10.411	-0.934	-0.079	1.00	0.00
ATOM	792	OE1 GLN A 570	-11.507	-0.680	-0.549	1.00	0.00
ATOM	793	NE2 GLN A 570	-9.663	-0.034	0.566	1.00	0.00
ATOM	794	HN GLN A 570	-9.315	-5.093	-0.714	1.00	0.00
ATOM	795	HA GLN A 570	-11.711	-3.886	-1.560	1.00	0.00
ATOM	796	1HB GLN A 570	-10.072	-2.022	-2.342	1.00	0.00
ATOM	797	2HB GLN A 570	-8.776	-3.100	-1.915	1.00	0.00
ATOM	798	1HG GLN A 570	-8.767	-2.289	0.165	1.00	0.00
ATOM	799	2HG GLN A 570	-10.334	-3.011	0.452	1.00	0.00
ATOM	800	1HE2 GLN A 570	-8.752	-0.195	0.949	1.00	0.00
ATOM	801	2HE2 GLN A 570	-10.037	0.888	0.666	1.00	0.00
ATOM	802	N VAL A 571	-9.829	-5.086	-3.988	1.00	0.00
ATOM	803	CA VAL A 571	-9.746	-5.296	-5.400	1.00	0.00
ATOM	804	C VAL A 571	-10.979	-5.988	-5.885	1.00	0.00
ATOM	805	O VAL A 571	-11.453	-5.695	-6.980	1.00	0.00
ATOM	806	CB VAL A 571	-8.564	-6.113	-5.838	1.00	0.00
ATOM	807	CG1 VAL A 571	-8.809	-7.579	-5.465	1.00	0.00
ATOM	808	CG2 VAL A 571	-8.355	-5.896	-7.346	1.00	0.00
ATOM	809	HN VAL A 571	-9.145	-5.485	-3.377	1.00	0.00
ATOM	810	HA VAL A 571	-9.697	-4.306	-5.853	1.00	0.00
ATOM	811	HB VAL A 571	-7.661	-5.751	-5.347	1.00	0.00
ATOM	812	1HG1 VAL A 571	-9.464	-8.058	-6.194	1.00	0.00
ATOM	813	2HG1 VAL A 571	-9.288	-7.645	-4.488	1.00	0.00
ATOM	814	3HG1 VAL A 571	-7.866	-8.126	-5.449	1.00	0.00
ATOM	815	1HG2 VAL A 571	-8.168	-4.845	-7.562	1.00	0.00
ATOM	816	2HG2 VAL A 571	-9.245	-6.200	-7.897	1.00	0.00
ATOM	817	3HG2 VAL A 571	-7.496	-6.470	-7.693	1.00	0.00
ATOM	818	N ILE A 572	-11.533	-6.934	-5.099	1.00	0.00
ATOM	819	CA ILE A 572	-12.701	-7.619	-5.569	1.00	0.00
ATOM	820	C ILE A 572	-13.819	-6.633	-5.718	1.00	0.00
ATOM	821	O ILE A 572	-14.523	-6.622	-6.725	1.00	0.00
ATOM	822	CB ILE A 572	-13.177	-8.716	-4.653	1.00	0.00
ATOM	823	CG1 ILE A 572	-13.637	-8.160	-3.296	1.00	0.00
ATOM	824	CG2 ILE A 572	-12.047	-9.754	-4.539	1.00	0.00
ATOM	825	CD1 ILE A 572	-14.406	-9.173	-2.447	1.00	0.00
ATOM	826	HN ILE A 572	-11.136	-7.152	-4.207	1.00	0.00
ATOM	827	HA ILE A 572	-12.442	-8.035	-6.542	1.00	0.00
ATOM	828	HB ILE A 572	-14.076	-9.181	-5.057	1.00	0.00
ATOM	829	1HG2 ILE A 572	-11.145	-9.299	-4.131	1.00	0.00
ATOM	830	2HG2 ILE A 572	-11.806	-10.157	-5.523	1.00	0.00
ATOM	831	3HG2 ILE A 572	-12.346	-10.564	-3.874	1.00	0.00
ATOM	832	1HG1 ILE A 572	-14.276	-7.296	-3.471	1.00	0.00

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ATOM	833	2HG1 ILE A 572	-12.761	-7.831	-2.738	1.00	0.00
ATOM	834	1HD1 ILE A 572	-13.787	-10.046	-2.234	1.00	0.00
ATOM	835	2HD1 ILE A 572	-15.295	-9.512	-2.978	1.00	0.00
ATOM	836	3HD1 ILE A 572	-14.695	-8.726	-1.496	1.00	0.00
ATOM	837	N ALA A 573	-13.995	-5.749	-4.721	1.00	0.00
ATOM	838	CA ALA A 573	-15.062	-4.793	-4.764	1.00	0.00
ATOM	839	C ALA A 573	-14.833	-3.877	-5.920	1.00	0.00
ATOM	840	O ALA A 573	-15.775	-3.457	-6.590	1.00	0.00
ATOM	841	CB ALA A 573	-15.137	-3.928	-3.494	1.00	0.00
ATOM	842	HN ALA A 573	-13.372	-5.759	-3.939	1.00	0.00
ATOM	843	HA ALA A 573	-15.985	-5.359	-4.888	1.00	0.00
ATOM	844	1HB ALA A 573	-14.292	-3.242	-3.444	1.00	0.00
ATOM	845	2HB ALA A 573	-15.110	-4.560	-2.606	1.00	0.00
ATOM	846	3HB ALA A 573	-16.052	-3.336	-3.495	1.00	0.00
ATOM	847	N ALA A 574	-13.554	-3.564	-6.190	1.00	0.00
ATOM	848	CA ALA A 574	-13.203	-2.632	-7.220	1.00	0.00
ATOM	849	C ALA A 574	-13.693	-3.097	-8.553	1.00	0.00
ATOM	850	O ALA A 574	-14.242	-2.312	-9.323	1.00	0.00
ATOM	851	CB ALA A 574	-11.683	-2.427	-7.337	1.00	0.00
ATOM	852	HN ALA A 574	-12.827	-3.994	-5.655	1.00	0.00
ATOM	853	HA ALA A 574	-13.691	-1.690	-6.971	1.00	0.00
ATOM	854	1HB ALA A 574	-11.184	-3.368	-7.569	1.00	0.00
ATOM	855	2HB ALA A 574	-11.280	-2.055	-6.395	1.00	0.00
ATOM	856	3HB ALA A 574	-11.459	-1.721	-8.137	1.00	0.00
ATOM	857	N VAL A 575	-13.530	-4.399	-8.853	1.00	0.00
ATOM	858	CA VAL A 575	-13.925	-4.888	-10.141	1.00	0.00
ATOM	859	C VAL A 575	-15.398	-4.687	-10.298	1.00	0.00
ATOM	860	O VAL A 575	-15.870	-4.340	-11.381	1.00	0.00
ATOM	861	CB VAL A 575	-13.632	-6.348	-10.347	1.00	0.00
ATOM	862	CG1 VAL A 575	-14.518	-7.183	-9.409	1.00	0.00
ATOM	863	CG2 VAL A 575	-13.839	-6.673	-11.835	1.00	0.00
ATOM	864	HN VAL A 575	-13.134	-5.023	-8.179	1.00	0.00
ATOM	865	HA VAL A 575	-13.384	-4.293	-10.877	1.00	0.00
ATOM	866	HB VAL A 575	-12.581	-6.547	-10.136	1.00	0.00
ATOM	867	1HG1 VAL A 575	-15.377	-7.584	-9.947	1.00	0.00
ATOM	868	2HG1 VAL A 575	-14.890	-6.565	-8.592	1.00	0.00
ATOM	869	3HG1 VAL A 575	-13.952	-8.023	-9.005	1.00	0.00
ATOM	870	1HG2 VAL A 575	-13.305	-5.960	-12.463	1.00	0.00
ATOM	871	2HG2 VAL A 575	-14.897	-6.619	-12.089	1.00	0.00
ATOM	872	3HG2 VAL A 575	-13.459	-7.670	-12.059	1.00	0.00
ATOM	873	N LYS A 576	-16.162	-4.895	-9.209	1.00	0.00
ATOM	874	CA LYS A 576	-17.590	-4.759	-9.248	1.00	0.00
ATOM	875	C LYS A 576	-17.917	-3.345	-9.608	1.00	0.00
ATOM	876	O LYS A 576	-18.759	-3.086	-10.468	1.00	0.00
ATOM	877	CB LYS A 576	-18.241	-4.998	-7.873	1.00	0.00
ATOM	878	CG LYS A 576	-17.958	-6.373	-7.268	1.00	0.00
ATOM	879	CD LYS A 576	-18.478	-7.544	-8.101	1.00	0.00
ATOM	880	CE LYS A 576	-18.182	-8.907	-7.472	1.00	0.00
ATOM	881	NZ LYS A 576	-18.714	-9.988	-8.331	1.00	0.00

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ATOM	882	HN	LYS	A	576	-15.722	-5.152	-8.349	1.00	0.00
ATOM	883	HA	LYS	A	576	-17.956	-5.490	-9.969	1.00	0.00
ATOM	884	IHB	LYS	A	576	-19.319	-4.882	-7.977	1.00	0.00
ATOM	885	2HB	LYS	A	576	-17.879	-4.236	-7.184	1.00	0.00
ATOM	886	IHG	LYS	A	576	-18.419	-6.419	-6.282	1.00	0.00
ATOM	887	2HG	LYS	A	576	-16.881	-6.484	-7.149	1.00	0.00
ATOM	888	IHD	LYS	A	576	-18.017	-7.506	-9.088	1.00	0.00
ATOM	889	2HD	LYS	A	576	-19.555	-7.439	-8.222	1.00	0.00
ATOM	890	IHE	LYS	A	576	-18.657	-8.984	-6.494	1.00	0.00
ATOM	891	2HE	LYS	A	576	-17.107	-9.052	-7.369	1.00	0.00
ATOM	892	IHZ	LYS	A	576	-18.266	-9.940	-9.267	1.00	0.00
ATOM	893	2HZ	LYS	A	576	-19.743	-9.875	-8.433	1.00	0.00
ATOM	894	3HZ	LYS	A	576	-18.509	-10.910	-7.895	1.00	0.00
ATOM	895	N	TRP	A	577	-17.222	-2.390	-8.964	1.00	0.00
ATOM	896	CA	TRP	A	577	-17.460	-0.991	-9.166	1.00	0.00
ATOM	897	C	TRP	A	577	-17.218	-0.636	-10.591	1.00	0.00
ATOM	898	O	TRP	A	577	-17.991	0.096	-11.206	1.00	0.00
ATOM	899	CB	TRP	A	577	-16.491	-0.113	-8.355	1.00	0.00
ATOM	900	CG	TRP	A	577	-16.575	1.365	-8.665	1.00	0.00
ATOM	901	CD1	TRP	A	577	-17.346	2.331	-8.087	1.00	0.00
ATOM	902	CD2	TRP	A	577	-15.783	2.025	-9.667	1.00	0.00
ATOM	903	NE1	TRP	A	577	-17.099	3.546	-8.679	1.00	0.00
ATOM	904	CE2	TRP	A	577	-16.136	3.374	-9.651	1.00	0.00
ATOM	905	CE3	TRP	A	577	-14.836	1.549	-10.529	1.00	0.00
ATOM	906	CZ2	TRP	A	577	-15.548	4.269	-10.500	1.00	0.00
ATOM	907	CZ3	TRP	A	577	-14.245	2.455	-11.383	1.00	0.00
ATOM	908	CH2	TRP	A	577	-14.593	3.789	-11.370	1.00	0.00
ATOM	909	HN	TRP	A	577	-16.511	-2.669	-8.319	1.00	0.00
ATOM	910	HA	TRP	A	577	-18.489	-0.799	-8.860	1.00	0.00
ATOM	911	IHB	TRP	A	577	-15.471	-0.439	-8.555	1.00	0.00
ATOM	912	2HB	TRP	A	577	-16.703	-0.245	-7.294	1.00	0.00
ATOM	913	HE3	TRP	A	577	-14.563	0.505	-10.542	1.00	0.00
ATOM	914	HD1	TRP	A	577	-18.047	2.165	-7.283	1.00	0.00
ATOM	915	HE1	TRP	A	577	-17.534	4.393	-8.450	1.00	0.00
ATOM	916	HZ2	TRP	A	577	-15.821	5.314	-10.490	1.00	0.00
ATOM	917	HZ3	TRP	A	577	-13.492	2.113	-12.077	1.00	0.00
ATOM	918	HH2	TRP	A	577	-14.109	4.470	-12.054	1.00	0.00
ATOM	919	N	ALA	A	578	-16.141	-1.186	-11.164	1.00	0.00
ATOM	920	CA	ALA	A	578	-15.751	-0.831	-12.495	1.00	0.00
ATOM	921	C	ALA	A	578	-16.858	-1.134	-13.453	1.00	0.00
ATOM	922	O	ALA	A	578	-17.130	-0.350	-14.361	1.00	0.00
ATOM	923	CB	ALA	A	578	-14.504	-1.599	-12.969	1.00	0.00
ATOM	924	HN	ALA	A	578	-15.601	-1.856	-10.654	1.00	0.00
ATOM	925	HA	ALA	A	578	-15.554	0.240	-12.488	1.00	0.00
ATOM	926	IHB	ALA	A	578	-14.737	-2.651	-13.130	1.00	0.00
ATOM	927	2HB	ALA	A	578	-13.717	-1.539	-12.217	1.00	0.00
ATOM	928	3HB	ALA	A	578	-14.143	-1.185	-13.910	1.00	0.00
ATOM	929	N	LYS	A	579	-17.560	-2.259	-13.246	1.00	0.00
ATOM	930	CA	LYS	A	579	-18.569	-2.685	-14.173	1.00	0.00

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ATOM	931	C	LYS A 579	-19.602	-1.613	-14.317	1.00	0.00
ATOM	932	O	LYS A 579	-20.149	-1.402	-15.396	1.00	0.00
ATOM	933	CB	LYS A 579	-19.301	-3.950	-13.690	1.00	0.00
ATOM	934	CG	LYS A 579	-18.376	-5.153	-13.491	1.00	0.00
ATOM	935	CD	LYS A 579	-17.692	-5.639	-14.770	1.00	0.00
ATOM	936	CE	LYS A 579	-18.527	-6.650	-15.559	1.00	0.00
ATOM	937	NZ	LYS A 579	-17.774	-7.115	-16.747	1.00	0.00
ATOM	938	HN	LYS A 579	-17.377	-2.809	-12.431	1.00	0.00
ATOM	939	HA	LYS A 579	-18.066	-2.878	-15.120	1.00	0.00
ATOM	940	1HB	LYS A 579	-20.064	-4.212	-14.421	1.00	0.00
ATOM	941	2HB	LYS A 579	-19.795	-3.728	-12.745	1.00	0.00
ATOM	942	1HG	LYS A 579	-18.961	-5.974	-13.079	1.00	0.00
ATOM	943	2HG	LYS A 579	-17.608	-4.882	-12.769	1.00	0.00
ATOM	944	1HD	LYS A 579	-16.742	-6.101	-14.505	1.00	0.00
ATOM	945	2HD	LYS A 579	-17.489	-4.779	-15.407	1.00	0.00
ATOM	946	1HE	LYS A 579	-19.454	-6.190	-15.903	1.00	0.00
ATOM	947	2HE	LYS A 579	-18.756	-7.518	-14.941	1.00	0.00
ATOM	948	1HZ	LYS A 579	-17.214	-7.954	-16.495	1.00	0.00
ATOM	949	2HZ	LYS A 579	-17.139	-6.358	-17.072	1.00	0.00
ATOM	950	3HZ	LYS A 579	-18.441	-7.358	-17.507	1.00	0.00
ATOM	951	N	ALA A 580	-19.912	-0.937	-13.203	1.00	0.00
ATOM	952	CA	ALA A 580	-20.909	0.087	-13.093	1.00	0.00
ATOM	953	C	ALA A 580	-20.599	1.416	-13.730	1.00	0.00
ATOM	954	O	ALA A 580	-21.517	2.183	-14.014	1.00	0.00
ATOM	955	CB	ALA A 580	-21.275	0.329	-11.631	1.00	0.00
ATOM	956	HN	ALA A 580	-19.401	-1.166	-12.376	1.00	0.00
ATOM	957	HA	ALA A 580	-21.779	-0.250	-13.656	1.00	0.00
ATOM	958	1HB	ALA A 580	-20.701	-0.327	-10.976	1.00	0.00
ATOM	959	2HB	ALA A 580	-22.333	0.125	-11.469	1.00	0.00
ATOM	960	3HB	ALA A 580	-21.054	1.359	-11.353	1.00	0.00
ATOM	961	N	ILE A 581	-19.308	1.770	-13.915	1.00	0.00
ATOM	962	CA	ILE A 581	-19.009	3.067	-14.463	1.00	0.00
ATOM	963	C	ILE A 581	-19.485	3.141	-15.877	1.00	0.00
ATOM	964	O	ILE A 581	-19.052	2.378	-16.741	1.00	0.00
ATOM	965	CB	ILE A 581	-17.545	3.400	-14.445	1.00	0.00
ATOM	966	CG1	ILE A 581	-17.304	4.796	-15.038	1.00	0.00
ATOM	967	CG2	ILE A 581	-16.779	2.273	-15.149	1.00	0.00
ATOM	968	CD1	ILE A 581	-15.857	5.261	-14.898	1.00	0.00
ATOM	969	HN	ILE A 581	-18.571	1.139	-13.674	1.00	0.00
ATOM	970	HA	ILE A 581	-19.563	3.791	-13.865	1.00	0.00
ATOM	971	HB	ILE A 581	-17.198	3.501	-13.417	1.00	0.00
ATOM	972	1HG2	ILE A 581	-17.468	1.591	-15.648	1.00	0.00
ATOM	973	2HG2	ILE A 581	-16.203	1.699	-14.424	1.00	0.00
ATOM	974	3HG2	ILE A 581	-16.110	2.687	-15.903	1.00	0.00
ATOM	975	1HG1	ILE A 581	-17.954	5.510	-14.534	1.00	0.00
ATOM	976	2HG1	ILE A 581	-17.568	4.780	-16.095	1.00	0.00
ATOM	977	1HD1	ILE A 581	-15.168	4.438	-15.083	1.00	0.00
ATOM	978	2HD1	ILE A 581	-15.677	5.630	-13.888	1.00	0.00
ATOM	979	3HD1	ILE A 581	-15.643	6.049	-15.620	1.00	0.00

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ATOM	980	N	PRO A 582	-20.368	4.076	-16.116	1.00	0.00
ATOM	981	CA	PRO A 582	-20.989	4.240	-17.404	1.00	0.00
ATOM	982	C	PRO A 582	-19.969	4.258	-18.500	1.00	0.00
ATOM	983	O	PRO A 582	-19.001	5.010	-18.407	1.00	0.00
ATOM	984	CB	PRO A 582	-21.759	5.557	-17.322	1.00	0.00
ATOM	985	CG	PRO A 582	-20.958	6.369	-16.287	1.00	0.00
ATOM	986	CD	PRO A 582	-20.393	5.302	-15.335	1.00	0.00
ATOM	987	IHD	PRO A 582	-19.386	5.561	-15.006	1.00	0.00
ATOM	988	2HD	PRO A 582	-21.029	5.179	-14.458	1.00	0.00
ATOM	989	HA	PRO A 582	-21.661	3.406	-17.606	1.00	0.00
ATOM	990	1HB	PRO A 582	-22.786	5.397	-16.993	1.00	0.00
ATOM	991	2HB	PRO A 582	-21.785	6.062	-18.287	1.00	0.00
ATOM	992	1HG	PRO A 582	-20.158	6.934	-16.764	1.00	0.00
ATOM	993	2HG	PRO A 582	-21.601	7.070	-15.754	1.00	0.00
ATOM	994	N	GLY A 583	-20.176	3.417	-19.535	1.00	0.00
ATOM	995	CA	GLY A 583	-19.319	3.366	-20.683	1.00	0.00
ATOM	996	C	GLY A 583	-18.265	2.305	-20.568	1.00	0.00
ATOM	997	O	GLY A 583	-17.716	1.855	-21.571	1.00	0.00
ATOM	998	HN	GLY A 583	-20.964	2.802	-19.498	1.00	0.00
ATOM	999	1HA	GLY A 583	-18.842	4.341	-20.773	1.00	0.00
ATOM	1000	2HA	GLY A 583	-19.950	3.155	-21.547	1.00	0.00
ATOM	1001	N	PHE A 584	-17.960	1.858	-19.339	1.00	0.00
ATOM	1002	CA	PHE A 584	-16.904	0.905	-19.124	1.00	0.00
ATOM	1003	C	PHE A 584	-17.199	-0.427	-19.753	1.00	0.00
ATOM	1004	O	PHE A 584	-16.348	-1.026	-20.411	1.00	0.00
ATOM	1005	CB	PHE A 584	-16.664	0.684	-17.623	1.00	0.00
ATOM	1006	CG	PHE A 584	-15.471	-0.178	-17.407	1.00	0.00
ATOM	1007	CD1	PHE A 584	-14.204	0.322	-17.608	1.00	0.00
ATOM	1008	CD2	PHE A 584	-15.612	-1.384	-16.760	1.00	0.00
ATOM	1009	CE1	PHE A 584	-13.096	-0.406	-17.241	1.00	0.00
ATOM	1010	CE2	PHE A 584	-14.509	-2.100	-16.364	1.00	0.00
ATOM	1011	CZ	PHE A 584	-13.246	-1.619	-16.614	1.00	0.00
ATOM	1012	HN	PHE A 584	-18.479	2.197	-18.555	1.00	0.00
ATOM	1013	HA	PHE A 584	-16.008	1.303	-19.601	1.00	0.00
ATOM	1014	1HB	PHE A 584	-17.533	0.202	-17.177	1.00	0.00
ATOM	1015	2HB	PHE A 584	-16.501	1.643	-17.131	1.00	0.00
ATOM	1016	HD1	PHE A 584	-14.079	1.296	-18.058	1.00	0.00
ATOM	1017	HD2	PHE A 584	-16.600	-1.771	-16.561	1.00	0.00
ATOM	1018	HE1	PHE A 584	-12.107	-0.023	-17.446	1.00	0.00
ATOM	1019	HE2	PHE A 584	-14.635	-3.044	-15.854	1.00	0.00
ATOM	1020	HZ	PHE A 584	-12.378	-2.190	-16.320	1.00	0.00
ATOM	1021	N	ARG A 585	-18.450	-0.893	-19.595	1.00	0.00
ATOM	1022	CA	ARG A 585	-18.881	-2.187	-20.037	1.00	0.00
ATOM	1023	C	ARG A 585	-18.770	-2.297	-21.522	1.00	0.00
ATOM	1024	O	ARG A 585	-18.582	-3.387	-22.060	1.00	0.00
ATOM	1025	CB	ARG A 585	-20.341	-2.478	-19.653	1.00	0.00
ATOM	1026	CG	ARG A 585	-20.830	-3.866	-20.073	1.00	0.00
ATOM	1027	CD	ARG A 585	-22.284	-4.140	-19.683	1.00	0.00
ATOM	1028	NE	ARG A 585	-22.624	-5.515	-20.148	1.00	0.00

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ATOM	1029	CZ	ARG A 585	-23.782	-6.107	-19.736	1.00	0.00
ATOM	1030	NH1	ARG A 585	-24.095	-7.365	-20.161	1.00	0.00
ATOM	1031	NH2	ARG A 585	-24.629	-5.440	-18.897	1.00	0.00
ATOM	1032	HN	ARG A 585	-19.118	-0.302	-19.143	1.00	0.00
ATOM	1033	HA	ARG A 585	-18.217	-2.916	-19.573	1.00	0.00
ATOM	1034	1HB	ARG A 585	-20.979	-1.730	-20.120	1.00	0.00
ATOM	1035	2HB	ARG A 585	-20.441	-2.387	-18.572	1.00	0.00
ATOM	1036	1HG	ARG A 585	-20.194	-4.617	-19.605	1.00	0.00
ATOM	1037	2HG	ARG A 585	-20.732	-3.959	-21.154	1.00	0.00
ATOM	1038	1HD	ARG A 585	-22.963	-3.442	-20.172	1.00	0.00
ATOM	1039	2HD	ARG A 585	-22.418	-4.107	-18.603	1.00	0.00
ATOM	1040	HE	ARG A 585	-22.003	-6.004	-20.760	1.00	0.00
ATOM	1041	1HH1	ARG A 585	-23.475	-7.854	-20.775	1.00	0.00
ATOM	1042	2HH1	ARG A 585	-24.944	-7.798	-19.860	1.00	0.00
ATOM	1043	1HH2	ARG A 585	-24.480	-4.471	-18.703	1.00	0.00
ATOM	1044	2HH2	ARG A 585	-25.398	-5.922	-18.477	1.00	0.00
ATOM	1045	N	ASN A 586	-18.893	-1.162	-22.227	1.00	0.00
ATOM	1046	CA	ASN A 586	-18.871	-1.149	-23.658	1.00	0.00
ATOM	1047	C	ASN A 586	-17.577	-1.675	-24.203	1.00	0.00
ATOM	1048	O	ASN A 586	-17.544	-2.196	-25.315	1.00	0.00
ATOM	1049	CB	ASN A 586	-19.118	0.251	-24.236	1.00	0.00
ATOM	1050	CG	ASN A 586	-20.571	0.587	-23.938	1.00	0.00
ATOM	1051	OD1	ASN A 586	-21.465	-0.218	-24.195	1.00	0.00
ATOM	1052	ND2	ASN A 586	-20.815	1.795	-23.364	1.00	0.00
ATOM	1053	HN	ASN A 586	-19.004	-0.298	-21.736	1.00	0.00
ATOM	1054	HA	ASN A 586	-19.650	-1.836	-23.990	1.00	0.00
ATOM	1055	1HB	ASN A 586	-18.950	0.263	-25.312	1.00	0.00
ATOM	1056	2HB	ASN A 586	-18.466	0.987	-23.765	1.00	0.00
ATOM	1057	1HD2	ASN A 586	-20.132	2.522	-23.430	1.00	0.00
ATOM	1058	2HD2	ASN A 586	-21.669	1.973	-22.876	1.00	0.00
ATOM	1059	N	LEU A 587	-16.462	-1.528	-23.464	1.00	0.00
ATOM	1060	CA	LEU A 587	-15.216	-2.041	-23.971	1.00	0.00
ATOM	1061	C	LEU A 587	-15.207	-3.534	-23.839	1.00	0.00
ATOM	1062	O	LEU A 587	-15.985	-4.117	-23.087	1.00	0.00
ATOM	1063	CB	LEU A 587	-13.966	-1.549	-23.218	1.00	0.00
ATOM	1064	CG	LEU A 587	-13.683	-0.036	-23.312	1.00	0.00
ATOM	1065	CD1	LEU A 587	-14.647	0.804	-22.461	1.00	0.00
ATOM	1066	CD2	LEU A 587	-12.217	0.255	-22.978	1.00	0.00
ATOM	1067	HN	LEU A 587	-16.499	-1.069	-22.577	1.00	0.00
ATOM	1068	HA	LEU A 587	-15.162	-1.731	-25.014	1.00	0.00
ATOM	1069	1HB	LEU A 587	-13.102	-2.081	-23.612	1.00	0.00
ATOM	1070	2HB	LEU A 587	-14.080	-1.809	-22.167	1.00	0.00
ATOM	1071	HG	LEU A 587	-13.768	0.275	-24.352	1.00	0.00
ATOM	1072	1HD1	LEU A 587	-14.703	0.414	-21.445	1.00	0.00
ATOM	1073	2HD1	LEU A 587	-15.649	0.776	-22.889	1.00	0.00
ATOM	1074	3HD1	LEU A 587	-14.300	1.836	-22.407	1.00	0.00
ATOM	1075	1HD2	LEU A 587	-11.554	-0.262	-23.671	1.00	0.00
ATOM	1076	2HD2	LEU A 587	-11.985	-0.088	-21.970	1.00	0.00
ATOM	1077	3HD2	LEU A 587	-12.019	1.324	-23.056	1.00	0.00

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ATOM	1078	N	HIS A 588	-14.324	-4.224	-24.583	1.00	0.00
ATOM	1079	CA	HIS A 588	-14.302	-5.645	-24.394	1.00	0.00
ATOM	1080	C	HIS A 588	-13.680	-5.962	-23.057	1.00	0.00
ATOM	1081	O	HIS A 588	-13.397	-5.069	-22.263	1.00	0.00
ATOM	1082	CB	HIS A 588	-13.564	-6.456	-25.471	1.00	0.00
ATOM	1083	CG	HIS A 588	-14.329	-6.632	-26.751	1.00	0.00
ATOM	1084	ND1	HIS A 588	-14.228	-5.801	-27.843	1.00	0.00
ATOM	1085	CD2	HIS A 588	-15.196	-7.619	-27.114	1.00	0.00
ATOM	1086	CE1	HIS A 588	-15.033	-6.320	-28.805	1.00	0.00
ATOM	1087	NE2	HIS A 588	-15.641	-7.422	-28.409	1.00	0.00
ATOM	1088	HN	HIS A 588	-13.715	-3.769	-25.232	1.00	0.00
ATOM	1089	HA	HIS A 588	-15.346	-5.955	-24.360	1.00	0.00
ATOM	1090	1HB	HIS A 588	-13.344	-7.446	-25.075	1.00	0.00
ATOM	1091	2HB	HIS A 588	-12.627	-5.953	-25.708	1.00	0.00
ATOM	1092	HD2	HIS A 588	-15.494	-8.439	-26.479	1.00	0.00
ATOM	1093	HD1	HIS A 588	-13.681	-4.992	-27.913	1.00	0.00
ATOM	1094	HE1	HIS A 588	-15.160	-5.881	-29.783	1.00	0.00
ATOM	1095	N	LEU A 589	-13.524	-7.268	-22.754	1.00	0.00
ATOM	1096	CA	LEU A 589	-12.907	-7.782	-21.549	1.00	0.00
ATOM	1097	C	LEU A 589	-11.421	-7.545	-21.600	1.00	0.00
ATOM	1098	O	LEU A 589	-10.690	-7.638	-20.621	1.00	0.00
ATOM	1099	CB	LEU A 589	-13.182	-9.270	-21.281	1.00	0.00
ATOM	1100	CG	LEU A 589	-14.650	-9.519	-20.885	1.00	0.00
ATOM	1101	CD1	LEU A 589	-15.603	-9.313	-22.073	1.00	0.00
ATOM	1102	CD2	LEU A 589	-14.825	-10.869	-20.181	1.00	0.00
ATOM	1103	HN	LEU A 589	-13.862	-7.935	-23.416	1.00	0.00
ATOM	1104	HA	LEU A 589	-13.296	-7.182	-20.728	1.00	0.00
ATOM	1105	1HB	LEU A 589	-12.532	-9.615	-20.478	1.00	0.00
ATOM	1106	2HB	LEU A 589	-12.952	-9.844	-22.178	1.00	0.00
ATOM	1107	HG	LEU A 589	-14.925	-8.835	-20.083	1.00	0.00
ATOM	1108	1HD1	LEU A 589	-15.171	-9.716	-22.989	1.00	0.00
ATOM	1109	2HD1	LEU A 589	-15.789	-8.250	-22.227	1.00	0.00
ATOM	1110	3HD1	LEU A 589	-16.547	-9.827	-21.892	1.00	0.00
ATOM	1111	1HD2	LEU A 589	-14.225	-10.909	-19.272	1.00	0.00
ATOM	1112	2HD2	LEU A 589	-14.502	-11.679	-20.834	1.00	0.00
ATOM	1113	3HD2	LEU A 589	-15.868	-11.016	-19.902	1.00	0.00
ATOM	1114	N	ASP A 590	-11.031	-7.149	-22.805	1.00	0.00
ATOM	1115	CA	ASP A 590	-9.924	-6.818	-23.641	1.00	0.00
ATOM	1116	C	ASP A 590	-10.032	-5.373	-23.370	1.00	0.00
ATOM	1117	O	ASP A 590	-11.115	-4.836	-23.268	1.00	0.00
ATOM	1118	CB	ASP A 590	-10.004	-7.103	-25.178	1.00	0.00
ATOM	1119	CG	ASP A 590	-10.722	-6.130	-26.144	1.00	0.00
ATOM	1120	OD1	ASP A 590	-10.727	-6.510	-27.345	1.00	0.00
ATOM	1121	OD2	ASP A 590	-11.240	-5.041	-25.780	1.00	0.00
ATOM	1122	HN	ASP A 590	-11.837	-7.036	-23.342	1.00	0.00
ATOM	1123	HA	ASP A 590	-9.087	-7.380	-23.229	1.00	0.00
ATOM	1124	1HB	ASP A 590	-10.503	-8.061	-25.301	1.00	0.00
ATOM	1125	2HB	ASP A 590	-8.982	-7.178	-25.542	1.00	0.00
ATOM	1126	N	ASP A 591	-8.993	-4.639	-23.046	1.00	0.00

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ATOM	1127	CA	ASP A 591	-8.947	-3.488	-22.220	1.00	0.00
ATOM	1128	C	ASP A 591	-9.839	-3.337	-21.017	1.00	0.00
ATOM	1129	O	ASP A 591	-9.322	-2.693	-20.111	1.00	0.00
ATOM	1130	CB	ASP A 591	-9.244	-2.289	-23.151	1.00	0.00
ATOM	1131	CG	ASP A 591	-9.012	-0.909	-22.554	1.00	0.00
ATOM	1132	OD1	ASP A 591	-8.376	-0.782	-21.477	1.00	0.00
ATOM	1133	OD2	ASP A 591	-9.478	0.062	-23.206	1.00	0.00
ATOM	1134	HN	ASP A 591	-8.121	-4.930	-23.433	1.00	0.00
ATOM	1135	HA	ASP A 591	-7.953	-3.420	-21.779	1.00	0.00
ATOM	1136	1HB	ASP A 591	-10.289	-2.337	-23.455	1.00	0.00
ATOM	1137	2HB	ASF A 591	-8.611	-2.370	-24.034	1.00	0.00
ATOM	1138	N	GLN A 592	-11.100	-3.786	-20.880	1.00	0.00
ATOM	1139	CA	GLN A 592	-11.706	-3.638	-19.564	1.00	0.00
ATOM	1140	C	GLN A 592	-10.809	-4.237	-18.494	1.00	0.00
ATOM	1141	O	GLN A 592	-10.526	-3.611	-17.468	1.00	0.00
ATOM	1142	CB	GLN A 592	-13.062	-4.362	-19.519	1.00	0.00
ATOM	1143	CG	GLN A 592	-13.773	-4.302	-18.176	1.00	0.00
ATOM	1144	CD	GLN A 592	-15.098	-5.034	-18.326	1.00	0.00
ATOM	1145	OE1	GLN A 592	-15.704	-5.451	-17.341	1.00	0.00
ATOM	1146	NE2	GLN A 592	-15.565	-5.192	-19.595	1.00	0.00
ATOM	1147	HN	GLN A 592	-11.595	-4.199	-21.643	1.00	0.00
ATOM	1148	HA	GLN A 592	-11.832	-2.572	-19.381	1.00	0.00
ATOM	1149	1HB	GLN A 592	-12.902	-5.408	-19.776	1.00	0.00
ATOM	1150	2HB	GLN A 592	-13.713	-3.919	-20.272	1.00	0.00
ATOM	1151	1HG	GLN A 592	-13.961	-3.268	-17.886	1.00	0.00
ATOM	1152	2HG	GLN A 592	-13.177	-4.786	-17.402	1.00	0.00
ATOM	1153	1HE2	GLN A 592	-15.039	-4.833	-20.365	1.00	0.00
ATOM	1154	2HE2	GLN A 592	-16.429	-5.663	-19.774	1.00	0.00
ATOM	1155	N	MET A 593	-10.260	-5.437	-18.742	1.00	0.00
ATOM	1156	CA	MET A 593	-9.370	-6.015	-17.780	1.00	0.00
ATOM	1157	C	MET A 593	-8.169	-5.123	-17.698	1.00	0.00
ATOM	1158	O	MET A 593	-7.646	-4.868	-16.610	1.00	0.00
ATOM	1159	CB	MET A 593	-8.929	-7.431	-18.199	1.00	0.00
ATOM	1160	CG	MET A 593	-8.478	-8.331	-17.047	1.00	0.00
ATOM	1161	SD	MET A 593	-6.901	-7.880	-16.276	1.00	0.00
ATOM	1162	CE	MET A 593	-6.846	-9.316	-15.164	1.00	0.00
ATOM	1163	HN	MET A 593	-10.471	-5.922	-19.591	1.00	0.00
ATOM	1164	HA	MET A 593	-9.905	-6.049	-16.831	1.00	0.00
ATOM	1165	1HB	MET A 593	-8.104	-7.338	-18.905	1.00	0.00
ATOM	1166	2HB	MET A 593	-9.762	-7.914	-18.707	1.00	0.00
ATOM	1167	1HG	MET A 593	-8.383	-9.350	-17.420	1.00	0.00
ATOM	1168	2HG	MET A 593	-9.242	-8.309	-16.271	1.00	0.00
ATOM	1169	1HE	MET A 593	-6.846	-10.232	-15.754	1.00	0.00
ATOM	1170	2HE	MET A 593	-7.723	-9.318	-14.517	1.00	0.00
ATOM	1171	3HE	MET A 593	-5.935	-9.286	-14.566	1.00	0.00
ATOM	1172	N	THR A 594	-7.699	-4.597	-18.851	1.00	0.00
ATOM	1173	CA	THR A 594	-6.500	-3.820	-18.739	1.00	0.00
ATOM	1174	C	THR A 594	-6.684	-2.533	-17.985	1.00	0.00
ATOM	1175	O	THR A 594	-5.791	-2.161	-17.226	1.00	0.00

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ATOM 1176 CB THR A 594	-5.721	-3.609	-20.009	1.00	0.00
ATOM 1177 OG1 THR A 594	-4.434	-3.097	-19.695	1.00	0.00
ATOM 1178 CG2 THR A 594	-6.449	-2.635	-20.928	1.00	0.00
ATOM 1179 HN THR A 594	-8.159	-4.741	-19.727	1.00	0.00
ATOM 1180 HA THR A 594	-5.875	-4.345	-18.016	1.00	0.00
ATOM 1181 HB THR A 594	-5.596	-4.552	-20.541	1.00	0.00
ATOM 1182 HG1 THR A 594	-4.553	-2.470	-18.995	1.00	0.00
ATOM 1183 1HG2 THR A 594	-5.913	-1.688	-20.989	1.00	0.00
ATOM 1184 2HG2 THR A 594	-7.449	-2.432	-20.545	1.00	0.00
ATOM 1185 3HG2 THR A 594	-6.519	-3.048	-21.935	1.00	0.00
ATOM 1186 N LEU A 595	-7.840	-1.833	-18.125	1.00	0.00
ATOM 1187 CA LEU A 595	-7.992	-0.587	-17.402	1.00	0.00
ATOM 1188 C LEU A 595	-7.869	-0.929	-15.955	1.00	0.00
ATOM 1189 O LEU A 595	-7.238	-0.225	-15.165	1.00	0.00
ATOM 1190 CB LEU A 595	-9.378	0.113	-17.468	1.00	0.00
ATOM 1191 CG LEU A 595	-9.880	0.767	-18.781	1.00	0.00
ATOM 1192 CD1 LEU A 595	-8.871	1.762	-19.367	1.00	0.00
ATOM 1193 CD2 LEU A 595	-10.458	-0.238	-19.780	1.00	0.00
ATOM 1194 HN LEU A 595	-8.572	-2.172	-18.715	1.00	0.00
ATOM 1195 HA LEU A 595	-7.237	0.081	-17.815	1.00	0.00
ATOM 1196 1HB LEU A 595	-9.370	0.895	-16.713	1.00	0.00
ATOM 1197 2HB LEU A 595	-10.118	-0.633	-17.189	1.00	0.00
ATOM 1198 HG LEU A 595	-10.816	1.288	-18.582	1.00	0.00
ATOM 1199 1HD1 LEU A 595	-7.996	1.240	-19.756	1.00	0.00
ATOM 1200 2HD1 LEU A 595	-8.534	2.455	-18.596	1.00	0.00
ATOM 1201 3HD1 LEU A 595	-9.323	2.318	-20.188	1.00	0.00
ATOM 1202 1HD2 LEU A 595	-11.538	-0.117	-19.866	1.00	0.00
ATOM 1203 2HD2 LEU A 595	-10.259	-1.257	-19.447	1.00	0.00
ATOM 1204 3HD2 LEU A 595	-10.022	-0.082	-20.766	1.00	0.00
ATOM 1205 N LEU A 596	-8.477	-2.053	-15.561	1.00	0.00
ATOM 1206 CA LEU A 596	-8.431	-2.348	-14.173	1.00	0.00
ATOM 1207 C LEU A 596	-7.005	-2.577	-13.776	1.00	0.00
ATOM 1208 O LEU A 596	-6.529	-2.006	-12.796	1.00	0.00
ATOM 1209 CB LEU A 596	-9.288	-3.570	-13.814	1.00	0.00
ATOM 1210 CG LEU A 596	-9.576	-3.691	-12.312	1.00	0.00
ATOM 1211 CD1 LEU A 596	-10.386	-2.487	-11.801	1.00	0.00
ATOM 1212 CD2 LEU A 596	-10.268	-5.021	-11.996	1.00	0.00
ATOM 1213 HN LEU A 596	-8.941	-2.654	-16.211	1.00	0.00
ATOM 1214 HA LEU A 596	-8.795	-1.465	-13.649	1.00	0.00
ATOM 1215 1HB LEU A 596	-8.772	-4.470	-14.146	1.00	0.00
ATOM 1216 2HB LEU A 596	-10.235	-3.502	-14.348	1.00	0.00
ATOM 1217 HG LEU A 596	-8.634	-3.749	-11.768	1.00	0.00
ATOM 1218 1HD1 LEU A 596	-11.255	-2.310	-12.434	1.00	0.00
ATOM 1219 2HD1 LEU A 596	-9.771	-1.587	-11.813	1.00	0.00
ATOM 1220 3HD1 LEU A 596	-10.740	-2.674	-10.787	1.00	0.00
ATOM 1221 1HD2 LEU A 596	-9.639	-5.862	-12.290	1.00	0.00
ATOM 1222 2HD2 LEU A 596	-11.208	-5.096	-12.542	1.00	0.00
ATOM 1223 3HD2 LEU A 596	-10.459	-5.102	-10.926	1.00	0.00
ATOM 1224 N GLN A 597	-6.254	-3.356	-14.577	1.00	0.00

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ATOM	1225	CA	GLN A 597	-4.895	-3.650	-14.216	1.00	0.00
ATOM	1226	C	GLN A 597	-4.138	-2.371	-14.131	1.00	0.00
ATOM	1227	O	GLN A 597	-3.312	-2.175	-13.242	1.00	0.00
ATOM	1228	CB	GLN A 597	-4.169	-4.488	-15.273	1.00	0.00
ATOM	1229	CG	GLN A 597	-4.725	-5.897	-15.424	1.00	0.00
ATOM	1230	CD	GLN A 597	-3.981	-6.553	-16.577	1.00	0.00
ATOM	1231	OE1	GLN A 597	-3.425	-7.638	-16.436	1.00	0.00
ATOM	1232	NE2	GLN A 597	-3.972	-5.874	-17.757	1.00	0.00
ATOM	1233	HN	GLN A 597	-6.641	-3.728	-15.421	1.00	0.00
ATOM	1234	HA	GLN A 597	-4.932	-4.189	-13.270	1.00	0.00
ATOM	1235	1HB	GLN A 597	-3.117	-4.556	-15.001	1.00	0.00
ATOM	1236	2HB	GLN A 597	-4.243	-3.979	-16.233	1.00	0.00
ATOM	1237	1HG	GLN A 597	-5.791	-5.870	-15.647	1.00	0.00
ATOM	1238	2HG	GLN A 597	-4.566	-6.474	-14.513	1.00	0.00
ATOM	1239	1HE2	GLN A 597	-4.441	-4.994	-17.826	1.00	0.00
ATOM	1240	2HE2	GLN A 597	-3.505	-6.240	-18.561	1.00	0.00
ATOM	1241	N	TYR A 598	-4.409	-1.463	-15.078	1.00	0.00
ATOM	1242	CA	TYR A 598	-3.683	-0.231	-15.173	1.00	0.00
ATOM	1243	C	TYR A 598	-3.830	0.698	-14.007	1.00	0.00
ATOM	1244	O	TYR A 598	-2.830	1.205	-13.499	1.00	0.00
ATOM	1245	CB	TYR A 598	-4.094	0.568	-16.422	1.00	0.00
ATOM	1246	CG	TYR A 598	-3.326	1.843	-16.414	1.00	0.00
ATOM	1247	CD1	TYR A 598	-2.013	1.869	-16.821	1.00	0.00
ATOM	1248	CD2	TYR A 598	-3.932	3.021	-16.038	1.00	0.00
ATOM	1249	CE1	TYR A 598	-1.307	3.047	-16.831	1.00	0.00
ATOM	1250	CE2	TYR A 598	-3.231	4.204	-16.048	1.00	0.00
ATOM	1251	CZ	TYR A 598	-1.914	4.216	-16.440	1.00	0.00
ATOM	1252	OH	TYR A 598	-1.187	5.426	-16.448	1.00	0.00
ATOM	1253	HN	TYR A 598	-5.138	-1.650	-15.736	1.00	0.00
ATOM	1254	HA	TYR A 598	-2.624	-0.488	-15.217	1.00	0.00
ATOM	1255	1HB	TYR A 598	-5.162	0.784	-16.403	1.00	0.00
ATOM	1256	2HB	TYR A 598	-3.864	0.008	-17.328	1.00	0.00
ATOM	1257	HD1	TYR A 598	-1.532	0.954	-17.137	1.00	0.00
ATOM	1258	HE1	TYR A 598	-0.274	3.055	-17.146	1.00	0.00
ATOM	1259	HD2	TYR A 598	-4.968	3.015	-15.733	1.00	0.00
ATOM	1260	HE2	TYR A 598	-3.715	5.122	-15.749	1.00	0.00
ATOM	1261	HH	TYR A 598	-1.413	5.935	-15.680	1.00	0.00
ATOM	1262	N	SER A 599	-5.066	0.937	-13.524	1.00	0.00
ATOM	1263	CA	SER A 599	-5.201	1.987	-12.548	1.00	0.00
ATOM	1264	C	SER A 599	-5.623	1.487	-11.203	1.00	0.00
ATOM	1265	O	SER A 599	-6.170	2.237	-10.397	1.00	0.00
ATOM	1266	CB	SER A 599	-6.228	3.049	-13.002	1.00	0.00
ATOM	1267	OG	SER A 599	-6.261	4.154	-12.109	1.00	0.00
ATOM	1268	HN	SER A 599	-5.856	0.407	-13.831	1.00	0.00
ATOM	1269	HA	SER A 599	-4.216	2.438	-12.425	1.00	0.00
ATOM	1270	1HB	SER A 599	-7.227	2.613	-13.032	1.00	0.00
ATOM	1271	2HB	SER A 599	-5.964	3.424	-13.991	1.00	0.00
ATOM	1272	HG	SER A 599	-7.009	4.682	-12.355	1.00	0.00
ATOM	1273	N	TRP A 600	-5.374	0.197	-10.930	1.00	0.00

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ATOM 1274 CA TRP A 600	-5.750	-0.339	-9.618	1.00	0.00
ATOM 1275 C TRP A 600	-5.235	0.537	-8.454	1.00	0.00
ATOM 1276 O TRP A 600	-5.982	0.998	-7.602	1.00	0.00
ATOM 1277 CB TRP A 600	-5.158	-1.745	-9.508	1.00	0.00
ATOM 1278 CG TRP A 600	-5.055	-2.226	-8.069	1.00	0.00
ATOM 1279 CD1 TRP A 600	-3.885	-2.666	-7.450	1.00	0.00
ATOM 1280 CD2 TRP A 600	-6.086	-2.286	-7.065	1.00	0.00
ATOM 1281 NE1 TRP A 600	-4.138	-2.989	-6.162	1.00	0.00
ATOM 1282 CE2 TRP A 600	-5.478	-2.771	-5.881	1.00	0.00
ATOM 1283 CE3 TRP A 600	-7.415	-1.962	-7.073	1.00	0.00
ATOM 1284 CZ2 TRP A 600	-6.220	-2.924	-4.744	1.00	0.00
ATOM 1285 CZ3 TRP A 600	-8.169	-2.109	-5.914	1.00	0.00
ATOM 1286 CH2 TRP A 600	-7.572	-2.594	-4.754	1.00	0.00
ATOM 1287 HN TRP A 600	-5.041	-0.407	-11.658	1.00	0.00
ATOM 1288 HA TRP A 600	-6.840	-0.362	-9.586	1.00	0.00
ATOM 1289 1HB TRP A 600	-4.152	-1.676	-9.917	1.00	0.00
ATOM 1290 2HB TRP A 600	-5.714	-2.461	-10.115	1.00	0.00
ATOM 1291 HE3 TRP A 600	-7.881	-1.589	-7.972	1.00	0.00
ATOM 1292 HD1 TRP A 600	-2.918	-2.729	-7.926	1.00	0.00
ATOM 1293 HE1 TRP A 600	-3.470	-3.318	-5.525	1.00	0.00
ATOM 1294 HZ2 TRP A 600	-5.762	-3.299	-3.842	1.00	0.00
ATOM 1295 HZ3 TRP A 600	-9.212	-1.838	-5.907	1.00	0.00
ATOM 1296 HH2 TRP A 600	-8.161	-2.715	-3.864	1.00	0.00
ATOM 1297 N MET A 601	-3.903	0.714	-8.453	1.00	0.00
ATOM 1298 CA MET A 601	-3.290	1.376	-7.306	1.00	0.00
ATOM 1299 C MET A 601	-3.711	2.849	-7.232	1.00	0.00
ATOM 1300 O MET A 601	-3.783	3.435	-6.160	1.00	0.00
ATOM 1301 CB MET A 601	-1.761	1.224	-7.356	1.00	0.00
ATOM 1302 CG MET A 601	-1.317	-0.233	-7.166	1.00	0.00
ATOM 1303 SD MET A 601	-1.813	-0.871	-5.552	1.00	0.00
ATOM 1304 CE MET A 601	-0.700	-2.284	-5.450	1.00	0.00
ATOM 1305 HN MET A 601	-3.367	0.312	-9.194	1.00	0.00
ATOM 1306 HA MET A 601	-3.678	0.887	-6.410	1.00	0.00
ATOM 1307 1HB MET A 601	-1.305	1.830	-6.572	1.00	0.00
ATOM 1308 2HB MET A 601	-1.377	1.612	-8.300	1.00	0.00
ATOM 1309 1HG MET A 601	-0.235	-0.297	-7.234	1.00	0.00
ATOM 1310 2HG MET A 601	-1.700	-0.874	-7.957	1.00	0.00
ATOM 1311 1HE MET A 601	-1.012	-3.065	-6.143	1.00	0.00
ATOM 1312 2HE MET A 601	-0.682	-2.677	-4.433	1.00	0.00
ATOM 1313 3HE MET A 601	0.315	-1.986	-5.713	1.00	0.00
ATOM 1314 N PHE A 602	-4.012	3.399	-8.430	1.00	0.00
ATOM 1315 CA PHE A 602	-4.329	4.792	-8.552	1.00	0.00
ATOM 1316 C PHE A 602	-5.642	4.922	-7.841	1.00	0.00
ATOM 1317 O PHE A 602	-5.808	5.741	-6.936	1.00	0.00
ATOM 1318 CB PHE A 602	-4.600	5.152	-10.026	1.00	0.00
ATOM 1319 CG PHE A 602	-4.341	6.595	-10.299	1.00	0.00
ATOM 1320 CD1 PHE A 602	-3.197	6.950	-10.976	1.00	0.00
ATOM 1321 CD2 PHE A 602	-5.191	7.584	-9.864	1.00	0.00
ATOM 1322 CE1 PHE A 602	-2.935	8.262	-11.292	1.00	0.00

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ATOM	1323	CE2 PHE A 602	-4.909	8.902	-10.141	1.00	0.00
ATOM	1324	CZ PHE A 602	-3.804	9.242	-10.885	1.00	0.00
ATOM	1325	HN PHE A 602	-3.876	2.850	-9.254	1.00	0.00
ATOM	1326	HA PHE A 602	-3.478	5.353	-8.169	1.00	0.00
ATOM	1327	1HB PHE A 602	-5.640	4.934	-10.269	1.00	0.00
ATOM	1328	2HB PHE A 602	-3.955	4.556	-10.671	1.00	0.00
ATOM	1329	HD1 PHE A 602	-2.492	6.184	-11.265	1.00	0.00
ATOM	1330	HD2 PHE A 602	-6.079	7.328	-9.306	1.00	0.00
ATOM	1331	HE1 PHE A 602	-2.051	8.519	-11.857	1.00	0.00
ATOM	1332	HE2 PHE A 602	-5.562	9.677	-9.769	1.00	0.00
ATOM	1333	HZ PHE A 602	-3.622	10.274	-11.148	1.00	0.00
ATOM	1334	N LEU A 603	-6.582	4.031	-8.209	1.00	0.00
ATOM	1335	CA LEU A 603	-7.919	3.980	-7.692	1.00	0.00
ATOM	1336	C LEU A 603	-7.888	3.784	-6.209	1.00	0.00
ATOM	1337	O LEU A 603	-8.534	4.518	-5.462	1.00	0.00
ATOM	1338	CB LEU A 603	-8.662	2.763	-8.271	1.00	0.00
ATOM	1339	CG LEU A 603	-10.109	2.593	-7.789	1.00	0.00
ATOM	1340	CD1 LEU A 603	-11.000	3.712	-8.331	1.00	0.00
ATOM	1341	CD2 LEU A 603	-10.648	1.191	-8.117	1.00	0.00
ATOM	1342	HN LEU A 603	-6.327	3.352	-8.896	1.00	0.00
ATOM	1343	HA LEU A 603	-8.414	4.907	-7.979	1.00	0.00
ATOM	1344	1HB LEU A 603	-8.106	1.865	-8.005	1.00	0.00
ATOM	1345	2HB LEU A 603	-8.671	2.852	-9.356	1.00	0.00
ATOM	1346	HG LEU A 603	-10.132	2.607	-6.700	1.00	0.00
ATOM	1347	1HD1 LEU A 603	-10.542	4.183	-9.200	1.00	0.00
ATOM	1348	2HD1 LEU A 603	-11.146	4.478	-7.570	1.00	0.00
ATOM	1349	3HD1 LEU A 603	-11.966	3.310	-8.635	1.00	0.00
ATOM	1350	1HD2 LEU A 603	-10.043	0.423	-7.635	1.00	0.00
ATOM	1351	2HD2 LEU A 603	-10.618	1.018	-9.193	1.00	0.00
ATOM	1352	3HD2 LEU A 603	-11.672	1.088	-7.759	1.00	0.00
ATOM	1353	N MET A 604	-7.108	2.801	-5.735	1.00	0.00
ATOM	1354	CA MET A 604	-7.162	2.563	-4.295	1.00	0.00
ATOM	1355	C MET A 604	-6.553	3.736	-3.494	1.00	0.00
ATOM	1356	O MET A 604	-6.989	4.068	-2.394	1.00	0.00
ATOM	1357	CB MET A 604	-6.551	1.197	-3.954	1.00	0.00
ATOM	1358	CG MET A 604	-7.377	0.461	-2.891	1.00	0.00
ATOM	1359	SD MET A 604	-9.047	0.097	-3.483	1.00	0.00
ATOM	1360	CE MET A 604	-10.010	1.373	-2.647	1.00	0.00
ATOM	1361	HN MET A 604	-6.591	2.225	-6.370	1.00	0.00
ATOM	1362	HA MET A 604	-8.222	2.547	-4.050	1.00	0.00
ATOM	1363	1HB MET A 604	-5.513	1.302	-3.633	1.00	0.00
ATOM	1364	2HB MET A 604	-6.522	0.572	-4.849	1.00	0.00
ATOM	1365	1HG MET A 604	-7.413	1.016	-1.954	1.00	0.00
ATOM	1366	2HG MET A 604	-6.900	-0.491	-2.669	1.00	0.00
ATOM	1367	1HE MET A 604	-10.288	2.160	-3.348	1.00	0.00
ATOM	1368	2HE MET A 604	-9.473	1.797	-1.800	1.00	0.00
ATOM	1369	3HE MET A 604	-10.936	0.941	-2.272	1.00	0.00
ATOM	1370	N ALA A 605	-5.545	4.363	-4.137	1.00	0.00
ATOM	1371	CA ALA A 605	-4.874	5.506	-3.532	1.00	0.00

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ATOM	1372	C	ALA A 605	-5.827	6.702	-3.362	1.00	0.00
ATOM	1373	O	ALA A 605	-5.878	7.310	-2.299	1.00	0.00
ATOM	1374	CB	ALA A 605	-3.646	5.903	-4.361	1.00	0.00
ATOM	1375	HN	ALA A 605	-5.229	4.030	-5.030	1.00	0.00
ATOM	1376	HA	ALA A 605	-4.552	5.187	-2.539	1.00	0.00
ATOM	1377	1HB	ALA A 605	-3.118	6.743	-3.908	1.00	0.00
ATOM	1378	2HB	ALA A 605	-3.918	6.189	-5.378	1.00	0.00
ATOM	1379	3HB	ALA A 605	-2.940	5.075	-4.429	1.00	0.00
ATOM	1380	N	PHE A 606	-6.591	7.014	-4.438	1.00	0.00
ATOM	1381	CA	PHE A 606	-7.447	8.165	-4.365	1.00	0.00
ATOM	1382	C	PHE A 606	-8.499	7.924	-3.332	1.00	0.00
ATOM	1383	O	PHE A 606	-8.914	8.843	-2.626	1.00	0.00
ATOM	1384	CB	PHE A 606	-8.128	8.482	-5.709	1.00	0.00
ATOM	1385	CG	PHE A 606	-8.764	9.826	-5.599	1.00	0.00
ATOM	1386	CD1	PHE A 606	-7.983	10.937	-5.380	1.00	0.00
ATOM	1387	CD2	PHE A 606	-10.075	10.011	-5.972	1.00	0.00
ATOM	1388	CE1	PHE A 606	-8.527	12.200	-5.390	1.00	0.00
ATOM	1389	CE2	PHE A 606	-10.612	11.275	-6.033	1.00	0.00
ATOM	1390	CZ	PHE A 606	-9.853	12.370	-5.702	1.00	0.00
ATOM	1391	HN	PHE A 606	-6.547	6.469	-5.275	1.00	0.00
ATOM	1392	HA	PHE A 606	-6.822	9.002	-4.055	1.00	0.00
ATOM	1393	1HB	PHE A 606	-8.890	7.736	-5.934	1.00	0.00
ATOM	1394	2HB	PHE A 606	-7.395	8.490	-6.515	1.00	0.00
ATOM	1395	HD1	PHE A 606	-6.926	10.816	-5.196	1.00	0.00
ATOM	1396	HD2	PHE A 606	-10.687	9.156	-6.219	1.00	0.00
ATOM	1397	HE1	PHE A 606	-7.912	13.056	-5.154	1.00	0.00
ATOM	1398	HE2	PHE A 606	-11.638	11.408	-6.342	1.00	0.00
ATOM	1399	HZ	PHE A 606	-10.295	13.356	-5.687	1.00	0.00
ATOM	1400	N	ALA A 607	-8.951	6.658	-3.251	1.00	0.00
ATOM	1401	CA	ALA A 607	-9.986	6.362	-2.267	1.00	0.00
ATOM	1402	C	ALA A 607	-9.485	6.561	-0.843	1.00	0.00
ATOM	1403	O	ALA A 607	-10.155	7.114	0.022	1.00	0.00
ATOM	1404	CB	ALA A 607	-10.490	4.929	-2.480	1.00	0.00
ATOM	1405	HN	ALA A 607	-8.636	5.964	-3.904	1.00	0.00
ATOM	1406	HA	ALA A 607	-10.759	7.108	-2.388	1.00	0.00
ATOM	1407	1HB	ALA A 607	-9.697	4.201	-2.307	1.00	0.00
ATOM	1408	2HB	ALA A 607	-10.839	4.790	-3.503	1.00	0.00
ATOM	1409	3HB	ALA A 607	-11.318	4.698	-1.809	1.00	0.00
ATOM	1410	N	LEU A 608	-8.251	6.069	-0.661	1.00	0.00
ATOM	1411	CA	LEU A 608	-7.589	6.185	0.626	1.00	0.00
ATOM	1412	C	LEU A 608	-7.499	7.666	1.051	1.00	0.00
ATOM	1413	O	LEU A 608	-7.854	8.037	2.161	1.00	0.00
ATOM	1414	CB	LEU A 608	-6.231	5.473	0.480	1.00	0.00
ATOM	1415	CG	LEU A 608	-5.341	5.404	1.730	1.00	0.00
ATOM	1416	CD1	LEU A 608	-4.488	6.666	1.889	1.00	0.00
ATOM	1417	CD2	LEU A 608	-6.131	5.062	3.000	1.00	0.00
ATOM	1418	HN	LEU A 608	-7.785	5.630	-1.434	1.00	0.00
ATOM	1419	HA	LEU A 608	-8.219	5.663	1.348	1.00	0.00
ATOM	1420	1HB	LEU A 608	-5.662	5.906	-0.342	1.00	0.00

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ATOM	1421	2HB	LEU	A	608	-6.446	4.453	0.166	1.00	0.00
ATOM	1422	HG	LEU	A	608	-4.638	4.586	1.562	1.00	0.00
ATOM	1423	1HD1	LEU	A	608	-3.936	6.889	0.977	1.00	0.00
ATOM	1424	2HD1	LEU	A	608	-3.758	6.534	2.684	1.00	0.00
ATOM	1425	3HD1	LEU	A	608	-5.087	7.542	2.119	1.00	0.00
ATOM	1426	1HD2	LEU	A	608	-5.464	4.811	3.825	1.00	0.00
ATOM	1427	2HD2	LEU	A	608	-6.776	4.201	2.829	1.00	0.00
ATOM	1428	3HD2	LEU	A	608	-6.760	5.891	3.325	1.00	0.00
ATOM	1429	N	GLY	A	609	-7.042	8.497	0.093	1.00	0.00
ATOM	1430	CA	GLY	A	609	-6.823	9.887	0.364	1.00	0.00
ATOM	1431	C	GLY	A	609	-8.130	10.530	0.702	1.00	0.00
ATOM	1432	O	GLY	A	609	-8.225	11.332	1.631	1.00	0.00
ATOM	1433	HN	GLY	A	609	-6.813	8.122	-0.806	1.00	0.00
ATOM	1434	IHA	GLY	A	609	-6.401	10.344	-0.530	1.00	0.00
ATOM	1435	2HA	GLY	A	609	-6.138	9.963	1.208	1.00	0.00
ATOM	1436	N	TRP	A	610	-9.180	10.177	-0.058	1.00	0.00
ATOM	1437	CA	TRP	A	610	-10.495	10.719	0.121	1.00	0.00
ATOM	1438	C	TRP	A	610	-11.037	10.406	1.478	1.00	0.00
ATOM	1439	O	TRP	A	610	-11.582	11.277	2.154	1.00	0.00
ATOM	1440	CB	TRP	A	610	-11.473	10.139	-0.913	1.00	0.00
ATOM	1441	CG	TRP	A	610	-12.929	10.398	-0.623	1.00	0.00
ATOM	1442	CD1	TRP	A	610	-13.862	9.539	-0.122	1.00	0.00
ATOM	1443	CD2	TRP	A	610	-13.576	11.671	-0.753	1.00	0.00
ATOM	1444	NE1	TRP	A	610	-15.063	10.187	0.033	1.00	0.00
ATOM	1445	CE2	TRP	A	610	-14.899	11.503	-0.345	1.00	0.00
ATOM	1446	CE3	TRP	A	610	-13.106	12.882	-1.173	1.00	0.00
ATOM	1447	CZ2	TRP	A	610	-15.777	12.548	-0.356	1.00	0.00
ATOM	1448	CZ3	TRP	A	610	-13.993	13.934	-1.180	1.00	0.00
ATOM	1449	CH2	TRP	A	610	-15.303	13.769	-0.781	1.00	0.00
ATOM	1450	HN	TRP	A	610	-9.037	9.503	-0.783	1.00	0.00
ATOM	1451	HA	TRP	A	610	-10.415	11.800	0.008	1.00	0.00
ATOM	1452	1HB	TRP	A	610	-11.331	9.060	-0.961	1.00	0.00
ATOM	1453	2HB	TRP	A	610	-11.246	10.569	-1.887	1.00	0.00
ATOM	1454	HE3	TRP	A	610	-12.080	13.008	-1.487	1.00	0.00
ATOM	1455	HD1	TRP	A	610	-13.682	8.502	0.119	1.00	0.00
ATOM	1456	HE1	TRP	A	610	-15.894	9.783	0.357	1.00	0.00
ATOM	1457	HZ2	TRP	A	610	-16.803	12.422	-0.044	1.00	0.00
ATOM	1458	HZ3	TRP	A	610	-13.657	14.907	-1.504	1.00	0.00
ATOM	1459	HH2	TRP	A	610	-15.971	14.617	-0.802	1.00	0.00
ATOM	1460	N	ARG	A	611	-10.908	9.137	1.904	1.00	0.00
ATOM	1461	CA	ARG	A	611	-11.485	8.823	3.212	1.00	0.00
ATOM	1462	C	ARG	A	611	-10.630	9.382	4.363	1.00	0.00
ATOM	1463	O	ARG	A	611	-11.108	9.620	5.463	1.00	0.00
ATOM	1464	CB	ARG	A	611	-11.704	7.323	3.367	1.00	0.00
ATOM	1465	CG	ARG	A	611	-12.850	6.806	2.484	1.00	0.00
ATOM	1466	CD	ARG	A	611	-13.346	5.416	2.901	1.00	0.00
ATOM	1467	NE	ARG	A	611	-12.276	4.442	2.750	1.00	0.00
ATOM	1468	CZ	ARG	A	611	-11.360	4.161	3.704	1.00	0.00
ATOM	1469	NH1	ARG	A	611	-11.429	4.663	4.939	1.00	0.00

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ATOM 1470 NH2 ARG A 611	-10.349	3.373	3.370	1.00	0.00
ATOM 1471 HN ARG A 611	-10.461	8.449	1.327	1.00	0.00
ATOM 1472 HA ARG A 611	-12.458	9.315	3.274	1.00	0.00
ATOM 1473 IHB ARG A 611	-11.960	7.134	4.408	1.00	0.00
ATOM 1474 2HB ARG A 611	-10.775	6.791	3.162	1.00	0.00
ATOM 1475 IHG ARG A 611	-12.533	6.795	1.440	1.00	0.00
ATOM 1476 2HG ARG A 611	-13.693	7.495	2.541	1.00	0.00
ATOM 1477 1HD ARG A 611	-14.154	5.084	2.248	1.00	0.00
ATOM 1478 2HD ARG A 611	-13.724	5.389	3.923	1.00	0.00
ATOM 1479 HE ARG A 611	-12.203	4.016	1.848	1.00	0.00
ATOM 1480 1HH1 ARG A 611	-12.239	5.161	5.293	1.00	0.00
ATOM 1481 2HH1 ARG A 611	-10.631	4.578	5.546	1.00	0.00
ATOM 1482 1HH2 ARG A 611	-9.738	2.982	4.066	1.00	0.00
ATOM 1483 2HH2 ARG A 611	-10.158	3.134	2.412	1.00	0.00
ATOM 1484 N SER A 612	-9.356	9.624	4.043	1.00	0.00
ATOM 1485 CA SER A 612	-8.434	10.203	4.984	1.00	0.00
ATOM 1486 C SER A 612	-8.651	11.664	5.221	1.00	0.00
ATOM 1487 O SER A 612	-8.081	12.237	6.147	1.00	0.00
ATOM 1488 CB SER A 612	-6.965	10.024	4.572	1.00	0.00
ATOM 1489 OG SER A 612	-6.605	8.656	4.662	1.00	0.00
ATOM 1490 HN SER A 612	-9.005	9.410	3.133	1.00	0.00
ATOM 1491 HA SER A 612	-8.617	9.712	5.940	1.00	0.00
ATOM 1492 IHB SER A 612	-6.313	10.595	5.233	1.00	0.00
ATOM 1493 2HB SER A 612	-6.817	10.351	3.543	1.00	0.00
ATOM 1494 HG SER A 612	-5.753	8.571	4.254	1.00	0.00
ATOM 1495 N TYR A 613	-9.470	12.302	4.372	1.00	0.00
ATOM 1496 CA TYR A 613	-9.629	13.727	4.326	1.00	0.00
ATOM 1497 C TYR A 613	-9.847	14.349	5.675	1.00	0.00
ATOM 1498 O TYR A 613	-9.040	15.171	6.102	1.00	0.00
ATOM 1499 CB TYR A 613	-10.852	14.052	3.449	1.00	0.00
ATOM 1500 CG TYR A 613	-10.984	15.506	3.166	1.00	0.00
ATOM 1501 CD1 TYR A 613	-11.417	16.382	4.134	1.00	0.00
ATOM 1502 CD2 TYR A 613	-10.952	15.928	1.857	1.00	0.00
ATOM 1503 CE1 TYR A 613	-11.756	17.674	3.804	1.00	0.00
ATOM 1504 CE2 TYR A 613	-11.302	17.211	1.518	1.00	0.00
ATOM 1505 CZ TYR A 613	-11.707	18.087	2.494	1.00	0.00
ATOM 1506 OH TYR A 613	-12.108	19.393	2.145	1.00	0.00
ATOM 1507 HN TYR A 613	-10.002	11.750	3.732	1.00	0.00
ATOM 1508 HA TYR A 613	-8.718	14.150	3.903	1.00	0.00
ATOM 1509 IHB TYR A 613	-11.757	13.718	3.955	1.00	0.00
ATOM 1510 2HB TYR A 613	-10.763	13.525	2.499	1.00	0.00
ATOM 1511 HD1 TYR A 613	-11.492	16.053	5.160	1.00	0.00
ATOM 1512 HE1 TYR A 613	-12.060	18.366	4.576	1.00	0.00
ATOM 1513 HD2 TYR A 613	-10.647	15.238	1.084	1.00	0.00
ATOM 1514 HE2 TYR A 613	-11.260	17.530	0.487	1.00	0.00
ATOM 1515 HH TYR A 613	-11.566	20.023	2.601	1.00	0.00
ATOM 1516 N ARG A 614	-10.901	13.979	6.422	1.00	0.00
ATOM 1517 CA ARG A 614	-11.083	14.637	7.689	1.00	0.00
ATOM 1518 C ARG A 614	-10.061	14.304	8.732	1.00	0.00

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ATOM	1519	O	ARG A 614	-9.739	15.139	9.577	1.00	0.00
ATOM	1520	CB	ARG A 614	-12.507	14.538	8.277	1.00	0.00
ATOM	1521	CG	ARG A 614	-13.137	13.148	8.278	1.00	0.00
ATOM	1522	CD	ARG A 614	-12.266	12.021	8.819	1.00	0.00
ATOM	1523	NE	ARG A 614	-13.095	10.787	8.732	1.00	0.00
ATOM	1524	CZ	ARG A 614	-13.441	10.285	7.509	1.00	0.00
ATOM	1525	NH1	ARG A 614	-13.181	11.003	6.378	1.00	0.00
ATOM	1526	NH2	ARG A 614	-14.083	9.085	7.418	1.00	0.00
ATOM	1527	HN	ARG A 614	-11.535	13.273	6.108	1.00	0.00
ATOM	1528	HA	ARG A 614	-10.827	15.683	7.525	1.00	0.00
ATOM	1529	1HB	ARG A 614	-13.154	15.201	7.705	1.00	0.00
ATOM	1530	2HB	ARG A 614	-12.472	14.894	9.305	1.00	0.00
ATOM	1531	1HG	ARG A 614	-13.411	12.900	7.255	1.00	0.00
ATOM	1532	2HG	ARG A 614	-14.045	13.190	8.878	1.00	0.00
ATOM	1533	1HD	ARG A 614	-11.998	12.183	9.862	1.00	0.00
ATOM	1534	2HD	ARG A 614	-11.371	11.878	8.215	1.00	0.00
ATOM	1535	HE	ARG A 614	-13.400	10.327	9.566	1.00	0.00
ATOM	1536	1HH1	ARG A 614	-12.608	11.822	6.425	1.00	0.00
ATOM	1537	2HH1	ARG A 614	-13.563	10.711	5.501	1.00	0.00
ATOM	1538	1HH2	ARG A 614	-14.302	8.571	8.247	1.00	0.00
ATOM	1539	2HH2	ARG A 614	-14.335	8.719	6.522	1.00	0.00
ATOM	1540	N	GLN A 615	-9.518	13.078	8.712	1.00	0.00
ATOM	1541	CA	GLN A 615	-8.577	12.675	9.719	1.00	0.00
ATOM	1542	C	GLN A 615	-7.221	13.187	9.341	1.00	0.00
ATOM	1543	O	GLN A 615	-6.452	12.503	8.664	1.00	0.00
ATOM	1544	CB	GLN A 615	-8.505	11.148	9.800	1.00	0.00
ATOM	1545	CG	GLN A 615	-9.842	10.488	10.155	1.00	0.00
ATOM	1546	CD	GLN A 615	-10.217	10.878	11.579	1.00	0.00
ATOM	1547	OE1	GLN A 615	-9.475	11.575	12.269	1.00	0.00
ATOM	1548	NE2	GLN A 615	-11.411	10.413	12.035	1.00	0.00
ATOM	1549	HN	GLN A 615	-9.771	12.437	7.987	1.00	0.00
ATOM	1550	HA	GLN A 615	-8.916	13.095	10.666	1.00	0.00
ATOM	1551	1HB	GLN A 615	-7.768	10.872	10.553	1.00	0.00
ATOM	1552	2HB	GLN A 615	-8.171	10.763	8.837	1.00	0.00
ATOM	1553	1HG	GLN A 615	-9.759	9.403	10.093	1.00	0.00
ATOM	1554	2HG	GLN A 615	-10.624	10.826	9.475	1.00	0.00
ATOM	1555	1HE2	GLN A 615	-11.913	9.731	11.502	1.00	0.00
ATOM	1556	2HE2	GLN A 615	-11.800	10.740	12.895	1.00	0.00
ATOM	1557	N	SER A 616	-6.865	14.393	9.825	1.00	0.00
ATOM	1558	CA	SER A 616	-5.661	15.027	9.371	1.00	0.00
ATOM	1559	C	SER A 616	-4.431	14.879	10.213	1.00	0.00
ATOM	1560	O	SER A 616	-4.477	14.649	11.421	1.00	0.00
ATOM	1561	CB	SER A 616	-5.840	16.541	9.163	1.00	0.00
ATOM	1562	OG	SER A 616	-4.622	17.122	8.721	1.00	0.00
ATOM	1563	HN	SER A 616	-7.443	14.848	10.504	1.00	0.00
ATOM	1564	HA	SER A 616	-5.388	14.547	8.432	1.00	0.00
ATOM	1565	1HB	SER A 616	-6.127	17.020	10.099	1.00	0.00
ATOM	1566	2HB	SER A 616	-6.603	16.731	8.407	1.00	0.00
ATOM	1567	HG	SER A 616	-4.480	16.816	7.835	1.00	0.00

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ATOM 1568 N SER A 617	-3.286	14.953	9.504	1.00	0.00
ATOM 1569 CA SER A 617	-1.945	15.132	9.987	1.00	0.00
ATOM 1570 C SER A 617	-1.302	14.020	10.728	1.00	0.00
ATOM 1571 O SER A 617	-0.091	13.825	10.625	1.00	0.00
ATOM 1572 CB SER A 617	-1.804	16.386	10.867	1.00	0.00
ATOM 1573 OG SER A 617	-2.536	16.222	12.072	1.00	0.00
ATOM 1574 HN SER A 617	-3.383	14.873	8.515	1.00	0.00
ATOM 1575 HA SER A 617	-1.303	15.212	9.110	1.00	0.00
ATOM 1576 1HB SER A 617	-2.195	17.260	10.346	1.00	0.00
ATOM 1577 2HB SER A 617	-0.757	16.553	11.123	1.00	0.00
ATOM 1578 HG SER A 617	-2.282	15.383	12.433	1.00	0.00
ATOM 1579 N ALA A 618	-2.055	13.181	11.440	1.00	0.00
ATOM 1580 CA ALA A 618	-1.297	12.170	12.109	1.00	0.00
ATOM 1581 C ALA A 618	-1.203	11.075	11.117	1.00	0.00
ATOM 1582 O ALA A 618	-1.451	9.937	11.510	1.00	0.00
ATOM 1583 CB ALA A 618	-2.014	11.587	13.336	1.00	0.00
ATOM 1584 HN ALA A 618	-3.048	13.253	11.500	1.00	0.00
ATOM 1585 HA ALA A 618	-0.359	12.634	12.411	1.00	0.00
ATOM 1586 1HB ALA A 618	-2.962	11.133	13.049	1.00	0.00
ATOM 1587 2HB ALA A 618	-2.222	12.375	14.060	1.00	0.00
ATOM 1588 3HB ALA A 618	-1.398	10.816	13.800	1.00	0.00
ATOM 1589 N ASN A 619	-0.796	11.421	9.859	1.00	0.00
ATOM 1590 CA ASN A 619	-0.825	10.611	8.670	1.00	0.00
ATOM 1591 C ASN A 619	-2.027	9.830	8.892	1.00	0.00
ATOM 1592 O ASN A 619	-1.981	8.604	8.928	1.00	0.00
ATOM 1593 CB ASN A 619	0.358	9.664	8.464	1.00	0.00
ATOM 1594 CG ASN A 619	0.176	8.729	7.272	1.00	0.00
ATOM 1595 OD1 ASN A 619	0.496	7.545	7.372	1.00	0.00
ATOM 1596 ND2 ASN A 619	-0.308	9.261	6.121	1.00	0.00
ATOM 1597 HN ASN A 619	-0.437	12.346	9.753	1.00	0.00
ATOM 1598 HA ASN A 619	-0.872	11.312	7.837	1.00	0.00
ATOM 1599 1HB ASN A 619	0.487	9.051	9.355	1.00	0.00
ATOM 1600 2HB ASN A 619	1.262	10.248	8.298	1.00	0.00
ATOM 1601 1HD2 ASN A 619	-0.165	8.782	5.255	1.00	0.00
ATOM 1602 2HD2 ASN A 619	-0.808	10.126	6.121	1.00	0.00
ATOM 1603 N LEU A 620	-3.132	10.545	9.137	1.00	0.00
ATOM 1604 CA LEU A 620	-4.225	9.747	9.520	1.00	0.00
ATOM 1605 C LEU A 620	-4.730	9.261	8.225	1.00	0.00
ATOM 1606 O LEU A 620	-5.412	9.965	7.478	1.00	0.00
ATOM 1607 CB LEU A 620	-5.288	10.498	10.341	1.00	0.00
ATOM 1608 CG LEU A 620	-6.190	9.548	11.155	1.00	0.00
ATOM 1609 CD1 LEU A 620	-7.024	10.322	12.191	1.00	0.00
ATOM 1610 CD2 LEU A 620	-7.029	8.637	10.242	1.00	0.00
ATOM 1611 HN LEU A 620	-3.174	11.538	9.056	1.00	0.00
ATOM 1612 HA LEU A 620	-3.815	8.927	10.108	1.00	0.00
ATOM 1613 1HB LEU A 620	-5.910	11.082	9.664	1.00	0.00
ATOM 1614 2HB LEU A 620	-4.789	11.183	11.024	1.00	0.00
ATOM 1615 HG LEU A 620	-5.570	8.814	11.667	1.00	0.00
ATOM 1616 1HD1 LEU A 620	-6.943	11.397	12.025	1.00	0.00

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ATOM	1617	2HD1 LEU A 620	-6.666	10.109	13.198	1.00	0.00
ATOM	1618	3HD1 LEU A 620	-8.075	10.047	12.110	1.00	0.00
ATOM	1619	1HD2 LEU A 620	-6.433	7.798	9.883	1.00	0.00
ATOM	1620	2HD2 LEU A 620	-7.383	9.195	9.376	1.00	0.00
ATOM	1621	3HD2 LEU A 620	-7.880	8.235	10.792	1.00	0.00
ATOM	1622	N LEU A 621	-4.250	8.020	7.935	1.00	0.00
ATOM	1623	CA LEU A 621	-4.711	7.307	6.773	1.00	0.00
ATOM	1624	C LEU A 621	-5.670	6.299	7.278	1.00	0.00
ATOM	1625	O LEU A 621	-5.333	5.304	7.915	1.00	0.00
ATOM	1626	CB LEU A 621	-3.721	6.649	5.792	1.00	0.00
ATOM	1627	CG LEU A 621	-2.520	7.497	5.409	1.00	0.00
ATOM	1628	CD1 LEU A 621	-1.471	6.654	4.663	1.00	0.00
ATOM	1629	CD2 LEU A 621	-2.900	8.754	4.603	1.00	0.00
ATOM	1630	HN LEU A 621	-3.596	7.614	8.584	1.00	0.00
ATOM	1631	HA LEU A 621	-5.268	8.045	6.264	1.00	0.00
ATOM	1632	1HB LEU A 621	-4.261	6.377	4.887	1.00	0.00
ATOM	1633	2HB LEU A 621	-3.363	5.699	6.173	1.00	0.00
ATOM	1634	HG LEU A 621	-2.110	7.785	6.370	1.00	0.00
ATOM	1635	1HD1 LEU A 621	-1.902	6.153	3.797	1.00	0.00
ATOM	1636	2HD1 LEU A 621	-1.059	5.885	5.317	1.00	0.00
ATOM	1637	3HD1 LEU A 621	-0.638	7.255	4.304	1.00	0.00
ATOM	1638	1HD2 LEU A 621	-3.553	9.411	5.177	1.00	0.00
ATOM	1639	2HD2 LEU A 621	-3.386	8.494	3.666	1.00	0.00
ATOM	1640	3HD2 LEU A 621	-2.029	9.340	4.318	1.00	0.00
ATOM	1641	N CYS A 622	-6.921	6.628	6.985	1.00	0.00
ATOM	1642	CA CYS A 622	-7.895	5.726	7.488	1.00	0.00
ATOM	1643	C CYS A 622	-7.990	4.641	6.469	1.00	0.00
ATOM	1644	O CYS A 622	-8.809	4.706	5.555	1.00	0.00
ATOM	1645	CB CYS A 622	-9.280	6.384	7.620	1.00	0.00
ATOM	1646	SG CYS A 622	-10.556	5.264	8.264	1.00	0.00
ATOM	1647	HN CYS A 622	-7.194	7.414	6.431	1.00	0.00
ATOM	1648	HA CYS A 622	-7.541	5.391	8.463	1.00	0.00
ATOM	1649	1HB CYS A 622	-9.601	6.735	6.640	1.00	0.00
ATOM	1650	2HB CYS A 622	-9.206	7.236	8.294	1.00	0.00
ATOM	1651	HG CYS A 622	-10.037	4.510	9.236	1.00	0.00
ATOM	1652	N PHE A 623	-7.120	3.616	6.603	1.00	0.00
ATOM	1653	CA PHE A 623	-7.232	2.532	5.627	1.00	0.00
ATOM	1654	C PHE A 623	-8.592	1.854	5.778	1.00	0.00
ATOM	1655	O PHE A 623	-9.217	1.491	4.790	1.00	0.00
ATOM	1656	CB PHE A 623	-6.106	1.494	5.696	1.00	0.00
ATOM	1657	CG PHE A 623	-4.839	1.984	5.052	1.00	0.00
ATOM	1658	CD1 PHE A 623	-3.876	2.685	5.771	1.00	0.00
ATOM	1659	CD2 PHE A 623	-4.619	1.727	3.704	1.00	0.00
ATOM	1660	CE1 PHE A 623	-2.708	3.107	5.147	1.00	0.00
ATOM	1661	CE2 PHE A 623	-3.457	2.152	3.080	1.00	0.00
ATOM	1662	CZ PHE A 623	-2.497	2.843	3.801	1.00	0.00
ATOM	1663	HN PHE A 623	-6.464	3.646	7.361	1.00	0.00
ATOM	1664	HA PHE A 623	-7.218	2.992	4.638	1.00	0.00
ATOM	1665	1HB PHE A 623	-6.416	0.606	5.143	1.00	0.00

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ATOM	1666	2HB	PHE	A	623	-5.923	1.144	6.704	1.00	0.00
ATOM	1667	HD1	PHE	A	623	-4.032	2.911	6.817	1.00	0.00
ATOM	1668	HD2	PHE	A	623	-5.362	1.190	3.135	1.00	0.00
ATOM	1669	HE1	PHE	A	623	-1.954	3.639	5.703	1.00	0.00
ATOM	1670	HE2	PHE	A	623	-3.306	1.942	2.035	1.00	0.00
ATOM	1671	HZ	PHE	A	623	-1.590	3.174	3.318	1.00	0.00
ATOM	1672	N	ALA	A	624	-9.041	1.779	7.044	1.00	0.00
ATOM	1673	CA	ALA	A	624	-10.350	1.267	7.317	1.00	0.00
ATOM	1674	C	ALA	A	624	-10.855	2.038	8.493	1.00	0.00
ATOM	1675	O	ALA	A	624	-10.065	2.613	9.241	1.00	0.00
ATOM	1676	CB	ALA	A	624	-10.355	-0.217	7.721	1.00	0.00
ATOM	1677	HN	ALA	A	624	-8.434	1.998	7.809	1.00	0.00
ATOM	1678	HA	ALA	A	624	-10.933	1.407	6.407	1.00	0.00
ATOM	1679	1HB	ALA	A	624	-10.609	-0.329	8.775	1.00	0.00
ATOM	1680	2HB	ALA	A	624	-9.368	-0.653	7.564	1.00	0.00
ATOM	1681	3HB	ALA	A	624	-11.094	-0.764	7.136	1.00	0.00
ATOM	1682	N	PRO	A	625	-12.151	2.098	8.664	1.00	0.00
ATOM	1683	CA	PRO	A	625	-12.727	2.784	9.789	1.00	0.00
ATOM	1684	C	PRO	A	625	-12.116	2.154	10.996	1.00	0.00
ATOM	1685	O	PRO	A	625	-11.963	2.805	12.029	1.00	0.00
ATOM	1686	CB	PRO	A	625	-14.224	2.503	9.706	1.00	0.00
ATOM	1687	CG	PRO	A	625	-14.283	1.125	9.020	1.00	0.00
ATOM	1688	CD	PRO	A	625	-13.055	1.114	8.094	1.00	0.00
ATOM	1689	1HD	PRO	A	625	-12.583	0.132	8.076	1.00	0.00
ATOM	1690	2HD	PRO	A	625	-13.327	1.393	7.076	1.00	0.00
ATOM	1691	HA	PRO	A	625	-12.524	3.853	9.724	1.00	0.00
ATOM	1692	1HB	PRO	A	625	-14.739	3.261	9.117	1.00	0.00
ATOM	1693	2HB	PRO	A	625	-14.679	2.473	10.696	1.00	0.00
ATOM	1694	1HG	PRO	A	625	-14.230	0.320	9.753	1.00	0.00
ATOM	1695	2HG	PRO	A	625	-15.205	1.009	8.452	1.00	0.00
ATOM	1696	N	ASP	A	626	-11.833	0.854	10.863	1.00	0.00
ATOM	1697	CA	ASP	A	626	-11.223	-0.014	11.814	1.00	0.00
ATOM	1698	C	ASP	A	626	-9.743	0.240	11.957	1.00	0.00
ATOM	1699	O	ASP	A	626	-9.180	0.039	13.029	1.00	0.00
ATOM	1700	CB	ASP	A	626	-11.465	-1.471	11.380	1.00	0.00
ATOM	1701	CG	ASP	A	626	-10.953	-2.418	12.437	1.00	0.00
ATOM	1702	OD1	ASP	A	626	-9.716	-2.411	12.662	1.00	0.00
ATOM	1703	OD2	ASP	A	626	-11.780	-3.159	13.032	1.00	0.00
ATOM	1704	HN	ASP	A	626	-12.081	0.441	9.989	1.00	0.00
ATOM	1705	HA	ASP	A	626	-11.677	0.186	12.785	1.00	0.00
ATOM	1706	1HB	ASP	A	626	-10.944	-1.674	10.445	1.00	0.00
ATOM	1707	2HB	ASP	A	626	-12.532	-1.647	11.239	1.00	0.00
ATOM	1708	N	LEU	A	627	-9.066	0.665	10.865	1.00	0.00
ATOM	1709	CA	LEU	A	627	-7.633	0.818	10.880	1.00	0.00
ATOM	1710	C	LEU	A	627	-7.271	2.255	10.627	1.00	0.00
ATOM	1711	O	LEU	A	627	-7.550	2.793	9.558	1.00	0.00
ATOM	1712	CB	LEU	A	627	-7.009	-0.060	9.768	1.00	0.00
ATOM	1713	CG	LEU	A	627	-5.475	-0.052	9.587	1.00	0.00
ATOM	1714	CD1	LEU	A	627	-4.957	1.295	9.077	1.00	0.00

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ATOM	1715	CD2 LEU A 627	-4.745	-0.561	10.841	1.00	0.00
ATOM	1716	HN LEU A 627	-9.573	0.878	10.029	1.00	0.00
ATOM	1717	HA LEU A 627	-7.280	0.508	11.864	1.00	0.00
ATOM	1718	1HB LEU A 627	-7.448	0.254	8.824	1.00	0.00
ATOM	1719	2HB LEU A 627	-7.306	-1.088	9.963	1.00	0.00
ATOM	1720	HG LEU A 627	-5.197	-0.831	8.878	1.00	0.00
ATOM	1721	1HD1 LEU A 627	-4.551	1.887	9.897	1.00	0.00
ATOM	1722	2HD1 LEU A 627	-5.768	1.862	8.621	1.00	0.00
ATOM	1723	3HD1 LEU A 627	-4.163	1.140	8.347	1.00	0.00
ATOM	1724	1HD2 LEU A 627	-5.167	-1.509	11.174	1.00	0.00
ATOM	1725	2HD2 LEU A 627	-4.846	0.158	11.653	1.00	0.00
ATOM	1726	3HD2 LEU A 627	-3.689	-0.721	10.622	1.00	0.00
ATOM	1727	N ILE A 628	-6.627	2.909	11.619	1.00	0.00
ATOM	1728	CA ILE A 628	-6.196	4.272	11.489	1.00	0.00
ATOM	1729	C ILE A 628	-4.708	4.248	11.691	1.00	0.00
ATOM	1730	O ILE A 628	-4.206	3.906	12.759	1.00	0.00
ATOM	1731	CB ILE A 628	-6.840	5.162	12.519	1.00	0.00
ATOM	1732	CG1 ILE A 628	-6.414	6.624	12.342	1.00	0.00
ATOM	1733	CG2 ILE A 628	-6.587	4.587	13.923	1.00	0.00
ATOM	1734	CD1 ILE A 628	-7.235	7.570	13.214	1.00	0.00
ATOM	1735	HN ILE A 628	-6.445	2.426	12.474	1.00	0.00
ATOM	1736	HA ILE A 628	-6.467	4.596	10.485	1.00	0.00
ATOM	1737	HB ILE A 628	-7.912	5.225	12.334	1.00	0.00
ATOM	1738	1HG2 ILE A 628	-5.586	4.844	14.270	1.00	0.00
ATOM	1739	2HG2 ILE A 628	-6.669	3.500	13.904	1.00	0.00
ATOM	1740	3HG2 ILE A 628	-7.305	4.997	14.633	1.00	0.00
ATOM	1741	1HG1 ILE A 628	-6.534	6.906	11.297	1.00	0.00
ATOM	1742	2HG1 ILE A 628	-5.361	6.722	12.604	1.00	0.00
ATOM	1743	1HD1 ILE A 628	-7.708	7.028	14.033	1.00	0.00
ATOM	1744	2HD1 ILE A 628	-8.022	8.039	12.622	1.00	0.00
ATOM	1745	3HD1 ILE A 628	-6.593	8.338	13.644	1.00	0.00
ATOM	1746	N ILE A 629	-3.950	4.627	10.651	1.00	0.00
ATOM	1747	CA ILE A 629	-2.526	4.519	10.716	1.00	0.00
ATOM	1748	C ILE A 629	-2.067	5.921	10.908	1.00	0.00
ATOM	1749	O ILE A 629	-2.791	6.847	10.547	1.00	0.00
ATOM	1750	CB ILE A 629	-2.017	3.951	9.416	1.00	0.00
ATOM	1751	CG1 ILE A 629	-0.621	3.322	9.516	1.00	0.00
ATOM	1752	CG2 ILE A 629	-2.118	5.071	8.367	1.00	0.00
ATOM	1753	CD1 ILE A 629	0.507	4.329	9.632	1.00	0.00
ATOM	1754	HN ILE A 629	-4.384	4.987	9.826	1.00	0.00
ATOM	1755	HA ILE A 629	-2.282	3.862	11.551	1.00	0.00
ATOM	1756	HB ILE A 629	-2.617	3.092	9.115	1.00	0.00
ATOM	1757	1HG2 ILE A 629	-1.666	5.990	8.740	1.00	0.00
ATOM	1758	2HG2 ILE A 629	-3.164	5.279	8.139	1.00	0.00
ATOM	1759	3HG2 ILE A 629	-1.594	4.783	7.456	1.00	0.00
ATOM	1760	1HG1 ILE A 629	-0.451	2.712	8.629	1.00	0.00
ATOM	1761	2HG1 ILE A 629	-0.596	2.671	10.389	1.00	0.00
ATOM	1762	1HD1 ILE A 629	0.483	4.823	10.604	1.00	0.00
ATOM	1763	2HD1 ILE A 629	0.409	5.095	8.862	1.00	0.00

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ATOM 1764 3HD1 ILE A 629	1.470	3.829	9.532	1.00	0.00
ATOM 1765 N ASN A 630	-0.885	6.114	11.532	1.00	0.00
ATOM 1766 CA ASN A 630	-0.400	7.444	11.749	1.00	0.00
ATOM 1767 C ASN A 630	0.924	7.601	11.071	1.00	0.00
ATOM 1768 O ASN A 630	1.551	6.630	10.661	1.00	0.00
ATOM 1769 CB ASN A 630	-0.253	7.854	13.235	1.00	0.00
ATOM 1770 CG ASN A 630	0.838	7.047	13.930	1.00	0.00
ATOM 1771 OD1 ASN A 630	1.458	6.163	13.344	1.00	0.00
ATOM 1772 ND2 ASN A 630	1.082	7.357	15.231	1.00	0.00
ATOM 1773 HN ASN A 630	-0.349	5.328	11.841	1.00	0.00
ATOM 1774 HA ASN A 630	-1.110	8.108	11.256	1.00	0.00
ATOM 1775 IHB ASN A 630	-1.194	7.683	13.759	1.00	0.00
ATOM 1776 2HB ASN A 630	0.006	8.910	13.302	1.00	0.00
ATOM 1777 1HD2 ASN A 630	1.675	6.766	15.779	1.00	0.00
ATOM 1778 2HD2 ASN A 630	0.680	8.168	15.655	1.00	0.00
ATOM 1779 N GLU A 631	1.406	8.849	10.956	1.00	0.00
ATOM 1780 CA GLU A 631	2.599	9.081	10.196	1.00	0.00
ATOM 1781 C GLU A 631	3.753	8.273	10.685	1.00	0.00
ATOM 1782 O GLU A 631	4.423	7.610	9.898	1.00	0.00
ATOM 1783 CB GLU A 631	2.986	10.570	10.200	1.00	0.00
ATOM 1784 CG GLU A 631	4.040	10.927	9.155	1.00	0.00
ATOM 1785 CD GLU A 631	3.969	12.424	8.908	1.00	0.00
ATOM 1786 OE1 GLU A 631	4.594	12.887	7.918	1.00	0.00
ATOM 1787 OE2 GLU A 631	3.280	13.124	9.698	1.00	0.00
ATOM 1788 HN GLU A 631	0.934	9.612	11.398	1.00	0.00
ATOM 1789 HA GLU A 631	2.402	8.742	9.179	1.00	0.00
ATOM 1790 IHB GLU A 631	3.370	10.829	11.185	1.00	0.00
ATOM 1791 2HB GLU A 631	2.093	11.164	10.013	1.00	0.00
ATOM 1792 IHG GLU A 631	3.847	10.399	8.221	1.00	0.00
ATOM 1793 2HG GLU A 631	5.036	10.667	9.511	1.00	0.00
ATOM 1794 N GLN A 632	3.989	8.256	12.002	1.00	0.00
ATOM 1795 CA GLN A 632	5.122	7.551	12.527	1.00	0.00
ATOM 1796 C GLN A 632	5.005	6.083	12.267	1.00	0.00
ATOM 1797 O GLN A 632	6.003	5.400	12.040	1.00	0.00
ATOM 1798 CB GLN A 632	5.289	7.747	14.043	1.00	0.00
ATOM 1799 CG GLN A 632	5.656	9.183	14.423	1.00	0.00
ATOM 1800 CD GLN A 632	5.770	9.271	15.938	1.00	0.00
ATOM 1801 OE1 GLN A 632	5.297	10.231	16.543	1.00	0.00
ATOM 1802 NE2 GLN A 632	6.417	8.255	16.568	1.00	0.00
ATOM 1803 HN GLN A 632	3.371	8.738	12.623	1.00	0.00
ATOM 1804 HA GLN A 632	5.998	7.930	12.000	1.00	0.00
ATOM 1805 IHB GLN A 632	6.071	7.077	14.400	1.00	0.00
ATOM 1806 2HB GLN A 632	4.357	7.478	14.538	1.00	0.00
ATOM 1807 IHG GLN A 632	4.886	9.875	14.081	1.00	0.00
ATOM 1808 2HG GLN A 632	6.610	9.463	13.975	1.00	0.00
ATOM 1809 IHE2 GLN A 632	6.919	7.578	16.030	1.00	0.00
ATOM 1810 2HE2 GLN A 632	6.402	8.170	17.564	1.00	0.00
ATOM 1811 N ARG A 633	3.764	5.568	12.261	1.00	0.00
ATOM 1812 CA ARG A 633	3.523	4.160	12.139	1.00	0.00

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ATOM 1813 C ARG A 633	4.131	3.680	10.869	1.00	0.00
ATOM 1814 O ARG A 633	4.547	2.529	10.774	1.00	0.00
ATOM 1815 CB ARG A 633	2.030	3.797	12.093	1.00	0.00
ATOM 1816 CG ARG A 633	1.725	2.310	12.292	1.00	0.00
ATOM 1817 CD ARG A 633	1.890	1.851	13.742	1.00	0.00
ATOM 1818 NE ARG A 633	1.264	2.893	14.605	1.00	0.00
ATOM 1819 CZ ARG A 633	-0.083	2.891	14.828	1.00	0.00
ATOM 1820 NH1 ARG A 633	-0.871	1.932	14.259	1.00	0.00
ATOM 1821 NH2 ARG A 633	-0.645	3.856	15.614	1.00	0.00
ATOM 1822 HN ARG A 633	2.984	6.188	12.345	1.00	0.00
ATOM 1823 HA ARG A 633	3.994	3.689	13.001	1.00	0.00
ATOM 1824 1HB ARG A 633	1.631	4.103	11.127	1.00	0.00
ATOM 1825 2HB ARG A 633	1.515	4.361	12.870	1.00	0.00
ATOM 1826 1HG ARG A 633	2.393	1.727	11.660	1.00	0.00
ATOM 1827 2HG ARG A 633	0.700	2.117	11.977	1.00	0.00
ATOM 1828 1HD ARG A 633	2.941	1.769	14.017	1.00	0.00
ATOM 1829 2HD ARG A 633	1.376	0.907	13.922	1.00	0.00
ATOM 1830 HE ARG A 633	1.835	3.598	15.025	1.00	0.00
ATOM 1831 1HH1 ARG A 633	-0.461	1.228	13.678	1.00	0.00
ATOM 1832 2HH1 ARG A 633	-1.857	1.932	14.423	1.00	0.00
ATOM 1833 1HH2 ARG A 633	-0.070	4.562	16.027	1.00	0.00
ATOM 1834 2HH2 ARG A 633	-1.631	3.855	15.778	1.00	0.00
ATOM 1835 N MET A 634	4.194	4.586	9.871	1.00	0.00
ATOM 1836 CA MET A 634	4.756	4.246	8.570	1.00	0.00
ATOM 1837 C MET A 634	6.239	3.832	8.629	1.00	0.00
ATOM 1838 O MET A 634	6.849	3.485	7.623	1.00	0.00
ATOM 1839 CB MET A 634	4.684	5.489	7.677	1.00	0.00
ATOM 1840 CG MET A 634	5.822	6.509	7.893	1.00	0.00
ATOM 1841 SD MET A 634	5.311	8.055	7.121	1.00	0.00
ATOM 1842 CE MET A 634	6.623	9.183	7.556	1.00	0.00
ATOM 1843 HN MET A 634	3.844	5.517	10.017	1.00	0.00
ATOM 1844 HA MET A 634	4.138	3.444	8.169	1.00	0.00
ATOM 1845 1HB MET A 634	3.717	5.974	7.823	1.00	0.00
ATOM 1846 2HB MET A 634	4.706	5.183	6.635	1.00	0.00
ATOM 1847 1HG MET A 634	6.771	6.152	7.508	1.00	0.00
ATOM 1848 2HG MET A 634	6.077	6.655	8.938	1.00	0.00
ATOM 1849 1HE MET A 634	7.173	9.429	6.652	1.00	0.00
ATOM 1850 2HE MET A 634	7.254	8.773	8.343	1.00	0.00
ATOM 1851 3HE MET A 634	6.206	10.122	7.903	1.00	0.00
ATOM 1852 N THR A 635	6.805	3.946	9.834	1.00	0.00
ATOM 1853 CA THR A 635	8.166	3.585	10.197	1.00	0.00
ATOM 1854 C THR A 635	8.562	2.126	10.015	1.00	0.00
ATOM 1855 O THR A 635	9.434	1.608	10.711	1.00	0.00
ATOM 1856 CB THR A 635	8.480	3.949	11.621	1.00	0.00
ATOM 1857 OG1 THR A 635	9.877	3.870	11.867	1.00	0.00
ATOM 1858 CG2 THR A 635	7.724	2.979	12.544	1.00	0.00
ATOM 1859 HN THR A 635	6.292	4.442	10.530	1.00	0.00
ATOM 1860 HA THR A 635	8.828	4.118	9.515	1.00	0.00
ATOM 1861 HB THR A 635	8.158	4.970	11.827	1.00	0.00

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ATOM 1862 HG1 THR A 635	10.134	2.975	11.694	1.00	0.00
ATOM 1863 IHG2 THR A 635	8.151	1.978	12.483	1.00	0.00
ATOM 1864 2HG2 THR A 635	6.677	2.918	12.248	1.00	0.00
ATOM 1865 3HG2 THR A 635	7.794	3.313	13.579	1.00	0.00
ATOM 1866 N LEU A 636	7.821	1.446	9.104	1.00	0.00
ATOM 1867 CA LEU A 636	8.154	0.172	8.494	1.00	0.00
ATOM 1868 C LEU A 636	8.817	0.534	7.166	1.00	0.00
ATOM 1869 O LEU A 636	8.410	0.111	6.097	1.00	0.00
ATOM 1870 CB LEU A 636	6.897	-0.722	8.320	1.00	0.00
ATOM 1871 CG LEU A 636	5.812	-0.400	7.243	1.00	0.00
ATOM 1872 CD1 LEU A 636	5.590	1.062	6.929	1.00	0.00
ATOM 1873 CD2 LEU A 636	5.875	-1.271	5.970	1.00	0.00
ATOM 1874 HN LEU A 636	7.059	1.888	8.645	1.00	0.00
ATOM 1875 HA LEU A 636	8.869	-0.331	9.147	1.00	0.00
ATOM 1876 IHB LEU A 636	6.408	-0.765	9.294	1.00	0.00
ATOM 1877 2HB LEU A 636	7.246	-1.734	8.137	1.00	0.00
ATOM 1878 HG LEU A 636	4.857	-0.636	7.692	1.00	0.00
ATOM 1879 IHD1 LEU A 636	5.311	1.582	7.839	1.00	0.00
ATOM 1880 2HD1 LEU A 636	4.765	1.181	6.233	1.00	0.00
ATOM 1881 3HD1 LEU A 636	6.470	1.511	6.482	1.00	0.00
ATOM 1882 IHD2 LEU A 636	6.080	-2.315	6.206	1.00	0.00
ATOM 1883 2HD2 LEU A 636	6.622	-0.946	5.252	1.00	0.00
ATOM 1884 3HD2 LEU A 636	4.921	-1.241	5.443	1.00	0.00
ATOM 1885 N PRO A 637	9.812	1.437	7.273	1.00	0.00
ATOM 1886 CA PRO A 637	10.350	2.125	6.111	1.00	0.00
ATOM 1887 C PRO A 637	10.363	1.662	4.692	1.00	0.00
ATOM 1888 O PRO A 637	10.335	0.477	4.364	1.00	0.00
ATOM 1889 CB PRO A 637	11.736	2.648	6.492	1.00	0.00
ATOM 1890 CG PRO A 637	12.187	1.711	7.606	1.00	0.00
ATOM 1891 CD PRO A 637	10.867	1.322	8.280	1.00	0.00
ATOM 1892 IHD PRO A 637	10.912	0.298	8.651	1.00	0.00
ATOM 1893 2HD PRO A 637	10.651	1.989	9.115	1.00	0.00
ATOM 1894 HA PRO A 637	9.692	2.949	5.834	1.00	0.00
ATOM 1895 IHB PRO A 637	11.685	3.679	6.841	1.00	0.00
ATOM 1896 2HB PRO A 637	12.419	2.609	5.643	1.00	0.00
ATOM 1897 IHG PRO A 637	12.702	0.837	7.207	1.00	0.00
ATOM 1898 2HG PRO A 637	12.857	2.214	8.303	1.00	0.00
ATOM 1899 N CYS A 638	10.449	2.743	3.865	1.00	0.00
ATOM 1900 CA CYS A 638	10.294	2.855	2.427	1.00	0.00
ATOM 1901 C CYS A 638	8.818	3.110	2.059	1.00	0.00
ATOM 1902 O CYS A 638	8.523	3.510	0.936	1.00	0.00
ATOM 1903 CB CYS A 638	10.982	1.745	1.628	1.00	0.00
ATOM 1904 SG CYS A 638	10.969	2.069	-0.161	1.00	0.00
ATOM 1905 HN CYS A 638	10.630	3.611	4.327	1.00	0.00
ATOM 1906 HA CYS A 638	10.814	3.783	2.192	1.00	0.00
ATOM 1907 IHB CYS A 638	10.524	0.785	1.832	1.00	0.00
ATOM 1908 2HB CYS A 638	12.019	1.656	1.951	1.00	0.00
ATOM 1909 HG CYS A 638	11.560	1.050	-0.793	1.00	0.00
ATOM 1910 N MET A 639	7.943	2.913	3.080	1.00	0.00

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ATOM 1911 CA MET A 639	6.573	3.419	3.022	1.00	0.00
ATOM 1912 C MET A 639	6.516	4.893	3.449	1.00	0.00
ATOM 1913 O MET A 639	5.612	5.614	3.065	1.00	0.00
ATOM 1914 CB MET A 639	5.630	2.616	3.935	1.00	0.00
ATOM 1915 CG MET A 639	4.149	2.912	3.646	1.00	0.00
ATOM 1916 SD MET A 639	3.022	1.729	4.408	1.00	0.00
ATOM 1917 CE MET A 639	2.363	2.759	5.733	1.00	0.00
ATOM 1918 HN MET A 639	8.222	2.383	3.879	1.00	0.00
ATOM 1919 HA MET A 639	6.243	3.341	1.983	1.00	0.00
ATOM 1920 IHB MET A 639	5.842	2.853	4.976	1.00	0.00
ATOM 1921 2HB MET A 639	5.812	1.549	3.817	1.00	0.00
ATOM 1922 IHG MET A 639	3.991	2.853	2.574	1.00	0.00
ATOM 1923 2HG MET A 639	3.875	3.928	3.931	1.00	0.00
ATOM 1924 IHE MET A 639	2.035	2.132	6.563	1.00	0.00
ATOM 1925 2HE MET A 639	1.522	3.354	5.376	1.00	0.00
ATOM 1926 3HE MET A 639	3.133	3.427	6.113	1.00	0.00
ATOM 1927 N TYR A 640	7.505	5.290	4.280	1.00	0.00
ATOM 1928 CA TYR A 640	7.618	6.639	4.842	1.00	0.00
ATOM 1929 C TYR A 640	7.155	7.706	3.865	1.00	0.00
ATOM 1930 O TYR A 640	6.223	8.472	4.087	1.00	0.00
ATOM 1931 CB TYR A 640	9.112	6.859	5.261	1.00	0.00
ATOM 1932 CG TYR A 640	9.494	8.274	5.672	1.00	0.00
ATOM 1933 CD1 TYR A 640	9.735	9.264	4.719	1.00	0.00
ATOM 1934 CD2 TYR A 640	9.594	8.630	7.016	1.00	0.00
ATOM 1935 CE1 TYR A 640	9.961	10.583	5.086	1.00	0.00
ATOM 1936 CE2 TYR A 640	9.828	9.953	7.392	1.00	0.00
ATOM 1937 CZ TYR A 640	9.977	10.941	6.424	1.00	0.00
ATOM 1938 OH TYR A 640	10.117	12.278	6.766	1.00	0.00
ATOM 1939 HN TYR A 640	8.092	4.572	4.641	1.00	0.00
ATOM 1940 HA TYR A 640	6.931	6.686	5.661	1.00	0.00
ATOM 1941 IHB TYR A 640	9.768	6.572	4.439	1.00	0.00
ATOM 1942 2HB TYR A 640	9.355	6.179	6.079	1.00	0.00
ATOM 1943 HD1 TYR A 640	9.757	9.027	3.668	1.00	0.00
ATOM 1944 HE1 TYR A 640	10.124	11.326	4.321	1.00	0.00
ATOM 1945 HD2 TYR A 640	9.464	7.879	7.782	1.00	0.00
ATOM 1946 HE2 TYR A 640	9.866	10.198	8.444	1.00	0.00
ATOM 1947 HH TYR A 640	10.860	12.349	7.362	1.00	0.00
ATOM 1948 N ASP A 641	7.900	7.689	2.756	1.00	0.00
ATOM 1949 CA ASP A 641	7.691	8.725	1.788	1.00	0.00
ATOM 1950 C ASP A 641	6.322	8.607	1.202	1.00	0.00
ATOM 1951 O ASP A 641	5.659	9.612	0.950	1.00	0.00
ATOM 1952 CB ASP A 641	8.725	8.718	0.644	1.00	0.00
ATOM 1953 CG ASP A 641	8.628	7.412	-0.130	1.00	0.00
ATOM 1954 OD1 ASP A 641	8.232	6.383	0.482	1.00	0.00
ATOM 1955 OD2 ASP A 641	8.951	7.425	-1.348	1.00	0.00
ATOM 1956 HN ASP A 641	8.594	6.986	2.603	1.00	0.00
ATOM 1957 HA ASP A 641	7.744	9.669	2.330	1.00	0.00
ATOM 1958 IHB ASP A 641	9.732	8.812	1.049	1.00	0.00
ATOM 1959 2HB ASP A 641	8.535	9.546	-0.038	1.00	0.00

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ATOM 1960 N GLN A 642	5.820	7.376	0.975	1.00	0.00
ATOM 1961 CA GLN A 642	4.539	7.246	0.288	1.00	0.00
ATOM 1962 C GLN A 642	3.405	7.741	1.196	1.00	0.00
ATOM 1963 O GLN A 642	2.481	8.398	0.744	1.00	0.00
ATOM 1964 CB GLN A 642	4.351	5.846	-0.336	1.00	0.00
ATOM 1965 CG GLN A 642	3.695	4.769	0.544	1.00	0.00
ATOM 1966 CD GLN A 642	2.169	4.926	0.592	1.00	0.00
ATOM 1967 OE1 GLN A 642	1.499	4.941	-0.429	1.00	0.00
ATOM 1968 NE2 GLN A 642	1.658	5.033	1.823	1.00	0.00
ATOM 1969 HN GLN A 642	6.396	6.590	1.211	1.00	0.00
ATOM 1970 HA GLN A 642	4.591	7.947	-0.548	1.00	0.00
ATOM 1971 IHB GLN A 642	5.329	5.487	-0.658	1.00	0.00
ATOM 1972 2HB GLN A 642	3.771	5.944	-1.256	1.00	0.00
ATOM 1973 IHG GLN A 642	4.104	4.785	1.547	1.00	0.00
ATOM 1974 2HG GLN A 642	3.903	3.782	0.131	1.00	0.00
ATOM 1975 IHE2 GLN A 642	2.223	5.000	2.645	1.00	0.00
ATOM 1976 2HE2 GLN A 642	0.669	5.157	1.891	1.00	0.00
ATOM 1977 N CYS A 643	3.555	7.450	2.506	1.00	0.00
ATOM 1978 CA CYS A 643	2.631	8.001	3.484	1.00	0.00
ATOM 1979 C CYS A 643	2.626	9.534	3.413	1.00	0.00
ATOM 1980 O CYS A 643	1.580	10.157	3.530	1.00	0.00
ATOM 1981 CB CYS A 643	3.045	7.537	4.885	1.00	0.00
ATOM 1982 SG CYS A 643	2.794	8.786	6.171	1.00	0.00
ATOM 1983 HN CYS A 643	4.332	6.879	2.775	1.00	0.00
ATOM 1984 HA CYS A 643	1.634	7.633	3.235	1.00	0.00
ATOM 1985 IHB CYS A 643	4.097	7.254	4.889	1.00	0.00
ATOM 1986 2HB CYS A 643	2.489	6.639	5.154	1.00	0.00
ATOM 1987 HG CYS A 643	2.847	8.193	7.368	1.00	0.00
ATOM 1988 N LYS A 644	3.835	10.104	3.196	1.00	0.00
ATOM 1989 CA LYS A 644	3.964	11.530	3.171	1.00	0.00
ATOM 1990 C LYS A 644	3.198	12.069	2.014	1.00	0.00
ATOM 1991 O LYS A 644	2.389	12.983	2.164	1.00	0.00
ATOM 1992 CB LYS A 644	5.421	11.993	2.987	1.00	0.00
ATOM 1993 CG LYS A 644	6.299	11.902	4.238	1.00	0.00
ATOM 1994 CD LYS A 644	5.885	12.868	5.350	1.00	0.00
ATOM 1995 CE LYS A 644	6.921	12.991	6.470	1.00	0.00
ATOM 1996 NZ LYS A 644	8.145	13.645	5.957	1.00	0.00
ATOM 1997 HN LYS A 644	4.648	9.527	3.117	1.00	0.00
ATOM 1998 HA LYS A 644	3.570	11.896	4.118	1.00	0.00
ATOM 1999 IHB LYS A 644	5.409	13.030	2.655	1.00	0.00
ATOM 2000 2HB LYS A 644	5.876	11.387	2.206	1.00	0.00
ATOM 2001 IHG LYS A 644	7.330	12.114	3.957	1.00	0.00
ATOM 2002 2HG LYS A 644	6.251	10.884	4.624	1.00	0.00
ATOM 2003 IHD LYS A 644	4.945	12.525	5.780	1.00	0.00
ATOM 2004 2HD LYS A 644	5.722	13.853	4.914	1.00	0.00
ATOM 2005 IHE LYS A 644	7.194	12.005	6.844	1.00	0.00
ATOM 2006 2HE LYS A 644	6.528	13.597	7.286	1.00	0.00
ATOM 2007 IHZ LYS A 644	7.909	14.595	5.604	1.00	0.00
ATOM 2008 2HZ LYS A 644	8.544	13.077	5.183	1.00	0.00

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ATOM 2009 3HZ LYS A 644	8.843	13.725	6.724	1.00	0.00
ATOM 2010 N HIS A 645	3.413	11.483	0.825	1.00	0.00
ATOM 2011 CA HIS A 645	2.750	11.978	-0.342	1.00	0.00
ATOM 2012 C HIS A 645	1.281	11.777	-0.183	1.00	0.00
ATOM 2013 O HIS A 645	0.485	12.612	-0.611	1.00	0.00
ATOM 2014 CB HIS A 645	3.245	11.314	-1.636	1.00	0.00
ATOM 2015 CG HIS A 645	4.645	11.751	-1.963	1.00	0.00
ATOM 2016 ND1 HIS A 645	5.461	11.146	-2.893	1.00	0.00
ATOM 2017 CD2 HIS A 645	5.363	12.796	-1.465	1.00	0.00
ATOM 2018 CE1 HIS A 645	6.623	11.848	-2.909	1.00	0.00
ATOM 2019 NE2 HIS A 645	6.610	12.858	-2.059	1.00	0.00
ATOM 2020 HN HIS A 645	4.035	10.704	0.756	1.00	0.00
ATOM 2021 HA HIS A 645	2.938	13.051	-0.376	1.00	0.00
ATOM 2022 1HB HIS A 645	2.590	11.588	-2.463	1.00	0.00
ATOM 2023 2HB HIS A 645	3.234	10.231	-1.521	1.00	0.00
ATOM 2024 HD2 HIS A 645	5.007	13.481	-0.711	1.00	0.00
ATOM 2025 HD1 HIS A 645	5.244	10.361	-3.438	1.00	0.00
ATOM 2026 HE1 HIS A 645	7.462	11.607	-3.544	1.00	0.00
ATOM 2027 N MET A 646	0.886	10.654	0.460	1.00	0.00
ATOM 2028 CA MET A 646	-0.539	10.371	0.669	1.00	0.00
ATOM 2029 C MET A 646	-1.199	11.378	1.633	1.00	0.00
ATOM 2030 O MET A 646	-2.362	11.742	1.495	1.00	0.00
ATOM 2031 CB MET A 646	-0.755	8.943	1.199	1.00	0.00
ATOM 2032 CG MET A 646	-0.620	7.867	0.116	1.00	0.00
ATOM 2033 SD MET A 646	-1.146	6.270	0.769	1.00	0.00
ATOM 2034 CE MET A 646	-2.105	5.669	-0.634	1.00	0.00
ATOM 2035 HN MET A 646	1.576	9.999	0.768	1.00	0.00
ATOM 2036 HA MET A 646	-1.022	10.471	-0.303	1.00	0.00
ATOM 2037 1HB MET A 646	-1.763	8.859	1.610	1.00	0.00
ATOM 2038 2HB MET A 646	-0.075	8.738	2.027	1.00	0.00
ATOM 2039 1HG MET A 646	0.406	7.791	-0.241	1.00	0.00
ATOM 2040 2HG MET A 646	-1.243	8.141	-0.735	1.00	0.00
ATOM 2041 1HE MET A 646	-2.864	4.977	-0.275	1.00	0.00
ATOM 2042 2HE MET A 646	-1.459	5.169	-1.356	1.00	0.00
ATOM 2043 3HE MET A 646	-2.632	6.484	-1.129	1.00	0.00
ATOM 2044 N LEU A 647	-0.416	11.831	2.622	1.00	0.00
ATOM 2045 CA LEU A 647	-0.963	12.840	3.484	1.00	0.00
ATOM 2046 C LEU A 647	-1.102	14.128	2.759	1.00	0.00
ATOM 2047 O LEU A 647	-2.124	14.808	2.872	1.00	0.00
ATOM 2048 CB LEU A 647	-0.078	13.164	4.691	1.00	0.00
ATOM 2049 CG LEU A 647	-0.153	12.091	5.768	1.00	0.00
ATOM 2050 CD1 LEU A 647	0.730	12.449	6.975	1.00	0.00
ATOM 2051 CD2 LEU A 647	-1.626	11.821	6.118	1.00	0.00
ATOM 2052 HN LEU A 647	0.457	11.394	2.840	1.00	0.00
ATOM 2053 HA LEU A 647	-1.929	12.466	3.822	1.00	0.00
ATOM 2054 1HB LEU A 647	-0.393	14.116	5.117	1.00	0.00
ATOM 2055 2HB LEU A 647	0.955	13.262	4.359	1.00	0.00
ATOM 2056 HG LEU A 647	0.175	11.139	5.351	1.00	0.00
ATOM 2057 1HD1 LEU A 647	0.117	12.701	7.840	1.00	0.00

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ATOM 2058 2HD1 LEU A 647	1.354	13.312	6.741	1.00	0.00
ATOM 2059 3HD1 LEU A 647	1.361	11.602	7.244	1.00	0.00
ATOM 2060 1HD2 LEU A 647	-2.243	11.826	5.219	1.00	0.00
ATOM 2061 2HD2 LEU A 647	-2.002	12.594	6.788	1.00	0.00
ATOM 2062 3HD2 LEU A 647	-1.728	10.844	6.591	1.00	0.00
ATOM 2063 N TYR A 648	-0.080	14.492	1.971	1.00	0.00
ATOM 2064 CA TYR A 648	-0.102	15.769	1.332	1.00	0.00
ATOM 2065 C TYR A 648	-1.285	15.860	0.425	1.00	0.00
ATOM 2066 O TYR A 648	-1.946	16.896	0.366	1.00	0.00
ATOM 2067 CB TYR A 648	1.167	16.042	0.507	1.00	0.00
ATOM 2068 CG TYR A 648	1.014	17.399	-0.087	1.00	0.00
ATOM 2069 CD1 TYR A 648	0.389	17.572	-1.299	1.00	0.00
ATOM 2070 CD2 TYR A 648	1.439	18.507	0.610	1.00	0.00
ATOM 2071 CE1 TYR A 648	0.206	18.831	-1.817	1.00	0.00
ATOM 2072 CE2 TYR A 648	1.257	19.769	0.098	1.00	0.00
ATOM 2073 CZ TYR A 648	0.640	19.932	-1.118	1.00	0.00
ATOM 2074 OH TYR A 648	0.444	21.226	-1.644	1.00	0.00
ATOM 2075 HN TYR A 648	0.692	13.872	1.832	1.00	0.00
ATOM 2076 HA TYR A 648	-0.202	16.513	2.123	1.00	0.00
ATOM 2077 1HB TYR A 648	1.277	15.303	-0.286	1.00	0.00
ATOM 2078 2HB TYR A 648	2.053	16.014	1.141	1.00	0.00
ATOM 2079 HD1 TYR A 648	0.038	16.711	-1.849	1.00	0.00
ATOM 2080 HE1 TYR A 648	-0.278	18.956	-2.774	1.00	0.00
ATOM 2081 HD2 TYR A 648	1.921	18.383	1.569	1.00	0.00
ATOM 2082 HE2 TYR A 648	1.599	20.631	0.652	1.00	0.00
ATOM 2083 HH TYR A 648	-0.245	21.202	-2.295	1.00	0.00
ATOM 2084 N VAL A 649	-1.593	14.783	-0.320	1.00	0.00
ATOM 2085 CA VAL A 649	-2.721	14.865	-1.204	1.00	0.00
ATOM 2086 C VAL A 649	-3.964	14.983	-0.384	1.00	0.00
ATOM 2087 O VAL A 649	-4.867	15.755	-0.707	1.00	0.00
ATOM 2088 CB VAL A 649	-2.861	13.681	-2.118	1.00	0.00
ATOM 2089 CG1 VAL A 649	-3.212	12.435	-1.292	1.00	0.00
ATOM 2090 CG2 VAL A 649	-3.907	14.026	-3.193	1.00	0.00
ATOM 2091 HN VAL A 649	-1.049	13.946	-0.260	1.00	0.00
ATOM 2092 HA VAL A 649	-2.586	15.773	-1.791	1.00	0.00
ATOM 2093 HB VAL A 649	-1.927	13.516	-2.655	1.00	0.00
ATOM 2094 1HG1 VAL A 649	-4.048	12.639	-0.623	1.00	0.00
ATOM 2095 2HG1 VAL A 649	-2.359	12.135	-0.683	1.00	0.00
ATOM 2096 3HG1 VAL A 649	-3.499	11.615	-1.950	1.00	0.00
ATOM 2097 1HG2 VAL A 649	-3.686	14.991	-3.650	1.00	0.00
ATOM 2098 2HG2 VAL A 649	-4.900	14.084	-2.747	1.00	0.00
ATOM 2099 3HG2 VAL A 649	-3.902	13.272	-3.979	1.00	0.00
ATOM 2100 N SER A 650	-4.023	14.232	0.732	1.00	0.00
ATOM 2101 CA SER A 650	-5.193	14.243	1.556	1.00	0.00
ATOM 2102 C SER A 650	-5.420	15.645	2.021	1.00	0.00
ATOM 2103 O SER A 650	-6.549	16.135	2.029	1.00	0.00
ATOM 2104 CB SER A 650	-5.044	13.361	2.807	1.00	0.00
ATOM 2105 OG SER A 650	-6.232	13.412	3.584	1.00	0.00
ATOM 2106 HN SER A 650	-3.241	13.662	0.986	1.00	0.00

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ATOM	2107	HA	SER A 650	-6.015	13.884	0.938	1.00	0.00
ATOM	2108	IHB	SER A 650	-4.217	13.714	3.423	1.00	0.00
ATOM	2109	2HB	SER A 650	-4.869	12.324	2.520	1.00	0.00
ATOM	2110	HG	SER A 650	-6.530	14.312	3.566	1.00	0.00
ATOM	2111	N	SER A 651	-4.335	16.334	2.416	1.00	0.00
ATOM	2112	CA	SER A 651	-4.456	17.677	2.903	1.00	0.00
ATOM	2113	C	SER A 651	-4.931	18.597	1.820	1.00	0.00
ATOM	2114	O	SER A 651	-5.771	19.464	2.059	1.00	0.00
ATOM	2115	CB	SER A 651	-3.139	18.242	3.471	1.00	0.00
ATOM	2116	OG	SER A 651	-2.170	18.402	2.446	1.00	0.00
ATOM	2117	HN	SER A 651	-3.434	15.904	2.369	1.00	0.00
ATOM	2118	HA	SER A 651	-5.219	17.657	3.680	1.00	0.00
ATOM	2119	IHB	SER A 651	-2.732	17.561	4.218	1.00	0.00
ATOM	2120	2HB	SER A 651	-3.315	19.218	3.924	1.00	0.00
ATOM	2121	HG	SER A 651	-2.577	18.115	1.639	1.00	0.00
ATOM	2122	N	GLU A 652	-4.421	18.421	0.586	1.00	0.00
ATOM	2123	CA	GLU A 652	-4.800	19.296	-0.486	1.00	0.00
ATOM	2124	C	GLU A 652	-6.268	19.145	-0.716	1.00	0.00
ATOM	2125	O	GLU A 652	-6.970	20.122	-0.969	1.00	0.00
ATOM	2126	CB	GLU A 652	-4.057	18.993	-1.797	1.00	0.00
ATOM	2127	CG	GLU A 652	-4.250	20.074	-2.862	1.00	0.00
ATOM	2128	CD	GLU A 652	-3.249	19.813	-3.976	1.00	0.00
ATOM	2129	OE1	GLU A 652	-2.042	19.647	-3.657	1.00	0.00
ATOM	2130	OE2	GLU A 652	-3.677	19.773	-5.160	1.00	0.00
ATOM	2131	HN	GLU A 652	-3.774	17.677	0.417	1.00	0.00
ATOM	2132	HA	GLU A 652	-4.576	20.310	-0.154	1.00	0.00
ATOM	2133	IHB	GLU A 652	-4.416	18.044	-2.192	1.00	0.00
ATOM	2134	2HB	GLU A 652	-2.994	18.897	-1.584	1.00	0.00
ATOM	2135	IHG	GLU A 652	-4.072	21.063	-2.441	1.00	0.00
ATOM	2136	2HG	GLU A 652	-5.261	20.036	-3.268	1.00	0.00
ATOM	2137	N	LEU A 653	-6.779	17.906	-0.610	1.00	0.00
ATOM	2138	CA	LEU A 653	-8.176	17.673	-0.822	1.00	0.00
ATOM	2139	C	LEU A 653	-8.916	18.459	0.215	1.00	0.00
ATOM	2140	O	LEU A 653	-9.976	19.020	-0.063	1.00	0.00
ATOM	2141	CB	LEU A 653	-8.555	16.191	-0.658	1.00	0.00
ATOM	2142	CG	LEU A 653	-7.855	15.278	-1.684	1.00	0.00
ATOM	2143	CD1	LEU A 653	-8.258	13.807	-1.496	1.00	0.00
ATOM	2144	CD2	LEU A 653	-8.074	15.782	-3.118	1.00	0.00
ATOM	2145	HN	LEU A 653	-6.177	17.141	-0.381	1.00	0.00
ATOM	2146	HA	LEU A 653	-8.401	18.010	-1.834	1.00	0.00
ATOM	2147	IHB	LEU A 653	-9.633	16.088	-0.772	1.00	0.00
ATOM	2148	2HB	LEU A 653	-8.284	15.867	0.346	1.00	0.00
ATOM	2149	HG	LEU A 653	-6.775	15.372	-1.571	1.00	0.00
ATOM	2150	IHD1	LEU A 653	-9.334	13.684	-1.619	1.00	0.00
ATOM	2151	2HD1	LEU A 653	-7.994	13.469	-0.494	1.00	0.00
ATOM	2152	3HD1	LEU A 653	-7.760	13.182	-2.237	1.00	0.00
ATOM	2153	IHD2	LEU A 653	-7.394	16.603	-3.347	1.00	0.00
ATOM	2154	2HD2	LEU A 653	-9.094	16.147	-3.238	1.00	0.00
ATOM	2155	3HD2	LEU A 653	-7.885	14.980	-3.832	1.00	0.00

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ATOM 2156 N HIS A 654	-8.355	18.527	1.440	1.00	0.00
ATOM 2157 CA HIS A 654	-8.965	19.245	2.528	1.00	0.00
ATOM 2158 C HIS A 654	-9.167	20.664	2.111	1.00	0.00
ATOM 2159 O HIS A 654	-10.270	21.201	2.179	1.00	0.00
ATOM 2160 CB HIS A 654	-8.019	19.455	3.728	1.00	0.00
ATOM 2161 CG HIS A 654	-7.730	18.335	4.681	1.00	0.00
ATOM 2162 ND1 HIS A 654	-8.058	18.419	6.018	1.00	0.00
ATOM 2163 CD2 HIS A 654	-6.904	17.262	4.569	1.00	0.00
ATOM 2164 CE1 HIS A 654	-7.416	17.402	6.643	1.00	0.00
ATOM 2165 NE2 HIS A 654	-6.709	16.666	5.803	1.00	0.00
ATOM 2166 HN HIS A 654	-7.485	18.062	1.597	1.00	0.00
ATOM 2167 HA HIS A 654	-9.834	18.662	2.835	1.00	0.00
ATOM 2168 1HB HIS A 654	-8.436	20.261	4.326	1.00	0.00
ATOM 2169 2HB HIS A 654	-7.058	19.766	3.327	1.00	0.00
ATOM 2170 HD2 HIS A 654	-6.461	16.921	3.645	1.00	0.00
ATOM 2171 HD1 HIS A 654	-8.643	19.085	6.435	1.00	0.00
ATOM 2172 HE1 HIS A 654	-7.476	17.215	7.704	1.00	0.00
ATOM 2173 N ARG A 655	-8.078	21.301	1.645	1.00	0.00
ATOM 2174 CA ARG A 655	-8.117	22.702	1.345	1.00	0.00
ATOM 2175 C ARG A 655	-9.090	23.001	0.254	1.00	0.00
ATOM 2176 O ARG A 655	-9.843	23.970	0.334	1.00	0.00
ATOM 2177 CB ARG A 655	-6.736	23.261	0.961	1.00	0.00
ATOM 2178 CG ARG A 655	-5.822	23.434	2.179	1.00	0.00
ATOM 2179 CD ARG A 655	-5.468	22.124	2.888	1.00	0.00
ATOM 2180 NE ARG A 655	-4.054	21.795	2.558	1.00	0.00
ATOM 2181 CZ ARG A 655	-3.045	22.307	3.323	1.00	0.00
ATOM 2182 NH1 ARG A 655	-3.338	23.121	4.379	1.00	0.00
ATOM 2183 NH2 ARG A 655	-1.746	22.004	3.036	1.00	0.00
ATOM 2184 HN ARG A 655	-7.230	20.790	1.506	1.00	0.00
ATOM 2185 HA ARG A 655	-8.490	23.203	2.238	1.00	0.00
ATOM 2186 1HB ARG A 655	-6.866	24.226	0.473	1.00	0.00
ATOM 2187 2HB ARG A 655	-6.261	22.582	0.253	1.00	0.00
ATOM 2188 1HG ARG A 655	-6.317	24.092	2.892	1.00	0.00
ATOM 2189 2HG ARG A 655	-4.899	23.913	1.854	1.00	0.00
ATOM 2190 1HD ARG A 655	-6.094	21.304	2.539	1.00	0.00
ATOM 2191 2HD ARG A 655	-5.545	22.228	3.970	1.00	0.00
ATOM 2192 HE ARG A 655	-3.843	21.202	1.781	1.00	0.00
ATOM 2193 1HH1 ARG A 655	-4.290	23.341	4.591	1.00	0.00
ATOM 2194 2HH1 ARG A 655	-2.601	23.497	4.940	1.00	0.00
ATOM 2195 1HH2 ARG A 655	-1.531	21.406	2.264	1.00	0.00
ATOM 2196 2HH2 ARG A 655	-1.009	22.380	3.598	1.00	0.00
ATOM 2197 N LEU A 656	-9.103	22.163	-0.792	1.00	0.00
ATOM 2198 CA LEU A 656	-10.001	22.337	-1.896	1.00	0.00
ATOM 2199 C LEU A 656	-11.407	22.100	-1.453	1.00	0.00
ATOM 2200 O LEU A 656	-12.349	22.583	-2.080	1.00	0.00
ATOM 2201 CB LEU A 656	-9.700	21.407	-3.087	1.00	0.00
ATOM 2202 CG LEU A 656	-8.472	21.835	-3.918	1.00	0.00
ATOM 2203 CD1 LEU A 656	-7.183	21.850	-3.084	1.00	0.00
ATOM 2204 CD2 LEU A 656	-8.342	20.980	-5.189	1.00	0.00

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ATOM 2205 HN LEU A 656	-8.466	21.392	-0.802	1.00	0.00
ATOM 2206 HA LEU A 656	-9.912	23.378	-2.205	1.00	0.00
ATOM 2207 1HB LEU A 656	-10.572	21.386	-3.740	1.00	0.00
ATOM 2208 2HB LEU A 656	-9.531	20.400	-2.709	1.00	0.00
ATOM 2209 HG LEU A 656	-8.646	22.832	-4.322	1.00	0.00
ATOM 2210 1HD1 LEU A 656	-6.878	20.835	-2.827	1.00	0.00
ATOM 2211 2HD1 LEU A 656	-7.341	22.399	-2.156	1.00	0.00
ATOM 2212 3HD1 LEU A 656	-6.374	22.311	-3.650	1.00	0.00
ATOM 2213 1HD2 LEU A 656	-9.227	21.085	-5.816	1.00	0.00
ATOM 2214 2HD2 LEU A 656	-8.238	19.928	-4.926	1.00	0.00
ATOM 2215 3HD2 LEU A 656	-7.477	21.300	-5.771	1.00	0.00
ATOM 2216 N GLN A 657	-11.597	21.333	-0.364	1.00	0.00
ATOM 2217 CA GLN A 657	-12.934	21.062	0.071	1.00	0.00
ATOM 2218 C GLN A 657	-13.598	20.292	-1.019	1.00	0.00
ATOM 2219 O GLN A 657	-14.683	20.641	-1.479	1.00	0.00
ATOM 2220 CB GLN A 657	-13.761	22.338	0.306	1.00	0.00
ATOM 2221 CG GLN A 657	-13.224	23.227	1.431	1.00	0.00
ATOM 2222 CD GLN A 657	-14.135	24.442	1.541	1.00	0.00
ATOM 2223 OE1 GLN A 657	-13.875	25.359	2.318	1.00	0.00
ATOM 2224 NE2 GLN A 657	-15.231	24.454	0.738	1.00	0.00
ATOM 2225 HN GLN A 657	-10.815	20.957	0.134	1.00	0.00
ATOM 2226 HA GLN A 657	-12.851	20.493	0.997	1.00	0.00
ATOM 2227 1HB GLN A 657	-14.783	22.051	0.549	1.00	0.00
ATOM 2228 2HB GLN A 657	-13.777	22.917	-0.616	1.00	0.00
ATOM 2229 1HG GLN A 657	-12.209	23.556	1.208	1.00	0.00
ATOM 2230 2HG GLN A 657	-13.224	22.688	2.378	1.00	0.00
ATOM 2231 1HE2 GLN A 657	-15.938	25.149	0.875	1.00	0.00
ATOM 2232 2HE2 GLN A 657	-15.347	23.780	0.009	1.00	0.00
ATOM 2233 N VAL A 658	-12.935	19.205	-1.457	1.00	0.00
ATOM 2234 CA VAL A 658	-13.459	18.405	-2.523	1.00	0.00
ATOM 2235 C VAL A 658	-14.729	17.748	-2.099	1.00	0.00
ATOM 2236 O VAL A 658	-14.827	17.196	-1.003	1.00	0.00
ATOM 2237 CB VAL A 658	-12.516	17.329	-2.978	1.00	0.00
ATOM 2238 CG1 VAL A 658	-11.249	17.994	-3.543	1.00	0.00
ATOM 2239 CG2 VAL A 658	-12.249	16.381	-1.797	1.00	0.00
ATOM 2240 HN VAL A 658	-12.065	18.954	-1.033	1.00	0.00
ATOM 2241 HA VAL A 658	-13.671	19.087	-3.346	1.00	0.00
ATOM 2242 HB VAL A 658	-12.991	16.718	-3.746	1.00	0.00
ATOM 2243 1HG1 VAL A 658	-10.668	18.456	-2.745	1.00	0.00
ATOM 2244 2HG1 VAL A 658	-11.519	18.772	-4.257	1.00	0.00
ATOM 2245 3HG1 VAL A 658	-10.620	17.250	-4.032	1.00	0.00
ATOM 2246 1HG2 VAL A 658	-13.032	16.474	-1.044	1.00	0.00
ATOM 2247 2HG2 VAL A 658	-11.298	16.627	-1.325	1.00	0.00
ATOM 2248 3HG2 VAL A 658	-12.232	15.347	-2.140	1.00	0.00
ATOM 2249 N SER A 659	-15.746	17.803	-2.984	1.00	0.00
ATOM 2250 CA SER A 659	-17.023	17.228	-2.686	1.00	0.00
ATOM 2251 C SER A 659	-17.056	15.801	-3.130	1.00	0.00
ATOM 2252 O SER A 659	-16.241	15.359	-3.938	1.00	0.00
ATOM 2253 CB SER A 659	-18.205	17.959	-3.344	1.00	0.00

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ATOM 2254 OG SER A 659	-18.194	17.764	-4.749	1.00	0.00
ATOM 2255 HN SER A 659	-15.604	18.255	-3.864	1.00	0.00
ATOM 2256 HA SER A 659	-17.128	17.258	-1.601	1.00	0.00
ATOM 2257 IHB SER A 659	-18.140	19.029	-3.150	1.00	0.00
ATOM 2258 2HB SER A 659	-19.148	17.574	-2.956	1.00	0.00
ATOM 2259 HG SER A 659	-18.584	18.538	-5.134	1.00	0.00
ATOM 2260 N TYR A 660	-18.026	15.044	-2.584	1.00	0.00
ATOM 2261 CA TYR A 660	-18.187	13.647	-2.862	1.00	0.00
ATOM 2262 C TYR A 660	-18.532	13.452	-4.305	1.00	0.00
ATOM 2263 O TYR A 660	-18.025	12.539	-4.953	1.00	0.00
ATOM 2264 CB TYR A 660	-19.292	13.024	-1.984	1.00	0.00
ATOM 2265 CG TYR A 660	-19.424	11.571	-2.291	1.00	0.00
ATOM 2266 CD1 TYR A 660	-20.300	11.128	-3.255	1.00	0.00
ATOM 2267 CD2 TYR A 660	-18.694	10.647	-1.579	1.00	0.00
ATOM 2268 CE1 TYR A 660	-20.449	9.782	-3.499	1.00	0.00
ATOM 2269 CE2 TYR A 660	-18.824	9.301	-1.832	1.00	0.00
ATOM 2270 CZ TYR A 660	-19.704	8.867	-2.793	1.00	0.00
ATOM 2271 OH TYR A 660	-19.835	7.489	-3.061	1.00	0.00
ATOM 2272 HN TYR A 660	-18.666	15.479	-1.952	1.00	0.00
ATOM 2273 HA TYR A 660	-17.228	13.169	-2.663	1.00	0.00
ATOM 2274 IHB TYR A 660	-20.245	13.517	-2.179	1.00	0.00
ATOM 2275 2HB TYR A 660	-19.043	13.144	-0.930	1.00	0.00
ATOM 2276 HD1 TYR A 660	-20.875	11.842	-3.826	1.00	0.00
ATOM 2277 HE1 TYR A 660	-21.152	9.443	-4.245	1.00	0.00
ATOM 2278 HD2 TYR A 660	-18.011	10.982	-0.812	1.00	0.00
ATOM 2279 HE2 TYR A 660	-18.235	8.587	-1.275	1.00	0.00
ATOM 2280 HH TYR A 660	-19.330	7.267	-3.832	1.00	0.00
ATOM 2281 N GLU A 661	-19.398	14.316	-4.864	1.00	0.00
ATOM 2282 CA GLU A 661	-19.761	14.171	-6.244	1.00	0.00
ATOM 2283 C GLU A 661	-18.536	14.346	-7.089	1.00	0.00
ATOM 2284 O GLU A 661	-18.372	13.667	-8.103	1.00	0.00
ATOM 2285 CB GLU A 661	-20.863	15.156	-6.680	1.00	0.00
ATOM 2286 CG GLU A 661	-20.651	16.585	-6.182	1.00	0.00
ATOM 2287 CD GLU A 661	-21.158	16.652	-4.749	1.00	0.00
ATOM 2288 OE1 GLU A 661	-20.840	17.652	-4.055	1.00	0.00
ATOM 2289 OE2 GLU A 661	-21.873	15.702	-4.330	1.00	0.00
ATOM 2290 HN GLU A 661	-19.787	15.057	-4.317	1.00	0.00
ATOM 2291 HA GLU A 661	-20.104	13.145	-6.370	1.00	0.00
ATOM 2292 IHB GLU A 661	-21.819	14.796	-6.303	1.00	0.00
ATOM 2293 2HB GLU A 661	-20.906	15.170	-7.768	1.00	0.00
ATOM 2294 IHG GLU A 661	-21.206	17.293	-6.797	1.00	0.00
ATOM 2295 2HG GLU A 661	-19.593	16.848	-6.204	1.00	0.00
ATOM 2296 N GLU A 662	-17.646	15.274	-6.688	1.00	0.00
ATOM 2297 CA GLU A 662	-16.412	15.526	-7.380	1.00	0.00
ATOM 2298 C GLU A 662	-15.564	14.293	-7.315	1.00	0.00
ATOM 2299 O GLU A 662	-15.021	13.830	-8.319	1.00	0.00
ATOM 2300 CB GLU A 662	-15.568	16.594	-6.662	1.00	0.00
ATOM 2301 CG GLU A 662	-16.170	17.997	-6.642	1.00	0.00
ATOM 2302 CD GLU A 662	-15.293	18.914	-7.473	1.00	0.00

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ATOM	2303	OE1	GLU	A	662	-14.265	18.432	-8.015	1.00	0.00
ATOM	2304	OE2	GLU	A	662	-15.631	20.123	-7.555	1.00	0.00
ATOM	2305	HN	GLU	A	662	-17.854	15.812	-5.871	1.00	0.00
ATOM	2306	HA	GLU	A	662	-16.672	15.859	-8.385	1.00	0.00
ATOM	2307	IHB	GLU	A	662	-14.597	16.646	-7.151	1.00	0.00
ATOM	2308	2HB	GLU	A	662	-15.418	16.273	-5.633	1.00	0.00
ATOM	2309	IHG	GLU	A	662	-16.217	18.376	-5.621	1.00	0.00
ATOM	2310	2HG	GLU	A	662	-17.175	17.985	-7.064	1.00	0.00
ATOM	2311	N	TYR	A	663	-15.466	13.711	-6.105	1.00	0.00
ATOM	2312	CA	TYR	A	663	-14.615	12.585	-5.853	1.00	0.00
ATOM	2313	C	TYR	A	663	-14.948	11.458	-6.774	1.00	0.00
ATOM	2314	O	TYR	A	663	-14.074	10.896	-7.433	1.00	0.00
ATOM	2315	CB	TYR	A	663	-14.789	12.093	-4.404	1.00	0.00
ATOM	2316	CG	TYR	A	663	-14.191	10.738	-4.252	1.00	0.00
ATOM	2317	CD1	TYR	A	663	-12.830	10.563	-4.239	1.00	0.00
ATOM	2318	CD2	TYR	A	663	-15.000	9.658	-3.983	1.00	0.00
ATOM	2319	CE1	TYR	A	663	-12.281	9.319	-4.041	1.00	0.00
ATOM	2320	CE2	TYR	A	663	-14.459	8.414	-3.759	1.00	0.00
ATOM	2321	CZ	TYR	A	663	-13.098	8.241	-3.803	1.00	0.00
ATOM	2322	OH	TYR	A	663	-12.537	6.964	-3.581	1.00	0.00
ATOM	2323	HN	TYR	A	663	-16.010	14.080	-5.352	1.00	0.00
ATOM	2324	HA	TYR	A	663	-13.589	12.909	-6.029	1.00	0.00
ATOM	2325	IHB	TYR	A	663	-15.849	12.044	-4.152	1.00	0.00
ATOM	2326	2HB	TYR	A	663	-14.295	12.779	-3.716	1.00	0.00
ATOM	2327	HD1	TYR	A	663	-12.182	11.414	-4.386	1.00	0.00
ATOM	2328	HE1	TYR	A	663	-11.209	9.189	-4.073	1.00	0.00
ATOM	2329	HD2	TYR	A	663	-16.071	9.788	-3.947	1.00	0.00
ATOM	2330	HE2	TYR	A	663	-15.105	7.574	-3.550	1.00	0.00
ATOM	2331	HH	TYR	A	663	-12.965	6.330	-4.140	1.00	0.00
ATOM	2332	N	LEU	A	664	-16.242	11.130	-6.887	1.00	0.00
ATOM	2333	CA	LEU	A	664	-16.646	10.024	-7.700	1.00	0.00
ATOM	2334	C	LEU	A	664	-16.277	10.231	-9.134	1.00	0.00
ATOM	2335	O	LEU	A	664	-15.938	9.278	-9.834	1.00	0.00
ATOM	2336	CB	LEU	A	664	-18.150	9.737	-7.595	1.00	0.00
ATOM	2337	CG	LEU	A	664	-18.516	9.035	-6.274	1.00	0.00
ATOM	2338	CD1	LEU	A	664	-18.042	7.572	-6.264	1.00	0.00
ATOM	2339	CD2	LEU	A	664	-17.958	9.802	-5.070	1.00	0.00
ATOM	2340	HN	LEU	A	664	-16.932	11.663	-6.397	1.00	0.00
ATOM	2341	HA	LEU	A	664	-16.074	9.160	-7.363	1.00	0.00
ATOM	2342	IHB	LEU	A	664	-18.452	9.105	-8.430	1.00	0.00
ATOM	2343	2HB	LEU	A	664	-18.697	10.677	-7.662	1.00	0.00
ATOM	2344	HG	LEU	A	664	-19.597	9.063	-6.140	1.00	0.00
ATOM	2345	IHD1	LEU	A	664	-17.391	7.372	-7.115	1.00	0.00
ATOM	2346	2HD1	LEU	A	664	-18.897	6.899	-6.329	1.00	0.00
ATOM	2347	3HD1	LEU	A	664	-17.481	7.364	-5.353	1.00	0.00
ATOM	2348	IHD2	LEU	A	664	-18.594	10.652	-4.826	1.00	0.00
ATOM	2349	2HD2	LEU	A	664	-16.961	10.181	-5.295	1.00	0.00
ATOM	2350	3HD2	LEU	A	664	-17.914	9.152	-4.196	1.00	0.00
ATOM	2351	N	CYS	A	665	-16.360	11.477	-9.628	1.00	0.00

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ATOM 2352 CA CYS A 665	-16.026	11.718	-11.002	1.00	0.00
ATOM 2353 C CYS A 665	-14.559	11.530	-11.271	1.00	0.00
ATOM 2354 O CYS A 665	-14.176	10.917	-12.267	1.00	0.00
ATOM 2355 CB CYS A 665	-16.440	13.121	-11.457	1.00	0.00
ATOM 2356 SG CYS A 665	-18.245	13.318	-11.386	1.00	0.00
ATOM 2357 HN CYS A 665	-16.652	12.231	-9.041	1.00	0.00
ATOM 2358 HA CYS A 665	-16.545	10.961	-11.590	1.00	0.00
ATOM 2359 IHB CYS A 665	-16.109	13.289	-12.482	1.00	0.00
ATOM 2360 2HB CYS A 665	-15.979	13.869	-10.812	1.00	0.00
ATOM 2361 HG CYS A 665	-18.563	14.157	-10.398	1.00	0.00
ATOM 2362 N MET A 666	-13.682	12.032	-10.379	1.00	0.00
ATOM 2363 CA MET A 666	-12.269	11.910	-10.626	1.00	0.00
ATOM 2364 C MET A 666	-11.910	10.462	-10.680	1.00	0.00
ATOM 2365 O MET A 666	-11.143	10.027	-11.537	1.00	0.00
ATOM 2366 CB MET A 666	-11.385	12.529	-9.528	1.00	0.00
ATOM 2367 CG MET A 666	-9.890	12.371	-9.834	1.00	0.00
ATOM 2368 SD MET A 666	-8.751	12.899	-8.518	1.00	0.00
ATOM 2369 CE MET A 666	-8.679	14.648	-8.996	1.00	0.00
ATOM 2370 HN MET A 666	-14.012	12.485	-9.551	1.00	0.00
ATOM 2371 HA MET A 666	-12.080	12.407	-11.577	1.00	0.00
ATOM 2372 IHB MET A 666	-11.607	12.046	-8.577	1.00	0.00
ATOM 2373 2HB MET A 666	-11.620	13.589	-9.437	1.00	0.00
ATOM 2374 IHG MET A 666	-9.656	12.955	-10.723	1.00	0.00
ATOM 2375 2HG MET A 666	-9.689	11.320	-10.038	1.00	0.00
ATOM 2376 IHE MET A 666	-9.197	15.250	-8.250	1.00	0.00
ATOM 2377 2HE MET A 666	-9.169	14.789	-9.959	1.00	0.00
ATOM 2378 3HE MET A 666	-7.641	14.975	-9.048	1.00	0.00
ATOM 2379 N LYS A 667	-12.496	9.665	-9.774	1.00	0.00
ATOM 2380 CA LYS A 667	-12.171	8.276	-9.706	1.00	0.00
ATOM 2381 C LYS A 667	-12.427	7.639	-11.042	1.00	0.00
ATOM 2382 O LYS A 667	-11.599	6.877	-11.541	1.00	0.00
ATOM 2383 CB LYS A 667	-13.029	7.561	-8.645	1.00	0.00
ATOM 2384 CG LYS A 667	-12.738	6.070	-8.521	1.00	0.00
ATOM 2385 CD LYS A 667	-13.243	5.424	-7.228	1.00	0.00
ATOM 2386 CE LYS A 667	-14.595	5.945	-6.740	1.00	0.00
ATOM 2387 NZ LYS A 667	-15.045	5.151	-5.575	1.00	0.00
ATOM 2388 HN LYS A 667	-13.166	10.049	-9.139	1.00	0.00
ATOM 2389 HA LYS A 667	-11.113	8.205	-9.454	1.00	0.00
ATOM 2390 IHB LYS A 667	-14.079	7.690	-8.903	1.00	0.00
ATOM 2391 2HB LYS A 667	-12.852	8.032	-7.680	1.00	0.00
ATOM 2392 IHG LYS A 667	-11.660	5.925	-8.579	1.00	0.00
ATOM 2393 2HG LYS A 667	-13.200	5.559	-9.364	1.00	0.00
ATOM 2394 IHD LYS A 667	-12.505	5.596	-6.446	1.00	0.00
ATOM 2395 2HD LYS A 667	-13.326	4.350	-7.390	1.00	0.00
ATOM 2396 IHE LYS A 667	-15.345	5.853	-7.526	1.00	0.00
ATOM 2397 2HE LYS A 667	-14.513	6.987	-6.432	1.00	0.00
ATOM 2398 IHZ LYS A 667	-14.346	5.234	-4.809	1.00	0.00
ATOM 2399 2HZ LYS A 667	-15.139	4.153	-5.851	1.00	0.00
ATOM 2400 3HZ LYS A 667	-15.964	5.508	-5.246	1.00	0.00

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ATOM 2401 N THR A 668	-13.575	7.951	-11.671	1.00	0.00
ATOM 2402 CA THR A 668	-13.899	7.362	-12.940	1.00	0.00
ATOM 2403 C THR A 668	-12.923	7.822	-13.968	1.00	0.00
ATOM 2404 O THR A 668	-12.511	7.056	-14.838	1.00	0.00
ATOM 2405 CB THR A 668	-15.262	7.745	-13.429	1.00	0.00
ATOM 2406 OG1 THR A 668	-15.314	9.130	-13.734	1.00	0.00
ATOM 2407 CG2 THR A 668	-16.267	7.419	-12.316	1.00	0.00
ATOM 2408 HN THR A 668	-14.208	8.600	-11.250	1.00	0.00
ATOM 2409 HA THR A 668	-13.840	6.282	-12.807	1.00	0.00
ATOM 2410 HB THR A 668	-15.506	7.190	-14.335	1.00	0.00
ATOM 2411 HG1 THR A 668	-14.822	9.577	-13.058	1.00	0.00
ATOM 2412 IHG2 THR A 668	-16.142	8.099	-11.473	1.00	0.00
ATOM 2413 2HG2 THR A 668	-16.112	6.403	-11.955	1.00	0.00
ATOM 2414 3HG2 THR A 668	-17.286	7.526	-12.686	1.00	0.00
ATOM 2415 N LEU A 669	-12.528	9.103	-13.882	1.00	0.00
ATOM 2416 CA LEU A 669	-11.627	9.672	-14.836	1.00	0.00
ATOM 2417 C LEU A 669	-10.377	8.854	-14.779	1.00	0.00
ATOM 2418 O LEU A 669	-9.848	8.427	-15.801	1.00	0.00
ATOM 2419 CB LEU A 669	-11.252	11.117	-14.451	1.00	0.00
ATOM 2420 CG LEU A 669	-10.406	11.869	-15.492	1.00	0.00
ATOM 2421 CD1 LEU A 669	-11.238	12.181	-16.744	1.00	0.00
ATOM 2422 CD2 LEU A 669	-9.759	13.126	-14.890	1.00	0.00
ATOM 2423 HN LEU A 669	-12.873	9.671	-13.134	1.00	0.00
ATOM 2424 HA LEU A 669	-12.129	9.653	-15.803	1.00	0.00
ATOM 2425 1HB LEU A 669	-10.697	11.089	-13.514	1.00	0.00
ATOM 2426 2HB LEU A 669	-12.172	11.677	-14.288	1.00	0.00
ATOM 2427 HG LEU A 669	-9.547	11.259	-15.769	1.00	0.00
ATOM 2428 1HD1 LEU A 669	-12.097	12.801	-16.491	1.00	0.00
ATOM 2429 2HD1 LEU A 669	-11.609	11.258	-17.189	1.00	0.00
ATOM 2430 3HD1 LEU A 669	-10.634	12.722	-17.472	1.00	0.00
ATOM 2431 1HD2 LEU A 669	-9.564	12.988	-13.827	1.00	0.00
ATOM 2432 2HD2 LEU A 669	-10.424	13.982	-15.003	1.00	0.00
ATOM 2433 3HD2 LEU A 669	-8.809	13.333	-15.383	1.00	0.00
ATOM 2434 N LEU A 670	-9.878	8.557	-13.571	1.00	0.00
ATOM 2435 CA LEU A 670	-8.653	7.820	-13.524	1.00	0.00
ATOM 2436 C LEU A 670	-8.775	6.453	-14.115	1.00	0.00
ATOM 2437 O LEU A 670	-7.844	5.969	-14.757	1.00	0.00
ATOM 2438 CB LEU A 670	-8.036	7.728	-12.123	1.00	0.00
ATOM 2439 CG LEU A 670	-7.389	9.061	-11.706	1.00	0.00
ATOM 2440 CD1 LEU A 670	-6.275	9.444	-12.693	1.00	0.00
ATOM 2441 CD2 LEU A 670	-8.411	10.188	-11.504	1.00	0.00
ATOM 2442 HN LEU A 670	-10.346	8.841	-12.735	1.00	0.00
ATOM 2443 HA LEU A 670	-7.963	8.326	-14.199	1.00	0.00
ATOM 2444 1HB LEU A 670	-7.280	6.943	-12.114	1.00	0.00
ATOM 2445 2HB LEU A 670	-8.812	7.464	-11.405	1.00	0.00
ATOM 2446 HG LEU A 670	-6.972	8.967	-10.703	1.00	0.00
ATOM 2447 1HD1 LEU A 670	-6.696	9.727	-13.658	1.00	0.00
ATOM 2448 2HD1 LEU A 670	-5.606	8.599	-12.852	1.00	0.00
ATOM 2449 3HD1 LEU A 670	-5.709	10.293	-12.311	1.00	0.00

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ATOM 2450 1HD2 LEU A 670	-9.306	9.812	-11.010	1.00	0.00
ATOM 2451 2HD2 LEU A 670	-8.707	10.604	-12.467	1.00	0.00
ATOM 2452 3HD2 LEU A 670	-7.986	10.974	-10.880	1.00	0.00
ATOM 2453 N LEU A 671	-9.926	5.787	-13.931	1.00	0.00
ATOM 2454 CA LEU A 671	-10.044	4.459	-14.453	1.00	0.00
ATOM 2455 C LEU A 671	-9.944	4.433	-15.955	1.00	0.00
ATOM 2456 O LEU A 671	-9.366	3.509	-16.522	1.00	0.00
ATOM 2457 CB LEU A 671	-11.309	3.731	-13.950	1.00	0.00
ATOM 2458 CG LEU A 671	-11.475	2.292	-14.479	1.00	0.00
ATOM 2459 CD1 LEU A 671	-12.424	1.474	-13.594	1.00	0.00
ATOM 2460 CD2 LEU A 671	-11.975	2.298	-15.931	1.00	0.00
ATOM 2461 HN LEU A 671	-10.685	6.211	-13.438	1.00	0.00
ATOM 2462 HA LEU A 671	-9.151	3.919	-14.139	1.00	0.00
ATOM 2463 1HB LEU A 671	-12.181	4.311	-14.250	1.00	0.00
ATOM 2464 2HB LEU A 671	-11.277	3.697	-12.862	1.00	0.00
ATOM 2465 HG LEU A 671	-10.501	1.805	-14.507	1.00	0.00
ATOM 2466 1HD1 LEU A 671	-13.450	1.827	-13.700	1.00	0.00
ATOM 2467 2HD1 LEU A 671	-12.140	1.571	-12.547	1.00	0.00
ATOM 2468 3HD1 LEU A 671	-12.398	0.424	-13.885	1.00	0.00
ATOM 2469 1HD2 LEU A 671	-12.110	3.319	-16.288	1.00	0.00
ATOM 2470 2HD2 LEU A 671	-12.936	1.787	-16.000	1.00	0.00
ATOM 2471 3HD2 LEU A 671	-11.251	1.806	-16.580	1.00	0.00
ATOM 2472 N LEU A 672	-10.499	5.448	-16.647	1.00	0.00
ATOM 2473 CA LEU A 672	-10.544	5.514	-18.089	1.00	0.00
ATOM 2474 C LEU A 672	-9.324	5.736	-18.977	1.00	0.00
ATOM 2475 O LEU A 672	-9.312	5.224	-20.093	1.00	0.00
ATOM 2476 CB LEU A 672	-11.620	6.488	-18.600	1.00	0.00
ATOM 2477 CG LEU A 672	-13.033	5.882	-18.591	1.00	0.00
ATOM 2478 CD1 LEU A 672	-13.210	4.877	-19.740	1.00	0.00
ATOM 2479 CD2 LEU A 672	-13.351	5.236	-17.239	1.00	0.00
ATOM 2480 HN LEU A 672	-10.904	6.201	-16.129	1.00	0.00
ATOM 2481 HA LEU A 672	-10.751	4.505	-18.444	1.00	0.00
ATOM 2482 1HB LEU A 672	-11.371	6.786	-19.618	1.00	0.00
ATOM 2483 2HB LEU A 672	-11.615	7.379	-17.972	1.00	0.00
ATOM 2484 HG LEU A 672	-13.769	6.679	-18.692	1.00	0.00
ATOM 2485 1HD1 LEU A 672	-12.388	4.161	-19.756	1.00	0.00
ATOM 2486 2HD1 LEU A 672	-13.222	5.398	-20.697	1.00	0.00
ATOM 2487 3HD1 LEU A 672	-14.139	4.321	-19.614	1.00	0.00
ATOM 2488 1HD2 LEU A 672	-12.588	5.489	-16.503	1.00	0.00
ATOM 2489 2HD2 LEU A 672	-13.379	4.151	-17.337	1.00	0.00
ATOM 2490 3HD2 LEU A 672	-14.310	5.596	-16.867	1.00	0.00
ATOM 2491 N SER A 673	-8.272	6.488	-18.577	1.00	0.00
ATOM 2492 CA SER A 673	-7.270	6.880	-19.559	1.00	0.00
ATOM 2493 C SER A 673	-6.215	5.842	-19.924	1.00	0.00
ATOM 2494 O SER A 673	-5.320	5.609	-19.119	1.00	0.00
ATOM 2495 CB SER A 673	-6.473	8.135	-19.153	1.00	0.00
ATOM 2496 OG SER A 673	-7.309	9.282	-19.137	1.00	0.00
ATOM 2497 HN SER A 673	-8.185	6.770	-17.621	1.00	0.00
ATOM 2498 HA SER A 673	-7.805	7.063	-20.491	1.00	0.00

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ATOM 2499 1HB SER A 673	-5.667	8.315	-19.866	1.00	0.00
ATOM 2500 2HB SER A 673	-6.055	8.007	-18.155	1.00	0.00
ATOM 2501 HG SER A 673	-8.075	9.053	-18.627	1.00	0.00
ATOM 2502 N SER A 674	-6.229	5.234	-21.156	1.00	0.00
ATOM 2503 CA SER A 674	-5.225	4.221	-21.490	1.00	0.00
ATOM 2504 C SER A 674	-5.519	3.470	-22.793	1.00	0.00
ATOM 2505 O SER A 674	-6.620	3.564	-23.322	1.00	0.00
ATOM 2506 CB SER A 674	-5.151	3.147	-20.380	1.00	0.00
ATOM 2507 OG SER A 674	-4.245	2.107	-20.714	1.00	0.00
ATOM 2508 HN SER A 674	-6.927	5.485	-21.827	1.00	0.00
ATOM 2509 HA SER A 674	-4.270	4.734	-21.594	1.00	0.00
ATOM 2510 1HB SER A 674	-6.133	2.699	-20.231	1.00	0.00
ATOM 2511 2HB SER A 674	-4.811	3.599	-19.448	1.00	0.00
ATOM 2512 HG SER A 674	-4.370	1.421	-20.072	1.00	0.00
ATOM 2513 N VAL A 675	-4.521	2.672	-23.293	1.00	0.00
ATOM 2514 CA VAL A 675	-4.423	1.847	-24.498	1.00	0.00
ATOM 2515 C VAL A 675	-5.492	0.778	-24.497	1.00	0.00
ATOM 2516 O VAL A 675	-6.542	1.113	-23.963	1.00	0.00
ATOM 2517 CB VAL A 675	-3.003	1.312	-24.570	1.00	0.00
ATOM 2518 CG1 VAL A 675	-2.839	0.093	-23.643	1.00	0.00
ATOM 2519 CG2 VAL A 675	-2.509	1.219	-26.026	1.00	0.00
ATOM 2520 HN VAL A 675	-3.705	2.649	-22.725	1.00	0.00
ATOM 2521 HA VAL A 675	-4.654	2.476	-25.357	1.00	0.00
ATOM 2522 HB VAL A 675	-2.304	2.093	-24.273	1.00	0.00
ATOM 2523 1HG1 VAL A 675	-3.780	-0.449	-23.550	1.00	0.00
ATOM 2524 2HG1 VAL A 675	-2.536	0.416	-22.647	1.00	0.00
ATOM 2525 3HG1 VAL A 675	-2.095	-0.591	-24.049	1.00	0.00
ATOM 2526 1HG2 VAL A 675	-1.874	2.069	-26.273	1.00	0.00
ATOM 2527 2HG2 VAL A 675	-3.357	1.221	-26.712	1.00	0.00
ATOM 2528 3HG2 VAL A 675	-1.925	0.310	-26.168	1.00	0.00
ATOM 2529 N PRO A 676	-5.477	-0.434	-25.043	1.00	0.00
ATOM 2530 CA PRO A 676	-4.453	-1.012	-25.884	1.00	0.00
ATOM 2531 C PRO A 676	-4.796	-0.749	-27.315	1.00	0.00
ATOM 2532 O PRO A 676	-5.914	-0.312	-27.586	1.00	0.00
ATOM 2533 CB PRO A 676	-4.440	-2.512	-25.580	1.00	0.00
ATOM 2534 CG PRO A 676	-5.840	-2.792	-25.019	1.00	0.00
ATOM 2535 CD PRO A 676	-6.217	-1.471	-24.338	1.00	0.00
ATOM 2536 1HD PRO A 676	-7.288	-1.284	-24.415	1.00	0.00
ATOM 2537 2HD PRO A 676	-5.937	-1.481	-23.285	1.00	0.00
ATOM 2538 HA PRO A 676	-3.487	-0.562	-25.656	1.00	0.00
ATOM 2539 1HB PRO A 676	-3.668	-2.759	-24.852	1.00	0.00
ATOM 2540 2HB PRO A 676	-4.255	-3.094	-26.483	1.00	0.00
ATOM 2541 1HG PRO A 676	-6.543	-3.044	-25.813	1.00	0.00
ATOM 2542 2HG PRO A 676	-5.823	-3.615	-24.304	1.00	0.00
ATOM 2543 N LYS A 677	-3.859	-1.003	-28.252	1.00	0.00
ATOM 2544 CA LYS A 677	-4.201	-0.796	-29.627	1.00	0.00
ATOM 2545 C LYS A 677	-4.195	-2.100	-30.367	1.00	0.00
ATOM 2546 O LYS A 677	-3.171	-2.541	-30.886	1.00	0.00
ATOM 2547 CB LYS A 677	-3.275	0.192	-30.374	1.00	0.00

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ATOM	2548	CG	LYS	A	677	-1.800	-0.215	-30.473	1.00	0.00
ATOM	2549	CD	LYS	A	677	-1.037	0.541	-31.565	1.00	0.00
ATOM	2550	CE	LYS	A	677	0.377	0.011	-31.813	1.00	0.00
ATOM	2551	NZ	LYS	A	677	0.959	0.660	-33.010	1.00	0.00
ATOM	2552	HN	LYS	A	677	-2.949	-1.328	-27.992	1.00	0.00
ATOM	2553	HA	LYS	A	677	-5.223	-0.419	-29.633	1.00	0.00
ATOM	2554	1HB	LYS	A	677	-3.327	1.153	-29.866	1.00	0.00
ATOM	2555	2HB	LYS	A	677	-3.659	0.316	-31.385	1.00	0.00
ATOM	2556	1HG	LYS	A	677	-1.743	-1.283	-30.680	1.00	0.00
ATOM	2557	2HG	LYS	A	677	-1.319	-0.026	-29.514	1.00	0.00
ATOM	2558	1HD	LYS	A	677	-0.970	1.590	-31.280	1.00	0.00
ATOM	2559	2HD	LYS	A	677	-1.601	0.474	-32.494	1.00	0.00
ATOM	2560	1HE	LYS	A	677	0.354	-1.065	-31.986	1.00	0.00
ATOM	2561	2HE	LYS	A	677	1.020	0.231	-30.961	1.00	0.00
ATOM	2562	1HZ	LYS	A	677	1.000	1.688	-32.862	1.00	0.00
ATOM	2563	2HZ	LYS	A	677	0.366	0.453	-33.839	1.00	0.00
ATOM	2564	3HZ	LYS	A	677	1.919	0.294	-33.171	1.00	0.00
ATOM	2565	N	ASP	A	678	-5.355	-2.780	-30.419	1.00	0.00
ATOM	2566	CA	ASP	A	678	-5.403	-3.975	-31.206	1.00	0.00
ATOM	2567	C	ASP	A	678	-5.302	-3.500	-32.613	1.00	0.00
ATOM	2568	O	ASP	A	678	-4.614	-4.095	-33.442	1.00	0.00
ATOM	2569	CB	ASP	A	678	-6.712	-4.768	-31.063	1.00	0.00
ATOM	2570	CG	ASP	A	678	-6.667	-5.508	-29.735	1.00	0.00
ATOM	2571	OD1	ASP	A	678	-7.705	-6.119	-29.363	1.00	0.00
ATOM	2572	OD2	ASP	A	678	-5.594	-5.476	-29.076	1.00	0.00
ATOM	2573	HN	ASP	A	678	-6.161	-2.459	-29.921	1.00	0.00
ATOM	2574	HA	ASP	A	678	-4.562	-4.588	-30.882	1.00	0.00
ATOM	2575	1HB	ASP	A	678	-6.815	-5.488	-31.875	1.00	0.00
ATOM	2576	2HB	ASP	A	678	-7.571	-4.096	-31.073	1.00	0.00
ATOM	2577	N	GLY	A	679	-5.989	-2.381	-32.908	1.00	0.00
ATOM	2578	CA	GLY	A	679	-5.943	-1.827	-34.223	1.00	0.00
ATOM	2579	C	GLY	A	679	-7.129	-0.938	-34.393	1.00	0.00
ATOM	2580	O	GLY	A	679	-7.322	0.016	-33.642	1.00	0.00
ATOM	2581	HN	GLY	A	679	-6.535	-1.934	-32.199	1.00	0.00
ATOM	2582	1HA	GLY	A	679	-5.978	-2.646	-34.940	1.00	0.00
ATOM	2583	2HA	GLY	A	679	-5.023	-1.253	-34.321	1.00	0.00
ATOM	2584	N	LEU	A	680	-7.974	-1.247	-35.390	1.00	0.00
ATOM	2585	CA	LEU	A	680	-9.110	-0.416	-35.644	1.00	0.00
ATOM	2586	C	LEU	A	680	-9.988	-0.447	-34.444	1.00	0.00
ATOM	2587	O	LEU	A	680	-10.549	0.573	-34.047	1.00	0.00
ATOM	2588	CB	LEU	A	680	-9.935	-0.874	-36.858	1.00	0.00
ATOM	2589	CG	LEU	A	680	-9.171	-0.731	-38.187	1.00	0.00
ATOM	2590	CD1	LEU	A	680	-7.937	-1.648	-38.224	1.00	0.00
ATOM	2591	CD2	LEU	A	680	-10.102	-0.926	-39.392	1.00	0.00
ATOM	2592	HN	LEU	A	680	-7.809	-2.056	-35.954	1.00	0.00
ATOM	2593	HA	LEU	A	680	-8.728	0.591	-35.810	1.00	0.00
ATOM	2594	1HB	LEU	A	680	-10.847	-0.280	-36.909	1.00	0.00
ATOM	2595	2HB	LEU	A	680	-10.214	-1.918	-36.722	1.00	0.00
ATOM	2596	HG	LEU	A	680	-8.853	0.304	-38.310	1.00	0.00

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ATOM	2597	1HD1	LEU	A	680	-8.164	-2.616	-37.778	1.00	0.00
ATOM	2598	2HD1	LEU	A	680	-7.118	-1.201	-37.661	1.00	0.00
ATOM	2599	3HD1	LEU	A	680	-7.625	-1.816	-39.255	1.00	0.00
ATOM	2600	1HD2	LEU	A	680	-10.902	-0.186	-39.385	1.00	0.00
ATOM	2601	2HD2	LEU	A	680	-10.558	-1.916	-39.359	1.00	0.00
ATOM	2602	3HD2	LEU	A	680	-9.544	-0.811	-40.321	1.00	0.00
ATOM	2603	N	LYS	A	681	-10.116	-1.628	-33.820	1.00	0.00
ATOM	2604	CA	LYS	A	681	-10.950	-1.737	-32.666	1.00	0.00
ATOM	2605	C	LYS	A	681	-10.397	-0.839	-31.612	1.00	0.00
ATOM	2606	O	LYS	A	681	-11.152	-0.186	-30.892	1.00	0.00
ATOM	2607	CB	LYS	A	681	-10.994	-3.159	-32.086	1.00	0.00
ATOM	2608	CG	LYS	A	681	-11.782	-4.143	-32.953	1.00	0.00
ATOM	2609	CD	LYS	A	681	-13.264	-3.791	-33.083	1.00	0.00
ATOM	2610	CE	LYS	A	681	-14.052	-4.774	-33.949	1.00	0.00
ATOM	2611	NZ	LYS	A	681	-13.595	-4.689	-35.355	1.00	0.00
ATOM	2612	HN	LYS	A	681	-9.628	-2.430	-34.164	1.00	0.00
ATOM	2613	HA	LYS	A	681	-11.949	-1.428	-32.973	1.00	0.00
ATOM	2614	1HB	LYS	A	681	-11.449	-3.121	-31.097	1.00	0.00
ATOM	2615	2HB	LYS	A	681	-9.974	-3.526	-31.979	1.00	0.00
ATOM	2616	1HG	LYS	A	681	-11.696	-5.138	-32.518	1.00	0.00
ATOM	2617	2HG	LYS	A	681	-11.339	-4.164	-33.947	1.00	0.00
ATOM	2618	1HD	LYS	A	681	-13.349	-2.796	-33.519	1.00	0.00
ATOM	2619	2HD	LYS	A	681	-13.707	-3.768	-32.089	1.00	0.00
ATOM	2620	1HE	LYS	A	681	-15.115	-4.536	-33.922	1.00	0.00
ATOM	2621	2HE	LYS	A	681	-13.897	-5.795	-33.601	1.00	0.00
ATOM	2622	1HZ	LYS	A	681	-12.583	-4.924	-35.405	1.00	0.00
ATOM	2623	2HZ	LYS	A	681	-13.744	-3.724	-35.711	1.00	0.00
ATOM	2624	3HZ	LYS	A	681	-14.135	-5.361	-35.937	1.00	0.00
ATOM	2625	N	SER	A	682	-9.058	-0.771	-31.496	1.00	0.00
ATOM	2626	CA	SER	A	682	-8.516	0.051	-30.459	1.00	0.00
ATOM	2627	C	SER	A	682	-8.919	1.467	-30.694	1.00	0.00
ATOM	2628	O	SER	A	682	-9.388	2.127	-29.772	1.00	0.00
ATOM	2629	CB	SER	A	682	-6.978	0.012	-30.339	1.00	0.00
ATOM	2630	OG	SER	A	682	-6.366	0.766	-31.373	1.00	0.00
ATOM	2631	HN	SER	A	682	-8.462	-1.280	-32.115	1.00	0.00
ATOM	2632	HA	SER	A	682	-8.965	-0.299	-29.529	1.00	0.00
ATOM	2633	1HB	SER	A	682	-6.623	-1.016	-30.417	1.00	0.00
ATOM	2634	2HB	SER	A	682	-6.667	0.434	-29.384	1.00	0.00
ATOM	2635	HG	SER	A	682	-7.010	0.857	-32.062	1.00	0.00
ATOM	2636	N	GLN	A	683	-8.804	1.975	-31.937	1.00	0.00
ATOM	2637	CA	GLN	A	683	-9.159	3.355	-32.108	1.00	0.00
ATOM	2638	C	GLN	A	683	-10.607	3.525	-31.795	1.00	0.00
ATOM	2639	O	GLN	A	683	-11.012	4.550	-31.250	1.00	0.00
ATOM	2640	CB	GLN	A	683	-8.907	3.961	-33.504	1.00	0.00
ATOM	2641	CG	GLN	A	683	-9.702	3.344	-34.655	1.00	0.00
ATOM	2642	CD	GLN	A	683	-8.737	2.506	-35.476	1.00	0.00
ATOM	2643	OE1	GLN	A	683	-7.665	2.128	-35.005	1.00	0.00
ATOM	2644	NE2	GLN	A	683	-9.115	2.226	-36.752	1.00	0.00
ATOM	2645	HN	GLN	A	683	-8.486	1.417	-32.703	1.00	0.00

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ATOM	2646	HA	GLN	A	683	-8.576	3.903	-31.368	1.00	0.00
ATOM	2647	IHB	GLN	A	683	-7.848	3.855	-33.731	1.00	0.00
ATOM	2648	2HB	GLN	A	683	-9.146	5.022	-33.459	1.00	0.00
ATOM	2649	IHG	GLN	A	683	-10.134	4.122	-35.285	1.00	0.00
ATOM	2650	2HG	GLN	A	683	-10.502	2.709	-34.274	1.00	0.00
ATOM	2651	IHE2	GLN	A	683	-8.460	1.811	-37.383	1.00	0.00
ATOM	2652	2HE2	GLN	A	683	-10.039	2.429	-37.075	1.00	0.00
ATOM	2653	N	GLU	A	684	-11.433	2.521	-32.140	1.00	0.00
ATOM	2654	CA	GLU	A	684	-12.839	2.607	-31.877	1.00	0.00
ATOM	2655	C	GLU	A	684	-13.018	2.688	-30.394	1.00	0.00
ATOM	2656	O	GLU	A	684	-13.812	3.478	-29.888	1.00	0.00
ATOM	2657	CB	GLU	A	684	-13.597	1.362	-32.363	1.00	0.00
ATOM	2658	CG	GLU	A	684	-15.098	1.590	-32.521	1.00	0.00
ATOM	2659	CD	GLU	A	684	-15.285	2.313	-33.845	1.00	0.00
ATOM	2660	OE1	GLU	A	684	-14.495	2.028	-34.784	1.00	0.00
ATOM	2661	OE2	GLU	A	684	-16.211	3.162	-33.936	1.00	0.00
ATOM	2662	HN	GLU	A	684	-11.061	1.706	-32.584	1.00	0.00
ATOM	2663	HA	GLU	A	684	-13.203	3.496	-32.392	1.00	0.00
ATOM	2664	IHB	GLU	A	684	-13.438	0.554	-31.649	1.00	0.00
ATOM	2665	2HB	GLU	A	684	-13.186	1.055	-33.324	1.00	0.00
ATOM	2666	IHG	GLU	A	684	-15.486	2.204	-31.708	1.00	0.00
ATOM	2667	2HG	GLU	A	684	-15.636	0.642	-32.540	1.00	0.00
ATOM	2668	N	LEU	A	685	-12.256	1.860	-29.660	1.00	0.00
ATOM	2669	CA	LEU	A	685	-12.333	1.834	-28.230	1.00	0.00
ATOM	2670	C	LEU	A	685	-11.900	3.180	-27.745	1.00	0.00
ATOM	2671	O	LEU	A	685	-12.485	3.719	-26.809	1.00	0.00
ATOM	2672	CB	LEU	A	685	-11.418	0.741	-27.624	1.00	0.00
ATOM	2673	CG	LEU	A	685	-11.464	0.523	-26.089	1.00	0.00
ATOM	2674	CD1	LEU	A	685	-10.495	-0.600	-25.688	1.00	0.00
ATOM	2675	CD2	LEU	A	685	-11.179	1.793	-25.269	1.00	0.00
ATOM	2676	HN	LEU	A	685	-11.618	1.246	-30.124	1.00	0.00
ATOM	2677	HA	LEU	A	685	-13.374	1.643	-27.972	1.00	0.00
ATOM	2678	IHB	LEU	A	685	-10.393	0.988	-27.890	1.00	0.00
ATOM	2679	2HB	LEU	A	685	-11.679	-0.203	-28.097	1.00	0.00
ATOM	2680	HG	LEU	A	685	-12.477	0.258	-25.787	1.00	0.00
ATOM	2681	IHD1	LEU	A	685	-9.565	-0.186	-25.300	1.00	0.00
ATOM	2682	2HD1	LEU	A	685	-10.254	-1.217	-26.554	1.00	0.00
ATOM	2683	3HD1	LEU	A	685	-10.939	-1.220	-24.909	1.00	0.00
ATOM	2684	IHD2	LEU	A	685	-12.108	2.238	-24.912	1.00	0.00
ATOM	2685	2HD2	LEU	A	685	-10.667	2.532	-25.886	1.00	0.00
ATOM	2686	3HD2	LEU	A	685	-10.566	1.552	-24.401	1.00	0.00
ATOM	2687	N	PHE	A	686	-10.863	3.764	-28.371	1.00	0.00
ATOM	2688	CA	PHE	A	686	-10.358	5.027	-27.916	1.00	0.00
ATOM	2689	C	PHE	A	686	-11.389	6.090	-28.050	1.00	0.00
ATOM	2690	O	PHE	A	686	-11.546	6.926	-27.162	1.00	0.00
ATOM	2691	CB	PHE	A	686	-9.101	5.529	-28.657	1.00	0.00
ATOM	2692	CG	PHE	A	686	-7.902	4.803	-28.143	1.00	0.00
ATOM	2693	CD1	PHE	A	686	-7.383	3.716	-28.806	1.00	0.00
ATOM	2694	CD2	PHE	A	686	-7.315	5.198	-26.963	1.00	0.00

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ATOM	2695	CE1 PHE A 686	-6.291	3.042	-28.311	1.00	0.00
ATOM	2696	CE2 PHE A 686	-6.225	4.527	-26.460	1.00	0.00
ATOM	2697	CZ PHE A 686	-5.709	3.448	-27.134	1.00	0.00
ATOM	2698	HN PHE A 686	-10.442	3.314	-29.159	1.00	0.00
ATOM	2699	HA PHE A 686	-10.131	4.898	-26.858	1.00	0.00
ATOM	2700	1HB PHE A 686	-8.971	6.599	-28.491	1.00	0.00
ATOM	2701	2HB PHE A 686	-9.199	5.348	-29.727	1.00	0.00
ATOM	2702	HD1 PHE A 686	-7.839	3.387	-29.728	1.00	0.00
ATOM	2703	HD2 PHE A 686	-7.715	6.044	-26.425	1.00	0.00
ATOM	2704	HE1 PHE A 686	-5.891	2.195	-28.848	1.00	0.00
ATOM	2705	HE2 PHE A 686	-5.773	4.850	-25.534	1.00	0.00
ATOM	2706	HZ PHE A 686	-4.852	2.920	-26.742	1.00	0.00
ATOM	2707	N ASP A 687	-12.135	6.092	-29.164	1.00	0.00
ATOM	2708	CA ASP A 687	-13.083	7.148	-29.329	1.00	0.00
ATOM	2709	C ASP A 687	-14.094	7.068	-28.235	1.00	0.00
ATOM	2710	O ASP A 687	-14.430	8.074	-27.612	1.00	0.00
ATOM	2711	CB ASP A 687	-13.841	7.083	-30.663	1.00	0.00
ATOM	2712	CG ASP A 687	-14.550	8.418	-30.818	1.00	0.00
ATOM	2713	OD1 ASP A 687	-14.445	9.244	-29.873	1.00	0.00
ATOM	2714	OD2 ASP A 687	-15.199	8.632	-31.876	1.00	0.00
ATOM	2715	HN ASP A 687	-12.030	5.378	-29.856	1.00	0.00
ATOM	2716	HA ASP A 687	-12.523	8.080	-29.263	1.00	0.00
ATOM	2717	1HB ASP A 687	-14.573	6.276	-30.656	1.00	0.00
ATOM	2718	2HB ASP A 687	-13.153	6.933	-31.495	1.00	0.00
ATOM	2719	N GLU A 688	-14.578	5.849	-27.942	1.00	0.00
ATOM	2720	CA GLU A 688	-15.609	5.742	-26.962	1.00	0.00
ATOM	2721	C GLU A 688	-15.131	6.282	-25.656	1.00	0.00
ATOM	2722	O GLU A 688	-15.805	7.105	-25.037	1.00	0.00
ATOM	2723	CB GLU A 688	-16.078	4.297	-26.724	1.00	0.00
ATOM	2724	CG GLU A 688	-17.293	4.220	-25.797	1.00	0.00
ATOM	2725	CD GLU A 688	-17.856	2.809	-25.859	1.00	0.00
ATOM	2726	OE1 GLU A 688	-17.087	1.874	-26.206	1.00	0.00
ATOM	2727	OE2 GLU A 688	-19.070	2.652	-25.564	1.00	0.00
ATOM	2728	HN GLU A 688	-14.223	5.035	-28.402	1.00	0.00
ATOM	2729	HA GLU A 688	-16.441	6.349	-27.319	1.00	0.00
ATOM	2730	1HB GLU A 688	-15.260	3.727	-26.283	1.00	0.00
ATOM	2731	2HB GLU A 688	-16.333	3.845	-27.681	1.00	0.00
ATOM	2732	1HG GLU A 688	-18.059	4.926	-26.116	1.00	0.00
ATOM	2733	2HG GLU A 688	-17.004	4.446	-24.771	1.00	0.00
ATOM	2734	N ILE A 689	-13.936	5.865	-25.202	1.00	0.00
ATOM	2735	CA ILE A 689	-13.526	6.370	-23.928	1.00	0.00
ATOM	2736	C ILE A 689	-13.262	7.842	-23.953	1.00	0.00
ATOM	2737	O ILE A 689	-13.552	8.537	-22.983	1.00	0.00
ATOM	2738	CB ILE A 689	-12.444	5.577	-23.235	1.00	0.00
ATOM	2739	CG1 ILE A 689	-11.151	5.446	-24.042	1.00	0.00
ATOM	2740	CG2 ILE A 689	-13.060	4.229	-22.839	1.00	0.00
ATOM	2741	CD1 ILE A 689	-10.067	4.699	-23.265	1.00	0.00
ATOM	2742	HN ILE A 689	-13.365	5.235	-25.728	1.00	0.00
ATOM	2743	HA ILE A 689	-14.422	6.382	-23.309	1.00	0.00

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ATOM	2744	HB	ILE A 689	-12.091	6.109	-22.350	1.00	0.00
ATOM	2745	1HG2	ILE A 689	-13.250	3.618	-23.722	1.00	0.00
ATOM	2746	2HG2	ILE A 689	-14.010	4.384	-22.327	1.00	0.00
ATOM	2747	3HG2	ILE A 689	-12.379	3.679	-22.189	1.00	0.00
ATOM	2748	1HG1	ILE A 689	-10.787	6.441	-24.298	1.00	0.00
ATOM	2749	2HG1	ILE A 689	-11.361	4.911	-24.968	1.00	0.00
ATOM	2750	1HD1	ILE A 689	-10.400	3.693	-23.010	1.00	0.00
ATOM	2751	2HD1	ILE A 689	-9.839	5.223	-22.337	1.00	0.00
ATOM	2752	3HD1	ILE A 689	-9.163	4.612	-23.868	1.00	0.00
ATOM	2753	N	ARG A 690	-12.745	8.378	-25.070	1.00	0.00
ATOM	2754	CA	ARG A 690	-12.504	9.793	-25.120	1.00	0.00
ATOM	2755	C	ARG A 690	-13.821	10.474	-24.910	1.00	0.00
ATOM	2756	O	ARG A 690	-13.918	11.457	-24.178	1.00	0.00
ATOM	2757	CB	ARG A 690	-11.949	10.243	-26.483	1.00	0.00
ATOM	2758	CG	ARG A 690	-10.620	9.572	-26.842	1.00	0.00
ATOM	2759	CD	ARG A 690	-10.025	10.023	-28.178	1.00	0.00
ATOM	2760	NE	ARG A 690	-9.259	11.276	-27.924	1.00	0.00
ATOM	2761	CZ	ARG A 690	-8.030	11.450	-28.490	1.00	0.00
ATOM	2762	NH1	ARG A 690	-7.500	10.477	-29.289	1.00	0.00
ATOM	2763	NH2	ARG A 690	-7.324	12.595	-28.252	1.00	0.00
ATOM	2764	HN	ARG A 690	-12.530	7.799	-25.857	1.00	0.00
ATOM	2765	HA	ARG A 690	-11.789	10.018	-24.328	1.00	0.00
ATOM	2766	1HB	ARG A 690	-11.804	11.323	-26.465	1.00	0.00
ATOM	2767	2HB	ARG A 690	-12.680	10.009	-27.256	1.00	0.00
ATOM	2768	1HG	ARG A 690	-10.776	8.495	-26.879	1.00	0.00
ATOM	2769	2HG	ARG A 690	-9.901	9.788	-26.053	1.00	0.00
ATOM	2770	1HD	ARG A 690	-10.805	10.246	-28.905	1.00	0.00
ATOM	2771	2HD	ARG A 690	-9.335	9.280	-28.576	1.00	0.00
ATOM	2772	HE	ARG A 690	-9.645	11.990	-27.339	1.00	0.00
ATOM	2773	1HH1	ARG A 690	-8.014	9.636	-29.460	1.00	0.00
ATOM	2774	2HH1	ARG A 690	-6.599	10.606	-29.703	1.00	0.00
ATOM	2775	1HH2	ARG A 690	-7.708	13.306	-27.663	1.00	0.00
ATOM	2776	2HH2	ARG A 690	-6.423	12.722	-28.667	1.00	0.00
ATOM	2777	N	MET A 691	-14.880	9.937	-25.544	1.00	0.00
ATOM	2778	CA	MET A 691	-16.196	10.500	-25.455	1.00	0.00
ATOM	2779	C	MET A 691	-16.711	10.474	-24.049	1.00	0.00
ATOM	2780	O	MET A 691	-17.297	11.450	-23.583	1.00	0.00
ATOM	2781	CB	MET A 691	-17.218	9.745	-26.318	1.00	0.00
ATOM	2782	CG	MET A 691	-18.627	10.331	-26.228	1.00	0.00
ATOM	2783	SD	MET A 691	-18.833	11.973	-26.976	1.00	0.00
ATOM	2784	CE	MET A 691	-20.569	12.136	-26.468	1.00	0.00
ATOM	2785	HN	MET A 691	-14.743	9.115	-26.097	1.00	0.00
ATOM	2786	HA	MET A 691	-16.117	11.536	-25.785	1.00	0.00
ATOM	2787	1HB	MET A 691	-17.248	8.705	-25.998	1.00	0.00
ATOM	2788	2HB	MET A 691	-16.891	9.774	-27.357	1.00	0.00
ATOM	2789	1HG	MET A 691	-18.904	10.410	-25.178	1.00	0.00
ATOM	2790	2HG	MET A 691	-19.318	9.652	-26.726	1.00	0.00
ATOM	2791	1HE	MET A 691	-20.636	12.085	-25.381	1.00	0.00
ATOM	2792	2HE	MET A 691	-21.157	11.321	-26.891	1.00	0.00

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ATOM	2793	3HE	MET A 691	-20.963	13.097	-26.797	1.00	0.00
ATOM	2794	N	THR A 692	-16.508	9.357	-23.329	1.00	0.00
ATOM	2795	CA	THR A 692	-16.995	9.258	-21.982	1.00	0.00
ATOM	2796	C	THR A 692	-16.283	10.306	-21.199	1.00	0.00
ATOM	2797	O	THR A 692	-16.863	10.948	-20.323	1.00	0.00
ATOM	2798	CB	THR A 692	-16.680	7.937	-21.344	1.00	0.00
ATOM	2799	OG1	THR A 692	-17.264	6.880	-22.089	1.00	0.00
ATOM	2800	CG2	THR A 692	-17.230	7.943	-19.907	1.00	0.00
ATOM	2801	HN	THR A 692	-16.014	8.588	-23.736	1.00	0.00
ATOM	2802	HA	THR A 692	-18.074	9.404	-22.029	1.00	0.00
ATOM	2803	HB	THR A 692	-15.602	7.779	-21.316	1.00	0.00
ATOM	2804	HG1	THR A 692	-16.785	6.824	-22.905	1.00	0.00
ATOM	2805	1HG2	THR A 692	-18.113	8.578	-19.836	1.00	0.00
ATOM	2806	2HG2	THR A 692	-16.480	8.329	-19.218	1.00	0.00
ATOM	2807	3HG2	THR A 692	-17.516	6.934	-19.610	1.00	0.00
ATOM	2808	N	TYR A 693	-14.990	10.511	-21.517	1.00	0.00
ATOM	2809	CA	TYR A 693	-14.227	11.517	-20.844	1.00	0.00
ATOM	2810	C	TYR A 693	-14.929	12.817	-20.883	1.00	0.00
ATOM	2811	O	TYR A 693	-15.150	13.421	-19.838	1.00	0.00
ATOM	2812	CB	TYR A 693	-12.888	11.823	-21.527	1.00	0.00
ATOM	2813	CG	TYR A 693	-11.895	10.964	-20.883	1.00	0.00
ATOM	2814	CD1	TYR A 693	-11.864	9.613	-21.108	1.00	0.00
ATOM	2815	CD2	TYR A 693	-11.090	11.555	-19.944	1.00	0.00
ATOM	2816	CE1	TYR A 693	-11.078	8.830	-20.307	1.00	0.00
ATOM	2817	CE2	TYR A 693	-10.292	10.784	-19.157	1.00	0.00
ATOM	2818	CZ	TYR A 693	-10.331	9.429	-19.322	1.00	0.00
ATOM	2819	OH	TYR A 693	-9.721	8.651	-18.344	1.00	0.00
ATOM	2820	HN	TYR A 693	-14.562	9.956	-22.230	1.00	0.00
ATOM	2821	HA	TYR A 693	-14.054	11.149	-19.833	1.00	0.00
ATOM	2822	1HB	TYR A 693	-12.616	12.871	-21.396	1.00	0.00
ATOM	2823	2HB	TYR A 693	-12.937	11.603	-22.594	1.00	0.00
ATOM	2824	HD1	TYR A 693	-12.448	9.174	-21.902	1.00	0.00
ATOM	2825	HE1	TYR A 693	-11.046	7.760	-20.446	1.00	0.00
ATOM	2826	HD2	TYR A 693	-11.089	12.629	-19.830	1.00	0.00
ATOM	2827	HE2	TYR A 693	-9.643	11.233	-18.420	1.00	0.00
ATOM	2828	HH	TYR A 693	-9.926	9.002	-17.487	1.00	0.00
ATOM	2829	N	ILE A 694	-15.324	13.266	-22.084	1.00	0.00
ATOM	2830	CA	ILE A 694	-15.905	14.570	-22.166	1.00	0.00
ATOM	2831	C	ILE A 694	-17.151	14.605	-21.352	1.00	0.00
ATOM	2832	O	ILE A 694	-17.425	15.590	-20.668	1.00	0.00
ATOM	2833	CB	ILE A 694	-16.243	15.008	-23.564	1.00	0.00
ATOM	2834	CG1	ILE A 694	-16.539	16.517	-23.576	1.00	0.00
ATOM	2835	CG2	ILE A 694	-17.401	14.145	-24.087	1.00	0.00
ATOM	2836	CD1	ILE A 694	-16.577	17.126	-24.977	1.00	0.00
ATOM	2837	HN	ILE A 694	-15.214	12.701	-22.902	1.00	0.00
ATOM	2838	HA	ILE A 694	-15.179	15.256	-21.730	1.00	0.00
ATOM	2839	HB	ILE A 694	-15.373	14.893	-24.210	1.00	0.00
ATOM	2840	1HG2	ILE A 694	-18.314	14.734	-24.170	1.00	0.00
ATOM	2841	2HG2	ILE A 694	-17.595	13.319	-23.402	1.00	0.00

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ATOM	2842	3HG2	ILE A 694	-17.162	13.753	-25.075	1.00	0.00
ATOM	2843	1HG1	ILE A 694	-15.771	17.028	-22.995	1.00	0.00
ATOM	2844	2HG1	ILE A 694	-17.502	16.688	-23.096	1.00	0.00
ATOM	2845	1HD1	ILE A 694	-17.351	16.652	-25.582	1.00	0.00
ATOM	2846	2HD1	ILE A 694	-15.621	16.978	-25.478	1.00	0.00
ATOM	2847	3HD1	ILE A 694	-16.801	18.191	-24.919	1.00	0.00
ATOM	2848	N	LYS A 695	-17.938	13.516	-21.384	1.00	0.00
ATOM	2849	CA	LYS A 695	-19.157	13.529	-20.639	1.00	0.00
ATOM	2850	C	LYS A 695	-18.843	13.722	-19.190	1.00	0.00
ATOM	2851	O	LYS A 695	-19.467	14.547	-18.523	1.00	0.00
ATOM	2852	CB	LYS A 695	-19.967	12.229	-20.781	1.00	0.00
ATOM	2853	CG	LYS A 695	-21.302	12.282	-20.036	1.00	0.00
ATOM	2854	CD	LYS A 695	-22.279	13.304	-20.617	1.00	0.00
ATOM	2855	CE	LYS A 695	-23.558	13.464	-19.793	1.00	0.00
ATOM	2856	NZ	LYS A 695	-23.266	14.222	-18.556	1.00	0.00
ATOM	2857	HN	LYS A 695	-17.674	12.713	-21.918	1.00	0.00
ATOM	2858	HA	LYS A 695	-19.739	14.373	-21.009	1.00	0.00
ATOM	2859	1HB	LYS A 695	-19.377	11.400	-20.390	1.00	0.00
ATOM	2860	2HB	LYS A 695	-20.158	12.045	-21.837	1.00	0.00
ATOM	2861	1HG	LYS A 695	-21.111	12.532	-18.993	1.00	0.00
ATOM	2862	2HG	LYS A 695	-21.763	11.296	-20.073	1.00	0.00
ATOM	2863	1HD	LYS A 695	-22.550	12.995	-21.626	1.00	0.00
ATOM	2864	2HD	LYS A 695	-21.780	14.270	-20.678	1.00	0.00
ATOM	2865	1HE	LYS A 695	-23.952	12.488	-19.510	1.00	0.00
ATOM	2866	2HE	LYS A 695	-24.310	14.013	-20.360	1.00	0.00
ATOM	2867	1HZ	LYS A 695	-22.898	15.162	-18.804	1.00	0.00
ATOM	2868	2HZ	LYS A 695	-22.557	13.709	-17.994	1.00	0.00
ATOM	2869	3HZ	LYS A 695	-24.139	14.328	-18.000	1.00	0.00
ATOM	2870	N	GLU A 696	-17.839	12.994	-18.659	1.00	0.00
ATOM	2871	CA	GLU A 696	-17.555	13.155	-17.265	1.00	0.00
ATOM	2872	C	GLU A 696	-17.124	14.559	-17.009	1.00	0.00
ATOM	2873	O	GLU A 696	-17.494	15.140	-15.989	1.00	0.00
ATOM	2874	CB	GLU A 696	-16.462	12.236	-16.677	1.00	0.00
ATOM	2875	CG	GLU A 696	-15.054	12.411	-17.246	1.00	0.00
ATOM	2876	CD	GLU A 696	-14.677	11.126	-17.965	1.00	0.00
ATOM	2877	OE1	GLU A 696	-15.592	10.298	-18.223	1.00	0.00
ATOM	2878	OE2	GLU A 696	-13.465	10.951	-18.262	1.00	0.00
ATOM	2879	HN	GLU A 696	-17.310	12.361	-19.224	1.00	0.00
ATOM	2880	HA	GLU A 696	-18.496	12.970	-16.749	1.00	0.00
ATOM	2881	1HB	GLU A 696	-16.766	11.204	-16.843	1.00	0.00
ATOM	2882	2HB	GLU A 696	-16.416	12.412	-15.604	1.00	0.00
ATOM	2883	1HG	GLU A 696	-14.338	12.600	-16.446	1.00	0.00
ATOM	2884	2HG	GLU A 696	-15.026	13.241	-17.952	1.00	0.00
ATOM	2885	N	LEU A 697	-16.332	15.163	-17.919	1.00	0.00
ATOM	2886	CA	LEU A 697	-15.923	16.501	-17.606	1.00	0.00
ATOM	2887	C	LEU A 697	-17.125	17.387	-17.521	1.00	0.00
ATOM	2888	O	LEU A 697	-17.223	18.217	-16.619	1.00	0.00
ATOM	2889	CB	LEU A 697	-14.934	17.177	-18.580	1.00	0.00
ATOM	2890	CG	LEU A 697	-13.522	16.555	-18.621	1.00	0.00

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ATOM	2891	CD1	LEU	A	697	-13.050	16.137	-17.219	1.00	0.00
ATOM	2892	CD2	LEU	A	697	-13.367	15.482	-19.702	1.00	0.00
ATOM	2893	HN	LEU	A	697	-16.049	14.705	-18.760	1.00	0.00
ATOM	2894	HA	LEU	A	697	-15.468	16.443	-16.618	1.00	0.00
ATOM	2895	1HB	LEU	A	697	-14.838	18.223	-18.297	1.00	0.00
ATOM	2896	2HB	LEU	A	697	-15.357	17.129	-19.582	1.00	0.00
ATOM	2897	HG	LEU	A	697	-12.821	17.280	-19.034	1.00	0.00
ATOM	2898	1HD1	LEU	A	697	-13.342	15.109	-17.005	1.00	0.00
ATOM	2899	2HD1	LEU	A	697	-13.501	16.780	-16.463	1.00	0.00
ATOM	2900	3HD1	LEU	A	697	-11.964	16.199	-17.153	1.00	0.00
ATOM	2901	1HD2	LEU	A	697	-12.720	15.834	-20.504	1.00	0.00
ATOM	2902	2HD2	LEU	A	697	-14.338	15.241	-20.134	1.00	0.00
ATOM	2903	3HD2	LEU	A	697	-12.921	14.583	-19.278	1.00	0.00
ATOM	2904	N	GLY	A	698	-18.088	17.215	-18.447	1.00	0.00
ATOM	2905	CA	GLY	A	698	-19.251	18.055	-18.451	1.00	0.00
ATOM	2906	C	GLY	A	698	-19.965	17.888	-17.151	1.00	0.00
ATOM	2907	O	GLY	A	698	-20.472	18.845	-16.571	1.00	0.00
ATOM	2908	HN	GLY	A	698	-17.990	16.497	-19.136	1.00	0.00
ATOM	2909	1HA	GLY	A	698	-19.891	17.744	-19.275	1.00	0.00
ATOM	2910	2HA	GLY	A	698	-18.923	19.087	-18.571	1.00	0.00
ATOM	2911	N	LYS	A	699	-20.020	16.646	-16.651	1.00	0.00
ATOM	2912	CA	LYS	A	699	-20.696	16.400	-15.419	1.00	0.00
ATOM	2913	C	LYS	A	699	-20.029	17.204	-14.345	1.00	0.00
ATOM	2914	O	LYS	A	699	-20.701	17.796	-13.502	1.00	0.00
ATOM	2915	CB	LYS	A	699	-20.667	14.897	-15.068	1.00	0.00
ATOM	2916	CG	LYS	A	699	-21.365	14.527	-13.762	1.00	0.00
ATOM	2917	CD	LYS	A	699	-20.564	14.961	-12.540	1.00	0.00
ATOM	2918	CE	LYS	A	699	-21.431	15.484	-11.408	1.00	0.00
ATOM	2919	NZ	LYS	A	699	-22.434	16.434	-11.943	1.00	0.00
ATOM	2920	HN	LYS	A	699	-19.587	15.891	-17.143	1.00	0.00
ATOM	2921	HA	LYS	A	699	-21.723	16.746	-15.540	1.00	0.00
ATOM	2922	1HB	LYS	A	699	-19.628	14.581	-15.002	1.00	0.00
ATOM	2923	2HB	LYS	A	699	-21.143	14.347	-15.879	1.00	0.00
ATOM	2924	1HG	LYS	A	699	-21.509	13.448	-13.729	1.00	0.00
ATOM	2925	2HG	LYS	A	699	-22.344	15.003	-13.734	1.00	0.00
ATOM	2926	1HD	LYS	A	699	-19.867	15.744	-12.838	1.00	0.00
ATOM	2927	2HD	LYS	A	699	-19.989	14.110	-12.178	1.00	0.00
ATOM	2928	1HE	LYS	A	699	-20.821	16.009	-10.673	1.00	0.00
ATOM	2929	2HE	LYS	A	699	-21.961	14.663	-10.925	1.00	0.00
ATOM	2930	1HZ	LYS	A	699	-23.137	15.914	-12.508	1.00	0.00
ATOM	2931	2HZ	LYS	A	699	-21.960	17.138	-12.543	1.00	0.00
ATOM	2932	3HZ	LYS	A	699	-22.911	16.915	-11.154	1.00	0.00
ATOM	2933	N	ALA	A	700	-18.684	17.255	-14.346	1.00	0.00
ATOM	2934	CA	ALA	A	700	-17.988	17.961	-13.307	1.00	0.00
ATOM	2935	C	ALA	A	700	-18.341	19.408	-13.349	1.00	0.00
ATOM	2936	O	ALA	A	700	-18.623	20.018	-12.318	1.00	0.00
ATOM	2937	CB	ALA	A	700	-16.460	17.857	-13.434	1.00	0.00
ATOM	2938	HN	ALA	A	700	-18.169	16.801	-15.072	1.00	0.00
ATOM	2939	HA	ALA	A	700	-18.316	17.528	-12.362	1.00	0.00

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ATOM	2940	IHB	ALA	A	700	-16.123	18.273	-14.384	1.00	0.00
ATOM	2941	2HB	ALA	A	700	-16.149	16.813	-13.394	1.00	0.00
ATOM	2942	3HB	ALA	A	700	-15.976	18.415	-12.633	1.00	0.00
ATOM	2943	N	ILE	A	701	-18.351	19.996	-14.557	1.00	0.00
ATOM	2944	CA	ILE	A	701	-18.652	21.390	-14.648	1.00	0.00
ATOM	2945	C	ILE	A	701	-20.060	21.594	-14.212	1.00	0.00
ATOM	2946	O	ILE	A	701	-20.382	22.623	-13.631	1.00	0.00
ATOM	2947	CB	ILE	A	701	-18.482	21.972	-16.021	1.00	0.00
ATOM	2948	CG1	ILE	A	701	-19.449	21.343	-17.031	1.00	0.00
ATOM	2949	CG2	ILE	A	701	-17.004	21.821	-16.406	1.00	0.00
ATOM	2950	CD1	ILE	A	701	-19.478	22.085	-18.362	1.00	0.00
ATOM	2951	HN	ILE	A	701	-18.151	19.465	-15.380	1.00	0.00
ATOM	2952	HA	ILE	A	701	-17.982	21.892	-13.950	1.00	0.00
ATOM	2953	HB	ILE	A	701	-18.767	23.024	-16.024	1.00	0.00
ATOM	2954	1HG2	ILE	A	701	-16.712	20.771	-16.411	1.00	0.00
ATOM	2955	2HG2	ILE	A	701	-16.372	22.343	-15.688	1.00	0.00
ATOM	2956	3HG2	ILE	A	701	-16.832	22.222	-17.405	1.00	0.00
ATOM	2957	1HG1	ILE	A	701	-20.452	21.342	-16.605	1.00	0.00
ATOM	2958	2HG1	ILE	A	701	-19.152	20.310	-17.208	1.00	0.00
ATOM	2959	1HD1	ILE	A	701	-18.490	22.088	-18.823	1.00	0.00
ATOM	2960	2HD1	ILE	A	701	-19.781	23.121	-18.210	1.00	0.00
ATOM	2961	3HD1	ILE	A	701	-20.170	21.598	-19.050	1.00	0.00
ATOM	2962	N	VAL	A	702	-20.949	20.622	-14.475	1.00	0.00
ATOM	2963	CA	VAL	A	702	-22.319	20.788	-14.085	1.00	0.00
ATOM	2964	C	VAL	A	702	-22.425	20.931	-12.597	1.00	0.00
ATOM	2965	O	VAL	A	702	-23.157	21.790	-12.105	1.00	0.00
ATOM	2966	CB	VAL	A	702	-23.172	19.627	-14.482	1.00	0.00
ATOM	2967	CG1	VAL	A	702	-24.594	19.863	-13.944	1.00	0.00
ATOM	2968	CG2	VAL	A	702	-23.084	19.481	-16.010	1.00	0.00
ATOM	2969	HN	VAL	A	702	-20.656	19.787	-14.941	1.00	0.00
ATOM	2970	HA	VAL	A	702	-22.675	21.698	-14.568	1.00	0.00
ATOM	2971	HB	VAL	A	702	-22.764	18.705	-14.067	1.00	0.00
ATOM	2972	1HG1	VAL	A	702	-24.650	20.809	-13.406	1.00	0.00
ATOM	2973	2HG1	VAL	A	702	-24.873	19.066	-13.255	1.00	0.00
ATOM	2974	3HG1	VAL	A	702	-25.306	19.901	-14.769	1.00	0.00
ATOM	2975	1HG2	VAL	A	702	-22.197	19.983	-16.395	1.00	0.00
ATOM	2976	2HG2	VAL	A	702	-23.958	19.930	-16.482	1.00	0.00
ATOM	2977	3HG2	VAL	A	702	-23.021	18.428	-16.285	1.00	0.00
ATOM	2978	N	LYS	A	703	-21.685	20.107	-11.829	1.00	0.00
ATOM	2979	CA	LYS	A	703	-21.780	20.209	-10.397	1.00	0.00
ATOM	2980	C	LYS	A	703	-21.344	21.580	-10.022	1.00	0.00
ATOM	2981	O	LYS	A	703	-21.933	22.232	-9.161	1.00	0.00
ATOM	2982	CB	LYS	A	703	-20.815	19.297	-9.622	1.00	0.00
ATOM	2983	CG	LYS	A	703	-21.180	17.821	-9.655	1.00	0.00
ATOM	2984	CD	LYS	A	703	-20.112	16.900	-9.058	1.00	0.00
ATOM	2985	CE	LYS	A	703	-18.706	17.078	-9.634	1.00	0.00
ATOM	2986	NZ	LYS	A	703	-18.598	16.389	-10.938	1.00	0.00
ATOM	2987	HN	LYS	A	703	-21.077	19.434	-12.250	1.00	0.00
ATOM	2988	HA	LYS	A	703	-22.809	19.955	-10.143	1.00	0.00

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ATOM	2989	1HB	LYS	A	703	-20.792	19.623	-8.583	1.00	0.00
ATOM	2990	2HB	LYS	A	703	-19.817	19.415	-10.041	1.00	0.00
ATOM	2991	1HG	LYS	A	703	-21.350	17.529	-10.691	1.00	0.00
ATOM	2992	2HG	LYS	A	703	-22.108	17.681	-9.103	1.00	0.00
ATOM	2993	1HD	LYS	A	703	-20.421	15.868	-9.220	1.00	0.00
ATOM	2994	2HD	LYS	A	703	-20.067	17.080	-7.985	1.00	0.00
ATOM	2995	1HE	LYS	A	703	-17.964	16.649	-8.961	1.00	0.00
ATOM	2996	2HE	LYS	A	703	-18.492	18.135	-9.790	1.00	0.00
ATOM	2997	1HZ	LYS	A	703	-19.292	16.791	-11.601	1.00	0.00
ATOM	2998	2HZ	LYS	A	703	-18.788	15.375	-10.811	1.00	0.00
ATOM	2999	3HZ	LYS	A	703	-17.639	16.517	-11.320	1.00	0.00
ATOM	3000	N	ARG	A	704	-20.273	22.026	-10.690	1.00	0.00
ATOM	3001	CA	ARG	A	704	-19.624	23.284	-10.496	1.00	0.00
ATOM	3002	C	ARG	A	704	-20.553	24.375	-10.917	1.00	0.00
ATOM	3003	O	ARG	A	704	-20.395	25.518	-10.507	1.00	0.00
ATOM	3004	CB	ARG	A	704	-18.371	23.420	-11.373	1.00	0.00
ATOM	3005	CG	ARG	A	704	-17.385	22.267	-11.197	1.00	0.00
ATOM	3006	CD	ARG	A	704	-16.448	22.425	-10.001	1.00	0.00
ATOM	3007	NE	ARG	A	704	-15.575	21.219	-9.975	1.00	0.00
ATOM	3008	CZ	ARG	A	704	-14.439	21.179	-10.732	1.00	0.00
ATOM	3009	NH1	ARG	A	704	-14.130	22.226	-11.549	1.00	0.00
ATOM	3010	NH2	ARG	A	704	-13.615	20.093	-10.666	1.00	0.00
ATOM	3011	HN	ARG	A	704	-19.893	21.422	-11.389	1.00	0.00
ATOM	3012	HA	ARG	A	704	-19.357	23.344	-9.441	1.00	0.00
ATOM	3013	1HB	ARG	A	704	-17.868	24.354	-11.123	1.00	0.00
ATOM	3014	2HB	ARG	A	704	-18.677	23.465	-12.417	1.00	0.00
ATOM	3015	1HG	ARG	A	704	-16.782	22.186	-12.100	1.00	0.00
ATOM	3016	2HG	ARG	A	704	-17.949	21.344	-11.076	1.00	0.00
ATOM	3017	1HD	ARG	A	704	-17.001	22.464	-9.064	1.00	0.00
ATOM	3018	2HD	ARG	A	704	-15.813	23.303	-10.105	1.00	0.00
ATOM	3019	HE	ARG	A	704	-15.820	20.437	-9.403	1.00	0.00
ATOM	3020	1HH1	ARG	A	704	-14.735	23.021	-11.593	1.00	0.00
ATOM	3021	2HH1	ARG	A	704	-13.299	22.198	-12.103	1.00	0.00
ATOM	3022	1HH2	ARG	A	704	-12.867	19.992	-11.323	1.00	0.00
ATOM	3023	2HH2	ARG	A	704	-13.759	19.398	-9.962	1.00	0.00
ATOM	3024	N	GLU	A	705	-21.526	24.047	-11.784	1.00	0.00
ATOM	3025	CA	GLU	A	705	-22.452	24.985	-12.346	1.00	0.00
ATOM	3026	C	GLU	A	705	-23.197	25.603	-11.225	1.00	0.00
ATOM	3027	O	GLU	A	705	-23.701	26.719	-11.350	1.00	0.00
ATOM	3028	CB	GLU	A	705	-23.467	24.326	-13.296	1.00	0.00
ATOM	3029	CG	GLU	A	705	-24.376	25.332	-14.004	1.00	0.00
ATOM	3030	CD	GLU	A	705	-23.519	26.124	-14.981	1.00	0.00
ATOM	3031	OE1	GLU	A	705	-23.147	27.278	-14.637	1.00	0.00
ATOM	3032	OE2	GLU	A	705	-23.216	25.584	-16.078	1.00	0.00
ATOM	3033	HN	GLU	A	705	-21.610	23.087	-12.052	1.00	0.00
ATOM	3034	HA	GLU	A	705	-21.859	25.724	-12.885	1.00	0.00
ATOM	3035	1HB	GLU	A	705	-24.086	23.637	-12.723	1.00	0.00
ATOM	3036	2HB	GLU	A	705	-22.924	23.755	-14.047	1.00	0.00
ATOM	3037	1HG	GLU	A	705	-24.829	26.014	-13.285	1.00	0.00

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ATOM	3038	2HG	GLU A 705	-25.166	24.816	-14.552	1.00	0.00
ATOM	3039	N	GLY A 706	-23.302	24.865	-10.105	1.00	0.00
ATOM	3040	CA	GLY A 706	-23.959	25.401	-8.954	1.00	0.00
ATOM	3041	C	GLY A 706	-23.259	26.696	-8.655	1.00	0.00
ATOM	3042	O	GLY A 706	-23.896	27.696	-8.328	1.00	0.00
ATOM	3043	HN	GLY A 706	-22.920	23.941	-10.078	1.00	0.00
ATOM	3044	1HA	GLY A 706	-23.850	24.701	-8.127	1.00	0.00
ATOM	3045	2HA	GLY A 706	-25.007	25.573	-9.194	1.00	0.00
ATOM	3046	N	ASN A 707	-21.914	26.694	-8.773	1.00	0.00
ATOM	3047	CA	ASN A 707	-21.090	27.862	-8.605	1.00	0.00
ATOM	3048	C	ASN A 707	-20.904	28.564	-9.933	1.00	0.00
ATOM	3049	O	ASN A 707	-21.800	28.531	-10.775	1.00	0.00
ATOM	3050	CB	ASN A 707	-19.699	27.572	-8.022	1.00	0.00
ATOM	3051	CG	ASN A 707	-19.889	27.364	-6.528	1.00	0.00
ATOM	3052	OD1	ASN A 707	-20.915	27.749	-5.970	1.00	0.00
ATOM	3053	ND2	ASN A 707	-18.874	26.755	-5.859	1.00	0.00
ATOM	3054	HN	ASN A 707	-21.465	25.829	-8.991	1.00	0.00
ATOM	3055	HA	ASN A 707	-21.637	28.529	-7.940	1.00	0.00
ATOM	3056	1HB	ASN A 707	-19.024	28.411	-8.192	1.00	0.00
ATOM	3057	2HB	ASN A 707	-19.270	26.674	-8.466	1.00	0.00
ATOM	3058	1HD2	ASN A 707	-18.885	26.730	-4.860	1.00	0.00
ATOM	3059	2HD2	ASN A 707	-18.114	26.329	-6.349	1.00	0.00
ATOM	3060	N	SER A 708	-19.744	29.240	-10.159	1.00	0.00
ATOM	3061	CA	SER A 708	-19.586	29.964	-11.400	1.00	0.00
ATOM	3062	C	SER A 708	-18.214	29.833	-12.019	1.00	0.00
ATOM	3063	O	SER A 708	-17.723	28.727	-12.234	1.00	0.00
ATOM	3064	CB	SER A 708	-19.894	31.469	-11.261	1.00	0.00
ATOM	3065	OG	SER A 708	-19.957	32.087	-12.539	1.00	0.00
ATOM	3066	HN	SER A 708	-19.014	29.235	-9.477	1.00	0.00
ATOM	3067	HA	SER A 708	-20.268	29.507	-12.117	1.00	0.00
ATOM	3068	1HB	SER A 708	-19.110	31.962	-10.685	1.00	0.00
ATOM	3069	2HB	SER A 708	-20.854	31.613	-10.767	1.00	0.00
ATOM	3070	HG	SER A 708	-20.537	31.556	-13.070	1.00	0.00
ATOM	3071	N	SER A 709	-17.553	30.988	-12.286	1.00	0.00
ATOM	3072	CA	SER A 709	-16.308	31.118	-13.009	1.00	0.00
ATOM	3073	C	SER A 709	-15.219	30.341	-12.359	1.00	0.00
ATOM	3074	O	SER A 709	-14.309	29.834	-13.014	1.00	0.00
ATOM	3075	CB	SER A 709	-15.830	32.578	-13.122	1.00	0.00
ATOM	3076	OG	SER A 709	-14.609	32.634	-13.845	1.00	0.00
ATOM	3077	HN	SER A 709	-17.968	31.831	-11.950	1.00	0.00
ATOM	3078	HA	SER A 709	-16.478	30.703	-14.002	1.00	0.00
ATOM	3079	1HB	SER A 709	-15.661	32.998	-12.130	1.00	0.00
ATOM	3080	2HB	SER A 709	-16.570	33.178	-13.651	1.00	0.00
ATOM	3081	HG	SER A 709	-14.089	31.895	-13.560	1.00	0.00
ATOM	3082	N	GLN A 710	-15.304	30.190	-11.034	1.00	0.00
ATOM	3083	CA	GLN A 710	-14.320	29.451	-10.309	1.00	0.00
ATOM	3084	C	GLN A 710	-14.284	28.076	-10.903	1.00	0.00
ATOM	3085	O	GLN A 710	-13.284	27.368	-10.796	1.00	0.00
ATOM	3086	CB	GLN A 710	-14.666	29.304	-8.816	1.00	0.00

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ATOM	3087	CG	GLN A 710	-14.694	30.629	-8.052	1.00	0.00
ATOM	3088	CD	GLN A 710	-15.988	31.361	-8.386	1.00	0.00
ATOM	3089	OE1	GLN A 710	-16.882	30.818	-9.034	1.00	0.00
ATOM	3090	NE2	GLN A 710	-16.096	32.635	-7.923	1.00	0.00
ATOM	3091	HN	GLN A 710	-16.071	30.602	-10.541	1.00	0.00
ATOM	3092	HA	GLN A 710	-13.378	29.988	-10.425	1.00	0.00
ATOM	3093	1HB	GLN A 710	-13.930	28.649	-8.352	1.00	0.00
ATOM	3094	2HB	GLN A 710	-15.645	28.833	-8.732	1.00	0.00
ATOM	3095	1HG	GLN A 710	-13.847	31.251	-8.341	1.00	0.00
ATOM	3096	2HG	GLN A 710	-14.653	30.448	-6.978	1.00	0.00
ATOM	3097	1HE2	GLN A 710	-15.346	33.036	-7.396	1.00	0.00
ATOM	3098	2HE2	GLN A 710	-16.913	33.183	-8.100	1.00	0.00
ATOM	3099	N	ASN A 711	-15.380	27.657	-11.559	1.00	0.00
ATOM	3100	CA	ASN A 711	-15.461	26.323	-12.067	1.00	0.00
ATOM	3101	C	ASN A 711	-14.298	25.993	-12.953	1.00	0.00
ATOM	3102	O	ASN A 711	-13.698	24.930	-12.804	1.00	0.00
ATOM	3103	CB	ASN A 711	-16.751	26.026	-12.870	1.00	0.00
ATOM	3104	CG	ASN A 711	-16.691	26.627	-14.274	1.00	0.00
ATOM	3105	OD1	ASN A 711	-16.897	25.908	-15.250	1.00	0.00
ATOM	3106	ND2	ASN A 711	-16.393	27.948	-14.394	1.00	0.00
ATOM	3107	HN	ASN A 711	-16.147	28.285	-11.693	1.00	0.00
ATOM	3108	HA	ASN A 711	-15.404	25.663	-11.202	1.00	0.00
ATOM	3109	1HB	ASN A 711	-17.611	26.448	-12.352	1.00	0.00
ATOM	3110	2HB	ASN A 711	-16.885	24.948	-12.964	1.00	0.00
ATOM	3111	1HD2	ASN A 711	-16.200	28.333	-15.296	1.00	0.00
ATOM	3112	2HD2	ASN A 711	-16.363	28.547	-13.594	1.00	0.00
ATOM	3113	N	TRP A 712	-13.916	26.884	-13.887	1.00	0.00
ATOM	3114	CA	TRP A 712	-12.853	26.497	-14.765	1.00	0.00
ATOM	3115	C	TRP A 712	-11.591	26.323	-13.993	1.00	0.00
ATOM	3116	O	TRP A 712	-10.832	25.390	-14.243	1.00	0.00
ATOM	3117	CB	TRP A 712	-12.619	27.465	-15.943	1.00	0.00
ATOM	3118	CG	TRP A 712	-12.309	28.896	-15.583	1.00	0.00
ATOM	3119	CD1	TRP A 712	-13.148	29.967	-15.494	1.00	0.00
ATOM	3120	CD2	TRP A 712	-10.988	29.388	-15.317	1.00	0.00
ATOM	3121	NE1	TRP A 712	-12.434	31.097	-15.174	1.00	0.00
ATOM	3122	CE2	TRP A 712	-11.101	30.754	-15.067	1.00	0.00
ATOM	3123	CE3	TRP A 712	-9.779	28.754	-15.292	1.00	0.00
ATOM	3124	CZ2	TRP A 712	-10.001	31.512	-14.785	1.00	0.00
ATOM	3125	CZ3	TRP A 712	-8.671	29.521	-15.011	1.00	0.00
ATOM	3126	CH2	TRP A 712	-8.781	30.873	-14.762	1.00	0.00
ATOM	3127	HN	TRP A 712	-14.356	27.778	-13.963	1.00	0.00
ATOM	3128	HA	TRP A 712	-13.116	25.510	-15.145	1.00	0.00
ATOM	3129	1HB	TRP A 712	-13.514	27.473	-16.563	1.00	0.00
ATOM	3130	2HB	TRP A 712	-11.783	27.091	-16.532	1.00	0.00
ATOM	3131	HE3	TRP A 712	-9.696	27.695	-15.485	1.00	0.00
ATOM	3132	HD1	TRP A 712	-14.216	29.933	-15.652	1.00	0.00
ATOM	3133	HE1	TRP A 712	-12.807	31.993	-15.043	1.00	0.00
ATOM	3134	HZ2	TRP A 712	-10.084	32.570	-14.587	1.00	0.00
ATOM	3135	HZ3	TRP A 712	-7.697	29.055	-14.985	1.00	0.00

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ATOM	3136	HH2 TRP A 712	-7.891	31.444	-14.544	1.00	0.00
ATOM	3137	N GLN A 713	-11.330	27.211	-13.017	1.00	0.00
ATOM	3138	CA GLN A 713	-10.107	27.075	-12.282	1.00	0.00
ATOM	3139	C GLN A 713	-10.089	25.802	-11.491	1.00	0.00
ATOM	3140	O GLN A 713	-9.093	25.080	-11.508	1.00	0.00
ATOM	3141	CB GLN A 713	-9.821	28.261	-11.342	1.00	0.00
ATOM	3142	CG GLN A 713	-10.838	28.460	-10.220	1.00	0.00
ATOM	3143	CD GLN A 713	-10.394	29.664	-9.403	1.00	0.00
ATOM	3144	OE1 GLN A 713	-9.241	29.755	-8.985	1.00	0.00
ATOM	3145	NE2 GLN A 713	-11.331	30.626	-9.180	1.00	0.00
ATOM	3146	HN GLN A 713	-11.973	27.947	-12.809	1.00	0.00
ATOM	3147	HA GLN A 713	-9.311	26.985	-13.021	1.00	0.00
ATOM	3148	1HB GLN A 713	-9.789	29.171	-11.939	1.00	0.00
ATOM	3149	2HB GLN A 713	-8.840	28.112	-10.892	1.00	0.00
ATOM	3150	1HG GLN A 713	-10.877	27.581	-9.577	1.00	0.00
ATOM	3151	2HG GLN A 713	-11.830	28.646	-10.630	1.00	0.00
ATOM	3152	1HE2 GLN A 713	-12.287	30.451	-9.415	1.00	0.00
ATOM	3153	2HE2 GLN A 713	-11.082	31.509	-8.783	1.00	0.00
ATOM	3154	N ARG A 714	-11.197	25.461	-10.801	1.00	0.00
ATOM	3155	CA ARG A 714	-11.173	24.266	-10.001	1.00	0.00
ATOM	3156	C ARG A 714	-10.968	23.072	-10.861	1.00	0.00
ATOM	3157	O ARG A 714	-10.272	22.135	-10.473	1.00	0.00
ATOM	3158	CB ARG A 714	-12.450	23.958	-9.200	1.00	0.00
ATOM	3159	CG ARG A 714	-12.332	22.584	-8.521	1.00	0.00
ATOM	3160	CD ARG A 714	-13.646	21.995	-8.004	1.00	0.00
ATOM	3161	NE ARG A 714	-13.923	22.565	-6.658	1.00	0.00
ATOM	3162	CZ ARG A 714	-13.668	21.828	-5.538	1.00	0.00
ATOM	3163	NH1 ARG A 714	-13.907	22.359	-4.303	1.00	0.00
ATOM	3164	NH2 ARG A 714	-13.186	20.556	-5.651	1.00	0.00
ATOM	3165	HN ARG A 714	-12.019	26.028	-10.846	1.00	0.00
ATOM	3166	HA ARG A 714	-10.337	24.388	-9.313	1.00	0.00
ATOM	3167	1HB ARG A 714	-13.310	23.963	-9.869	1.00	0.00
ATOM	3168	2HB ARG A 714	-12.601	24.728	-8.443	1.00	0.00
ATOM	3169	1HG ARG A 714	-11.647	22.677	-7.680	1.00	0.00
ATOM	3170	2HG ARG A 714	-11.905	21.885	-9.238	1.00	0.00
ATOM	3171	1HD ARG A 714	-13.576	20.913	-7.899	1.00	0.00
ATOM	3172	2HD ARG A 714	-14.478	22.260	-8.656	1.00	0.00
ATOM	3173	HE ARG A 714	-14.297	23.489	-6.573	1.00	0.00
ATOM	3174	1HH1 ARG A 714	-14.268	23.288	-4.219	1.00	0.00
ATOM	3175	2HH1 ARG A 714	-13.720	21.819	-3.482	1.00	0.00
ATOM	3176	1HH2 ARG A 714	-12.724	20.126	-4.876	1.00	0.00
ATOM	3177	2HH2 ARG A 714	-13.296	20.054	-6.509	1.00	0.00
ATOM	3178	N PHE A 715	-11.573	23.082	-12.059	1.00	0.00
ATOM	3179	CA PHE A 715	-11.501	21.952	-12.932	1.00	0.00
ATOM	3180	C PHE A 715	-10.049	21.682	-13.163	1.00	0.00
ATOM	3181	O PHE A 715	-9.574	20.558	-12.995	1.00	0.00
ATOM	3182	CB PHE A 715	-12.180	22.267	-14.278	1.00	0.00
ATOM	3183	CG PHE A 715	-12.190	21.056	-15.138	1.00	0.00
ATOM	3184	CD1 PHE A 715	-11.089	20.730	-15.896	1.00	0.00

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ATOM	3185	CD2 PHE A 715	-13.348	20.329	-15.286	1.00	0.00
ATOM	3186	CE1 PHE A 715	-11.142	19.685	-16.784	1.00	0.00
ATOM	3187	CE2 PHE A 715	-13.406	19.282	-16.173	1.00	0.00
ATOM	3188	CZ PHE A 715	-12.305	18.969	-16.931	1.00	0.00
ATOM	3189	HN PHE A 715	-12.083	23.893	-12.345	1.00	0.00
ATOM	3190	HA PHE A 715	-12.003	21.124	-12.432	1.00	0.00
ATOM	3191	1HB PHE A 715	-11.639	23.063	-14.790	1.00	0.00
ATOM	3192	2HB PHE A 715	-13.207	22.591	-14.109	1.00	0.00
ATOM	3193	HD1 PHE A 715	-10.178	21.300	-15.792	1.00	0.00
ATOM	3194	HD2 PHE A 715	-14.219	20.583	-14.700	1.00	0.00
ATOM	3195	HE1 PHE A 715	-10.271	19.426	-17.367	1.00	0.00
ATOM	3196	HE2 PHE A 715	-14.315	18.707	-16.273	1.00	0.00
ATOM	3197	HZ PHE A 715	-12.353	18.159	-17.643	1.00	0.00
ATOM	3198	N TYR A 716	-9.289	22.737	-13.493	1.00	0.00
ATOM	3199	CA TYR A 716	-7.900	22.550	-13.770	1.00	0.00
ATOM	3200	C TYR A 716	-7.194	22.064	-12.541	1.00	0.00
ATOM	3201	O TYR A 716	-6.394	21.132	-12.613	1.00	0.00
ATOM	3202	CB TYR A 716	-7.222	23.842	-14.256	1.00	0.00
ATOM	3203	CG TYR A 716	-5.825	23.506	-14.644	1.00	0.00
ATOM	3204	CD1 TYR A 716	-5.581	22.804	-15.802	1.00	0.00
ATOM	3205	CD2 TYR A 716	-4.758	23.997	-13.927	1.00	0.00
ATOM	3206	CE1 TYR A 716	-4.294	22.552	-16.214	1.00	0.00
ATOM	3207	CE2 TYR A 716	-3.468	23.756	-14.339	1.00	0.00
ATOM	3208	CZ TYR A 716	-3.235	23.028	-15.481	1.00	0.00
ATOM	3209	OH TYR A 716	-1.912	22.781	-15.905	1.00	0.00
ATOM	3210	HN TYR A 716	-9.693	23.650	-13.544	1.00	0.00
ATOM	3211	HA TYR A 716	-7.833	21.779	-14.537	1.00	0.00
ATOM	3212	1HB TYR A 716	-7.211	24.589	-13.462	1.00	0.00
ATOM	3213	2HB TYR A 716	-7.751	24.251	-15.116	1.00	0.00
ATOM	3214	HD1 TYR A 716	-6.411	22.446	-16.394	1.00	0.00
ATOM	3215	HE1 TYR A 716	-4.116	21.980	-17.113	1.00	0.00
ATOM	3216	HD2 TYR A 716	-4.936	24.578	-13.034	1.00	0.00
ATOM	3217	HE2 TYR A 716	-2.638	24.140	-13.764	1.00	0.00
ATOM	3218	HH TYR A 716	-1.407	22.435	-15.181	1.00	0.00
ATOM	3219	N GLN A 717	-7.480	22.658	-11.365	1.00	0.00
ATOM	3220	CA GLN A 717	-6.767	22.208	-10.203	1.00	0.00
ATOM	3221	C GLN A 717	-7.093	20.799	-9.825	1.00	0.00
ATOM	3222	O GLN A 717	-6.242	20.068	-9.319	1.00	0.00
ATOM	3223	CB GLN A 717	-6.848	23.111	-8.952	1.00	0.00
ATOM	3224	CG GLN A 717	-8.239	23.434	-8.409	1.00	0.00
ATOM	3225	CD GLN A 717	-8.473	24.912	-8.692	1.00	0.00
ATOM	3226	OE1 GLN A 717	-9.459	25.503	-8.254	1.00	0.00
ATOM	3227	NE2 GLN A 717	-7.511	25.541	-9.419	1.00	0.00
ATOM	3228	HN GLN A 717	-8.165	23.384	-11.305	1.00	0.00
ATOM	3229	HA GLN A 717	-5.726	22.118	-10.514	1.00	0.00
ATOM	3230	1HB GLN A 717	-6.359	24.053	-9.192	1.00	0.00
ATOM	3231	2HB GLN A 717	-6.287	22.625	-8.156	1.00	0.00
ATOM	3232	1HG GLN A 717	-8.292	23.251	-7.336	1.00	0.00
ATOM	3233	2HG GLN A 717	-9.002	22.838	-8.910	1.00	0.00

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ATOM 3234 1HE2 GLN A 717	-7.086	25.069	-10.191	1.00	0.00
ATOM 3235 2HE2 GLN A 717	-7.218	26.470	-9.196	1.00	0.00
ATOM 3236 N LEU A 718	-8.345	20.378	-10.043	1.00	0.00
ATOM 3237 CA LEU A 718	-8.759	19.061	-9.662	1.00	0.00
ATOM 3238 C LEU A 718	-7.997	18.065	-10.503	1.00	0.00
ATOM 3239 O LEU A 718	-7.428	17.099	-9.995	1.00	0.00
ATOM 3240 CB LEU A 718	-10.288	18.979	-9.871	1.00	0.00
ATOM 3241 CG LEU A 718	-11.062	17.937	-9.047	1.00	0.00
ATOM 3242 CD1 LEU A 718	-10.887	16.514	-9.571	1.00	0.00
ATOM 3243 CD2 LEU A 718	-10.734	18.069	-7.552	1.00	0.00
ATOM 3244 HN LEU A 718	-9.000	20.994	-10.479	1.00	0.00
ATOM 3245 HA LEU A 718	-8.493	18.913	-8.616	1.00	0.00
ATOM 3246 1HB LEU A 718	-10.466	18.767	-10.923	1.00	0.00
ATOM 3247 2HB LEU A 718	-10.705	19.958	-9.640	1.00	0.00
ATOM 3248 HG LEU A 718	-12.122	18.190	-9.065	1.00	0.00
ATOM 3249 1HD1 LEU A 718	-9.911	16.395	-10.041	1.00	0.00
ATOM 3250 2HD1 LEU A 718	-11.650	16.290	-10.315	1.00	0.00
ATOM 3251 3HD1 LEU A 718	-10.955	15.800	-8.750	1.00	0.00
ATOM 3252 1HD2 LEU A 718	-10.835	19.104	-7.226	1.00	0.00
ATOM 3253 2HD2 LEU A 718	-9.708	17.754	-7.363	1.00	0.00
ATOM 3254 3HD2 LEU A 718	-11.419	17.461	-6.962	1.00	0.00
ATOM 3255 N THR A 719	-7.913	18.326	-11.823	1.00	0.00
ATOM 3256 CA THR A 719	-7.266	17.449	-12.761	1.00	0.00
ATOM 3257 C THR A 719	-5.793	17.323	-12.512	1.00	0.00
ATOM 3258 O THR A 719	-5.244	16.230	-12.641	1.00	0.00
ATOM 3259 CB THR A 719	-7.433	17.911	-14.178	1.00	0.00
ATOM 3260 OG1 THR A 719	-6.820	19.179	-14.356	1.00	0.00
ATOM 3261 CG2 THR A 719	-8.936	18.002	-14.489	1.00	0.00
ATOM 3262 HN THR A 719	-8.322	19.171	-12.167	1.00	0.00
ATOM 3263 HA THR A 719	-7.712	16.463	-12.630	1.00	0.00
ATOM 3264 HB THR A 719	-6.963	17.206	-14.864	1.00	0.00
ATOM 3265 HG1 THR A 719	-5.901	19.069	-14.148	1.00	0.00
ATOM 3266 1HG2 THR A 719	-9.482	18.409	-13.638	1.00	0.00
ATOM 3267 2HG2 THR A 719	-9.337	17.011	-14.704	1.00	0.00
ATOM 3268 3HG2 THR A 719	-9.105	18.658	-15.343	1.00	0.00
ATOM 3269 N LYS A 720	-5.093	18.417	-12.150	1.00	0.00
ATOM 3270 CA LYS A 720	-3.672	18.243	-12.010	1.00	0.00
ATOM 3271 C LYS A 720	-3.334	17.332	-10.872	1.00	0.00
ATOM 3272 O LYS A 720	-2.267	16.722	-10.867	1.00	0.00
ATOM 3273 CB LYS A 720	-2.780	19.505	-11.921	1.00	0.00
ATOM 3274 CG LYS A 720	-2.797	20.308	-10.622	1.00	0.00
ATOM 3275 CD LYS A 720	-4.022	21.194	-10.462	1.00	0.00
ATOM 3276 CE LYS A 720	-4.127	22.275	-11.542	1.00	0.00
ATOM 3277 NZ LYS A 720	-2.912	23.122	-11.534	1.00	0.00
ATOM 3278 HN LYS A 720	-5.536	19.298	-11.988	1.00	0.00
ATOM 3279 HA LYS A 720	-3.369	17.661	-12.880	1.00	0.00
ATOM 3280 1HB LYS A 720	-3.081	20.175	-12.723	1.00	0.00
ATOM 3281 2HB LYS A 720	-1.753	19.192	-12.098	1.00	0.00
ATOM 3282 1HG LYS A 720	-1.907	20.935	-10.590	1.00	0.00

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ATOM	3283	2HG	LYS	A	720	-2.757	19.614	-9.784	1.00	0.00
ATOM	3284	1HD	LYS	A	720	-3.982	21.675	-9.485	1.00	0.00
ATOM	3285	2HD	LYS	A	720	-4.914	20.570	-10.501	1.00	0.00
ATOM	3286	1HE	LYS	A	720	-4.989	22.916	-11.355	1.00	0.00
ATOM	3287	2HE	LYS	A	720	-4.216	21.819	-12.528	1.00	0.00
ATOM	3288	1HZ	LYS	A	720	-2.077	22.532	-11.722	1.00	0.00
ATOM	3289	2HZ	LYS	A	720	-2.813	23.577	-10.604	1.00	0.00
ATOM	3290	3HZ	LYS	A	720	-2.993	23.852	-12.270	1.00	0.00
ATOM	3291	N	LEU	A	721	-4.227	17.216	-9.873	1.00	0.00
ATOM	3292	CA	LEU	A	721	-3.978	16.374	-8.733	1.00	0.00
ATOM	3293	C	LEU	A	721	-3.756	14.989	-9.260	1.00	0.00
ATOM	3294	O	LEU	A	721	-2.949	14.229	-8.726	1.00	0.00
ATOM	3295	CB	LEU	A	721	-5.180	16.384	-7.757	1.00	0.00
ATOM	3296	CG	LEU	A	721	-5.050	15.608	-6.423	1.00	0.00
ATOM	3297	CD1	LEU	A	721	-6.341	15.751	-5.601	1.00	0.00
ATOM	3298	CD2	LEU	A	721	-4.679	14.127	-6.606	1.00	0.00
ATOM	3299	HN	LEU	A	721	-5.085	17.728	-9.924	1.00	0.00
ATOM	3300	HA	LEU	A	721	-3.084	16.757	-8.241	1.00	0.00
ATOM	3301	1HB	LEU	A	721	-6.036	15.975	-8.290	1.00	0.00
ATOM	3302	2HB	LEU	A	721	-5.391	17.423	-7.510	1.00	0.00
ATOM	3303	HG	LEU	A	721	-4.208	15.999	-5.853	1.00	0.00
ATOM	3304	1HD1	LEU	A	721	-7.158	15.200	-6.068	1.00	0.00
ATOM	3305	2HD1	LEU	A	721	-6.634	16.799	-5.538	1.00	0.00
ATOM	3306	3HD1	LEU	A	721	-6.195	15.350	-4.598	1.00	0.00
ATOM	3307	1HD2	LEU	A	721	-3.597	13.999	-6.607	1.00	0.00
ATOM	3308	2HD2	LEU	A	721	-5.064	13.757	-7.556	1.00	0.00
ATOM	3309	3HD2	LEU	A	721	-5.088	13.534	-5.788	1.00	0.00
ATOM	3310	N	LEU	A	722	-4.443	14.633	-10.356	1.00	0.00
ATOM	3311	CA	LEU	A	722	-4.320	13.307	-10.888	1.00	0.00
ATOM	3312	C	LEU	A	722	-2.887	13.009	-11.191	1.00	0.00
ATOM	3313	O	LEU	A	722	-2.442	11.872	-11.040	1.00	0.00
ATOM	3314	CB	LEU	A	722	-5.125	13.093	-12.177	1.00	0.00
ATOM	3315	CG	LEU	A	722	-6.645	13.143	-11.952	1.00	0.00
ATOM	3316	CD1	LEU	A	722	-7.109	14.534	-11.493	1.00	0.00
ATOM	3317	CD2	LEU	A	722	-7.396	12.646	-13.191	1.00	0.00
ATOM	3318	HN	LEU	A	722	-5.044	15.296	-10.804	1.00	0.00
ATOM	3319	HA	LEU	A	722	-4.672	12.628	-10.111	1.00	0.00
ATOM	3320	1HB	LEU	A	722	-4.863	12.123	-12.598	1.00	0.00
ATOM	3321	2HB	LEU	A	722	-4.850	13.864	-12.895	1.00	0.00
ATOM	3322	HG	LEU	A	722	-6.920	12.407	-11.197	1.00	0.00
ATOM	3323	1HD1	LEU	A	722	-6.709	15.309	-12.147	1.00	0.00
ATOM	3324	2HD1	LEU	A	722	-6.756	14.733	-10.481	1.00	0.00
ATOM	3325	3HD1	LEU	A	722	-8.196	14.597	-11.521	1.00	0.00
ATOM	3326	1HD2	LEU	A	722	-6.803	11.906	-13.729	1.00	0.00
ATOM	3327	2HD2	LEU	A	722	-7.595	13.476	-13.869	1.00	0.00
ATOM	3328	3HD2	LEU	A	722	-8.336	12.178	-12.899	1.00	0.00
ATOM	3329	N	ASP	A	723	-2.119	14.019	-11.633	1.00	0.00
ATOM	3330	CA	ASP	A	723	-0.741	13.792	-11.962	1.00	0.00
ATOM	3331	C	ASP	A	723	-0.010	13.274	-10.759	1.00	0.00

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ATOM 3332 O ASP A 723	0.743	12.305	-10.854	1.00	0.00
ATOM 3333 CB ASP A 723	-0.030	15.083	-12.405	1.00	0.00
ATOM 3334 CG ASP A 723	1.370	14.732	-12.890	1.00	0.00
ATOM 3335 OD1 ASP A 723	2.107	15.674	-13.288	1.00	0.00
ATOM 3336 OD2 ASP A 723	1.720	13.522	-12.876	1.00	0.00
ATOM 3337 HN ASP A 723	-2.510	14.934	-11.733	1.00	0.00
ATOM 3338 HA ASP A 723	-0.725	13.057	-12.767	1.00	0.00
ATOM 3339 1HB ASP A 723	0.047	15.779	-11.569	1.00	0.00
ATOM 3340 2HB ASP A 723	-0.580	15.560	-13.216	1.00	0.00
ATOM 3341 N SER A 724	-0.232	13.895	-9.585	1.00	0.00
ATOM 3342 CA SER A 724	0.455	13.494	-8.388	1.00	0.00
ATOM 3343 C SER A 724	0.075	12.088	-8.070	1.00	0.00
ATOM 3344 O SER A 724	0.909	11.279	-7.664	1.00	0.00
ATOM 3345 CB SER A 724	0.076	14.348	-7.166	1.00	0.00
ATOM 3346 OG SER A 724	0.481	15.694	-7.363	1.00	0.00
ATOM 3347 HN SER A 724	-0.888	14.649	-9.546	1.00	0.00
ATOM 3348 HA SER A 724	1.521	13.587	-8.595	1.00	0.00
ATOM 3349 1HB SER A 724	0.573	13.970	-6.273	1.00	0.00
ATOM 3350 2HB SER A 724	-1.003	14.336	-7.016	1.00	0.00
ATOM 3351 HG SER A 724	1.389	15.668	-7.634	1.00	0.00
ATOM 3352 N MET A 725	-1.212	11.757	-8.261	1.00	0.00
ATOM 3353 CA MET A 725	-1.668	10.440	-7.944	1.00	0.00
ATOM 3354 C MET A 725	-0.915	9.461	-8.785	1.00	0.00
ATOM 3355 O MET A 725	-0.510	8.408	-8.298	1.00	0.00
ATOM 3356 CB MET A 725	-3.164	10.256	-8.196	1.00	0.00
ATOM 3357 CG MET A 725	-4.058	11.063	-7.257	1.00	0.00
ATOM 3358 SD MET A 725	-5.826	10.823	-7.583	1.00	0.00
ATOM 3359 CE MET A 725	-5.715	9.033	-7.303	1.00	0.00
ATOM 3360 HN MET A 725	-1.852	12.434	-8.625	1.00	0.00
ATOM 3361 HA MET A 725	-1.441	10.276	-6.890	1.00	0.00
ATOM 3362 1HB MET A 725	-3.408	9.200	-8.083	1.00	0.00
ATOM 3363 2HB MET A 725	-3.382	10.551	-9.221	1.00	0.00
ATOM 3364 1HG MET A 725	-3.832	12.123	-7.370	1.00	0.00
ATOM 3365 2HG MET A 725	-3.858	10.767	-6.228	1.00	0.00
ATOM 3366 1HE MET A 725	-5.897	8.818	-6.250	1.00	0.00
ATOM 3367 2HE MET A 725	-4.719	8.677	-7.564	1.00	0.00
ATOM 3368 3HE MET A 725	-6.469	8.517	-7.898	1.00	0.00
ATOM 3369 N HIS A 726	-0.694	9.788	-10.072	1.00	0.00
ATOM 3370 CA HIS A 726	0.036	8.910	-10.943	1.00	0.00
ATOM 3371 C HIS A 726	1.424	8.772	-10.390	1.00	0.00
ATOM 3372 O HIS A 726	2.024	7.699	-10.419	1.00	0.00
ATOM 3373 CB HIS A 726	0.161	9.465	-12.373	1.00	0.00
ATOM 3374 CG HIS A 726	0.837	8.528	-13.331	1.00	0.00
ATOM 3375 ND1 HIS A 726	0.193	7.499	-13.981	1.00	0.00
ATOM 3376 CD2 HIS A 726	2.124	8.498	-13.772	1.00	0.00
ATOM 3377 CE1 HIS A 726	1.115	6.900	-14.777	1.00	0.00
ATOM 3378 NE2 HIS A 726	2.302	7.471	-14.685	1.00	0.00
ATOM 3379 HN HIS A 726	-1.044	10.655	-10.426	1.00	0.00
ATOM 3380 HA HIS A 726	-0.500	7.962	-10.953	1.00	0.00

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ATOM 3381	IHB HIS A 726	0.734	10.391	-12.345	1.00	0.00
ATOM 3382	2HB HIS A 726	-0.836	9.679	-12.758	1.00	0.00
ATOM 3383	HD2 HIS A 726	2.899	9.179	-13.455	1.00	0.00
ATOM 3384	HD1 HIS A 726	-0.750	7.247	-13.886	1.00	0.00
ATOM 3385	HE1 HIS A 726	0.903	6.054	-15.412	1.00	0.00
ATOM 3386	N GLU A 727	1.986	9.871	-9.863	1.00	0.00
ATOM 3387	CA GLU A 727	3.321	9.790	-9.352	1.00	0.00
ATOM 3388	C GLU A 727	3.378	8.829	-8.205	1.00	0.00
ATOM 3389	O GLU A 727	4.243	7.955	-8.158	1.00	0.00
ATOM 3390	CB GLU A 727	3.841	11.150	-8.853	1.00	0.00
ATOM 3391	CG GLU A 727	5.295	11.127	-8.376	1.00	0.00
ATOM 3392	CD GLU A 727	5.332	10.686	-6.918	1.00	0.00
ATOM 3393	OE1 GLU A 727	6.457	10.435	-6.410	1.00	0.00
ATOM 3394	OE2 GLU A 727	4.242	10.600	-6.293	1.00	0.00
ATOM 3395	HN GLU A 727	1.479	10.733	-9.827	1.00	0.00
ATOM 3396	HA GLU A 727	3.947	9.424	-10.166	1.00	0.00
ATOM 3397	IHB GLU A 727	3.211	11.481	-8.028	1.00	0.00
ATOM 3398	2HB GLU A 727	3.754	11.873	-9.663	1.00	0.00
ATOM 3399	IHG GLU A 727	5.736	12.121	-8.458	1.00	0.00
ATOM 3400	2HG GLU A 727	5.879	10.428	-8.974	1.00	0.00
ATOM 3401	N VAL A 728	2.426	8.949	-7.260	1.00	0.00
ATOM 3402	CA VAL A 728	2.421	8.126	-6.084	1.00	0.00
ATOM 3403	C VAL A 728	2.245	6.693	-6.460	1.00	0.00
ATOM 3404	O VAL A 728	2.901	5.819	-5.893	1.00	0.00
ATOM 3405	CB VAL A 728	1.307	8.467	-5.137	1.00	0.00
ATOM 3406	CG1 VAL A 728	1.343	7.471	-3.965	1.00	0.00
ATOM 3407	CG2 VAL A 728	1.458	9.936	-4.705	1.00	0.00
ATOM 3408	HN VAL A 728	1.704	9.629	-7.382	1.00	0.00
ATOM 3409	HA VAL A 728	3.385	8.272	-5.597	1.00	0.00
ATOM 3410	HB VAL A 728	0.348	8.405	-5.650	1.00	0.00
ATOM 3411	IHG1 VAL A 728	2.370	7.266	-3.664	1.00	0.00
ATOM 3412	2HG1 VAL A 728	0.883	6.527	-4.259	1.00	0.00
ATOM 3413	3HG1 VAL A 728	0.816	7.883	-3.104	1.00	0.00
ATOM 3414	IHG2 VAL A 728	1.409	10.598	-5.570	1.00	0.00
ATOM 3415	2HG2 VAL A 728	2.420	10.088	-4.217	1.00	0.00
ATOM 3416	3HG2 VAL A 728	0.653	10.212	-4.023	1.00	0.00
ATOM 3417	N VAL A 729	1.351	6.419	-7.432	1.00	0.00
ATOM 3418	CA VAL A 729	1.114	5.066	-7.846	1.00	0.00
ATOM 3419	C VAL A 729	2.347	4.436	-8.386	1.00	0.00
ATOM 3420	O VAL A 729	2.634	3.280	-8.079	1.00	0.00
ATOM 3421	CB VAL A 729	0.025	4.898	-8.881	1.00	0.00
ATOM 3422	CG1 VAL A 729	-0.103	6.135	-9.771	1.00	0.00
ATOM 3423	CG2 VAL A 729	0.399	3.659	-9.717	1.00	0.00
ATOM 3424	HN VAL A 729	0.849	7.166	-7.868	1.00	0.00
ATOM 3425	HA VAL A 729	0.849	4.516	-6.943	1.00	0.00
ATOM 3426	HB VAL A 729	-0.924	4.719	-8.377	1.00	0.00
ATOM 3427	IHG1 VAL A 729	0.243	5.920	-10.781	1.00	0.00
ATOM 3428	2HG1 VAL A 729	0.502	6.949	-9.373	1.00	0.00
ATOM 3429	3HG1 VAL A 729	-1.145	6.449	-9.831	1.00	0.00

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ATOM 3430 1HG2 VAL A 729	0.802	2.871	-9.080	1.00	0.00
ATOM 3431 2HG2 VAL A 729	1.160	3.918	-10.454	1.00	0.00
ATOM 3432 3HG2 VAL A 729	-0.482	3.266	-10.223	1.00	0.00
ATOM 3433 N GLU A 730	3.121	5.177	-9.194	1.00	0.00
ATOM 3434 CA GLU A 730	4.298	4.583	-9.753	1.00	0.00
ATOM 3435 C GLU A 730	5.209	4.190	-8.637	1.00	0.00
ATOM 3436 O GLU A 730	5.754	3.088	-8.626	1.00	0.00
ATOM 3437 CB GLU A 730	5.081	5.542	-10.669	1.00	0.00
ATOM 3438 CG GLU A 730	4.352	5.894	-11.968	1.00	0.00
ATOM 3439 CD GLU A 730	5.250	6.829	-12.770	1.00	0.00
ATOM 3440 OE1 GLU A 730	4.873	7.167	-13.923	1.00	0.00
ATOM 3441 OE2 GLU A 730	6.327	7.211	-12.241	1.00	0.00
ATOM 3442 HN GLU A 730	2.880	6.125	-9.400	1.00	0.00
ATOM 3443 HA GLU A 730	3.967	3.712	-10.319	1.00	0.00
ATOM 3444 1HB GLU A 730	6.035	5.080	-10.920	1.00	0.00
ATOM 3445 2HB GLU A 730	5.278	6.462	-10.121	1.00	0.00
ATOM 3446 1HG GLU A 730	3.408	6.395	-11.755	1.00	0.00
ATOM 3447 2HG GLU A 730	4.154	4.995	-12.552	1.00	0.00
ATOM 3448 N ASN A 731	5.383	5.085	-7.649	1.00	0.00
ATOM 3449 CA ASN A 731	6.262	4.803	-6.553	1.00	0.00
ATOM 3450 C ASN A 731	5.724	3.642	-5.785	1.00	0.00
ATOM 3451 O ASN A 731	6.482	2.778	-5.346	1.00	0.00
ATOM 3452 CB ASN A 731	6.391	5.978	-5.566	1.00	0.00
ATOM 3453 CG ASN A 731	7.092	7.133	-6.272	1.00	0.00
ATOM 3454 OD1 ASN A 731	6.004	6.959	-5.719	1.00	0.00
ATOM 3455 ND2 ASN A 731	8.213	6.414	-6.535	1.00	0.00
ATOM 3456 HN ASN A 731	4.894	5.957	-7.679	1.00	0.00
ATOM 3457 HA ASN A 731	7.235	4.570	-6.986	1.00	0.00
ATOM 3458 1HB ASN A 731	6.978	5.682	-4.697	1.00	0.00
ATOM 3459 2HB ASN A 731	5.406	6.307	-5.236	1.00	0.00
ATOM 3460 1HD2 ASN A 731	8.909	6.788	-7.148	1.00	0.00
ATOM 3461 2HD2 ASN A 731	8.358	5.513	-6.126	1.00	0.00
ATOM 3462 N LEU A 732	4.389	3.608	-5.654	1.00	0.00
ATOM 3463 CA LEU A 732	3.673	2.603	-4.884	1.00	0.00
ATOM 3464 C LEU A 732	3.997	1.198	-5.395	1.00	0.00
ATOM 3465 O LEU A 732	4.352	0.318	-4.621	1.00	0.00
ATOM 3466 CB LEU A 732	2.167	2.913	-4.937	1.00	0.00
ATOM 3467 CG LEU A 732	1.276	2.084	-4.002	1.00	0.00
ATOM 3468 CD1 LEU A 732	-0.051	2.820	-3.762	1.00	0.00
ATOM 3469 CD2 LEU A 732	1.004	0.675	-4.542	1.00	0.00
ATOM 3470 HN LEU A 732	3.877	4.336	-6.105	1.00	0.00
ATOM 3471 HA LEU A 732	4.037	2.690	-3.860	1.00	0.00
ATOM 3472 1HB LEU A 732	1.790	2.817	-5.951	1.00	0.00
ATOM 3473 2HB LEU A 732	2.044	3.962	-4.666	1.00	0.00
ATOM 3474 HG LEU A 732	1.791	1.986	-3.050	1.00	0.00
ATOM 3475 1HD1 LEU A 732	-0.731	2.224	-3.158	1.00	0.00
ATOM 3476 2HD1 LEU A 732	-0.557	3.042	-4.701	1.00	0.00
ATOM 3477 3HD1 LEU A 732	0.112	3.764	-3.240	1.00	0.00
ATOM 3478 1HD2 LEU A 732	0.728	0.714	-5.592	1.00	0.00

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ATOM	3479	2HD2 LEU A 732	0.188	0.202	-3.998	1.00	0.00
ATOM	3480	3HD2 LEU A 732	1.865	0.018	-4.444	1.00	0.00
ATOM	3481	N LEU A 733	3.882	1.025	-6.730	1.00	0.00
ATOM	3482	CA LEU A 733	4.123	-0.307	-7.268	1.00	0.00
ATOM	3483	C LEU A 733	5.569	-0.716	-7.057	1.00	0.00
ATOM	3484	O LEU A 733	5.843	-1.876	-6.783	1.00	0.00
ATOM	3485	CB LEU A 733	3.761	-0.454	-8.753	1.00	0.00
ATOM	3486	CG LEU A 733	2.286	-0.825	-8.982	1.00	0.00
ATOM	3487	CD1 LEU A 733	1.429	0.428	-9.126	1.00	0.00
ATOM	3488	CD2 LEU A 733	2.141	-1.718	-10.214	1.00	0.00
ATOM	3489	HN LEU A 733	3.603	1.798	-7.310	1.00	0.00
ATOM	3490	HA LEU A 733	3.518	-0.998	-6.677	1.00	0.00
ATOM	3491	1HB LEU A 733	4.363	-1.258	-9.182	1.00	0.00
ATOM	3492	2HB LEU A 733	4.043	0.440	-9.313	1.00	0.00
ATOM	3493	HG LEU A 733	1.916	-1.402	-8.133	1.00	0.00
ATOM	3494	1HD1 LEU A 733	1.798	1.058	-9.937	1.00	0.00
ATOM	3495	2HD1 LEU A 733	1.450	1.008	-8.204	1.00	0.00
ATOM	3496	3HD1 LEU A 733	0.392	0.179	-9.350	1.00	0.00
ATOM	3497	1HD2 LEU A 733	2.708	-2.644	-10.104	1.00	0.00
ATOM	3498	2HD2 LEU A 733	2.518	-1.194	-11.090	1.00	0.00
ATOM	3499	3HD2 LEU A 733	1.101	-1.995	-10.389	1.00	0.00
ATOM	3500	N ASN A 734	6.483	0.268	-7.192	1.00	0.00
ATOM	3501	CA ASN A 734	7.872	-0.044	-7.046	1.00	0.00
ATOM	3502	C ASN A 734	8.076	-0.607	-5.680	1.00	0.00
ATOM	3503	O ASN A 734	8.776	-1.603	-5.507	1.00	0.00
ATOM	3504	CB ASN A 734	8.785	1.188	-7.172	1.00	0.00
ATOM	3505	CG ASN A 734	8.736	1.676	-8.611	1.00	0.00
ATOM	3506	OD1 ASN A 734	8.794	0.888	-9.554	1.00	0.00
ATOM	3507	ND2 ASN A 734	8.622	3.020	-8.790	1.00	0.00
ATOM	3508	HN ASN A 734	6.201	1.201	-7.415	1.00	0.00
ATOM	3509	HA ASN A 734	8.111	-0.767	-7.826	1.00	0.00
ATOM	3510	1HB ASN A 734	9.812	0.928	-6.916	1.00	0.00
ATOM	3511	2HB ASN A 734	8.444	1.984	-6.511	1.00	0.00
ATOM	3512	1HD2 ASN A 734	8.576	3.623	-7.994	1.00	0.00
ATOM	3513	2HD2 ASN A 734	8.584	3.419	-9.706	1.00	0.00
ATOM	3514	N TYR A 735	7.472	0.061	-4.663	1.00	0.00
ATOM	3515	CA TYR A 735	7.712	-0.419	-3.297	1.00	0.00
ATOM	3516	C TYR A 735	6.993	-1.750	-3.052	1.00	0.00
ATOM	3517	O TYR A 735	7.519	-2.627	-2.381	1.00	0.00
ATOM	3518	CB TYR A 735	7.350	0.616	-2.209	1.00	0.00
ATOM	3519	CG TYR A 735	7.674	0.144	-0.800	1.00	0.00
ATOM	3520	CD1 TYR A 735	8.850	-0.555	-0.517	1.00	0.00
ATOM	3521	CD2 TYR A 735	6.788	0.380	0.250	1.00	0.00
ATOM	3522	CE1 TYR A 735	9.119	-1.018	0.764	1.00	0.00
ATOM	3523	CE2 TYR A 735	7.061	-0.082	1.536	1.00	0.00
ATOM	3524	CZ TYR A 735	8.232	-0.775	1.800	1.00	0.00
ATOM	3525	OH TYR A 735	8.521	-1.222	3.077	1.00	0.00
ATOM	3526	HN TYR A 735	6.917	0.875	-4.864	1.00	0.00
ATOM	3527	HA TYR A 735	8.784	-0.616	-3.250	1.00	0.00

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ATOM	3528	IHB	TYR	A	735	6.287	0.852	-2.275	1.00	0.00
ATOM	3529	2HB	TYR	A	735	7.886	1.547	-2.393	1.00	0.00
ATOM	3530	HD1	TYR	A	735	9.577	-0.763	-1.285	1.00	0.00
ATOM	3531	HE1	TYR	A	735	10.023	-1.577	0.952	1.00	0.00
ATOM	3532	HD2	TYR	A	735	5.867	0.913	0.069	1.00	0.00
ATOM	3533	HE2	TYR	A	735	6.349	0.077	2.330	1.00	0.00
ATOM	3534	HH	TYR	A	735	9.007	-0.572	3.589	1.00	0.00
ATOM	3535	N	CYS	A	736	5.797	-1.868	-3.656	1.00	0.00
ATOM	3536	CA	CYS	A	736	5.021	-3.096	-3.545	1.00	0.00
ATOM	3537	C	CYS	A	736	5.847	-4.286	-4.026	1.00	0.00
ATOM	3538	O	CYS	A	736	5.925	-5.320	-3.369	1.00	0.00
ATOM	3539	CB	CYS	A	736	3.696	-2.947	-4.303	1.00	0.00
ATOM	3540	SG	CYS	A	736	2.461	-4.186	-3.834	1.00	0.00
ATOM	3541	HN	CYS	A	736	5.452	-1.090	-4.182	1.00	0.00
ATOM	3542	HA	CYS	A	736	4.829	-3.258	-2.490	1.00	0.00
ATOM	3543	IHB	CYS	A	736	3.856	-2.988	-5.382	1.00	0.00
ATOM	3544	2HB	CYS	A	736	3.270	-1.966	-4.093	1.00	0.00
ATOM	3545	HG	CYS	A	736	1.304	-3.914	-4.440	1.00	0.00
ATOM	3546	N	PHE	A	737	6.506	-4.064	-5.183	1.00	0.00
ATOM	3547	CA	PHE	A	737	7.249	-5.179	-5.733	1.00	0.00
ATOM	3548	C	PHE	A	737	8.514	-5.457	-4.926	1.00	0.00
ATOM	3549	O	PHE	A	737	8.950	-6.593	-4.862	1.00	0.00
ATOM	3550	CB	PHE	A	737	7.421	-5.145	-7.268	1.00	0.00
ATOM	3551	CG	PHE	A	737	8.665	-4.481	-7.801	1.00	0.00
ATOM	3552	CD1	PHE	A	737	8.577	-3.263	-8.460	1.00	0.00
ATOM	3553	CD2	PHE	A	737	9.914	-5.087	-7.676	1.00	0.00
ATOM	3554	CE1	PHE	A	737	9.711	-2.651	-8.980	1.00	0.00
ATOM	3555	CE2	PHE	A	737	11.052	-4.479	-8.191	1.00	0.00
ATOM	3556	CZ	PHE	A	737	10.951	-3.258	-8.843	1.00	0.00
ATOM	3557	HN	PHE	A	737	6.446	-3.190	-5.666	1.00	0.00
ATOM	3558	HA	PHE	A	737	6.610	-6.051	-5.573	1.00	0.00
ATOM	3559	IHB	PHE	A	737	6.537	-4.699	-7.727	1.00	0.00
ATOM	3560	2HB	PHE	A	737	7.444	-6.174	-7.632	1.00	0.00
ATOM	3561	HD1	PHE	A	737	7.613	-2.789	-8.574	1.00	0.00
ATOM	3562	HD2	PHE	A	737	10.007	-6.045	-7.184	1.00	0.00
ATOM	3563	HE1	PHE	A	737	9.625	-1.701	-9.490	1.00	0.00
ATOM	3564	HE2	PHE	A	737	12.014	-4.959	-8.085	1.00	0.00
ATOM	3565	HZ	PHE	A	737	11.833	-2.781	-9.246	1.00	0.00
ATOM	3566	N	GLN	A	738	9.120	-4.415	-4.322	1.00	0.00
ATOM	3567	CA	GLN	A	738	10.282	-4.659	-3.514	1.00	0.00
ATOM	3568	C	GLN	A	738	9.894	-5.407	-2.272	1.00	0.00
ATOM	3569	O	GLN	A	738	10.561	-6.363	-1.882	1.00	0.00
ATOM	3570	CB	GLN	A	738	11.000	-3.359	-3.105	1.00	0.00
ATOM	3571	CG	GLN	A	738	12.352	-3.577	-2.418	1.00	0.00
ATOM	3572	CD	GLN	A	738	12.102	-3.957	-0.966	1.00	0.00
ATOM	3573	OE1	GLN	A	738	11.251	-3.369	-0.301	1.00	0.00
ATOM	3574	NE2	GLN	A	738	12.856	-4.970	-0.462	1.00	0.00
ATOM	3575	HN	GLN	A	738	8.801	-3.479	-4.470	1.00	0.00
ATOM	3576	HA	GLN	A	738	10.949	-5.287	-4.104	1.00	0.00

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ATOM	3577	1HB	GLN	A	738	10.353	-2.805	-2.427	1.00	0.00
ATOM	3578	2HB	GLN	A	738	11.159	-2.756	-3.998	1.00	0.00
ATOM	3579	1HG	GLN	A	738	12.948	-2.665	-2.452	1.00	0.00
ATOM	3580	2HG	GLN	A	738	12.903	-4.381	-2.908	1.00	0.00
ATOM	3581	1HE2	GLN	A	738	13.630	-5.321	-0.989	1.00	0.00
ATOM	3582	2HE2	GLN	A	738	12.652	-5.374	0.429	1.00	0.00
ATOM	3583	N	THR	A	739	8.777	-4.983	-1.675	1.00	0.00
ATOM	3584	CA	THR	A	739	8.229	-5.599	-0.472	1.00	0.00
ATOM	3585	C	THR	A	739	7.769	-7.048	-0.725	1.00	0.00
ATOM	3586	O	THR	A	739	7.590	-7.863	0.163	1.00	0.00
ATOM	3587	CB	THR	A	739	7.024	-4.732	-0.074	1.00	0.00
ATOM	3588	OG1	THR	A	739	7.468	-3.420	0.223	1.00	0.00
ATOM	3589	CG2	THR	A	739	6.312	-5.263	1.159	1.00	0.00
ATOM	3590	HN	THR	A	739	8.305	-4.212	-2.093	1.00	0.00
ATOM	3591	HA	THR	A	739	9.007	-5.592	0.292	1.00	0.00
ATOM	3592	HB	THR	A	739	6.279	-4.716	-0.884	1.00	0.00
ATOM	3593	HG1	THR	A	739	7.587	-2.915	-0.587	1.00	0.00
ATOM	3594	1HG2	THR	A	739	6.996	-5.820	1.792	1.00	0.00
ATOM	3595	2HG2	THR	A	739	5.517	-5.941	0.871	1.00	0.00
ATOM	3596	3HG2	THR	A	739	5.874	-4.459	1.746	1.00	0.00
ATOM	3597	N	PHE	A	740	7.539	-7.292	-2.006	1.00	0.00
ATOM	3598	CA	PHE	A	740	7.217	-8.590	-2.519	1.00	0.00
ATOM	3599	C	PHE	A	740	8.461	-9.389	-2.770	1.00	0.00
ATOM	3600	O	PHE	A	740	8.539	-10.564	-2.415	1.00	0.00
ATOM	3601	CB	PHE	A	740	6.466	-8.465	-3.856	1.00	0.00
ATOM	3602	CG	PHE	A	740	6.007	-9.806	-4.302	1.00	0.00
ATOM	3603	CD1	PHE	A	740	6.865	-10.669	-4.944	1.00	0.00
ATOM	3604	CD2	PHE	A	740	4.676	-10.138	-4.199	1.00	0.00
ATOM	3605	CE1	PHE	A	740	6.402	-11.859	-5.454	1.00	0.00
ATOM	3606	CE2	PHE	A	740	4.207	-11.323	-4.709	1.00	0.00
ATOM	3607	CZ	PHE	A	740	5.072	-12.183	-5.342	1.00	0.00
ATOM	3608	HN	PHE	A	740	7.342	-6.493	-2.574	1.00	0.00
ATOM	3609	HA	PHE	A	740	6.596	-9.089	-1.774	1.00	0.00
ATOM	3610	1HB	PHE	A	740	7.124	-8.042	-4.615	1.00	0.00
ATOM	3611	2HB	PHE	A	740	5.601	-7.813	-3.738	1.00	0.00
ATOM	3612	HD1	PHE	A	740	7.908	-10.410	-5.047	1.00	0.00
ATOM	3613	HD2	PHE	A	740	3.992	-9.458	-3.712	1.00	0.00
ATOM	3614	HE1	PHE	A	740	7.085	-12.539	-5.941	1.00	0.00
ATOM	3615	HE2	PHE	A	740	3.163	-11.580	-4.612	1.00	0.00
ATOM	3616	HZ	PHE	A	740	4.706	-13.112	-5.753	1.00	0.00
ATOM	3617	N	LEU	A	741	9.481	-8.749	-3.373	1.00	0.00
ATOM	3618	CA	LEU	A	741	10.675	-9.435	-3.772	1.00	0.00
ATOM	3619	C	LEU	A	741	11.407	-10.008	-2.617	1.00	0.00
ATOM	3620	O	LEU	A	741	11.870	-11.146	-2.694	1.00	0.00
ATOM	3621	CB	LEU	A	741	11.668	-8.553	-4.549	1.00	0.00
ATOM	3622	CG	LEU	A	741	12.941	-9.319	-4.958	1.00	0.00
ATOM	3623	CD1	LEU	A	741	12.608	-10.522	-5.851	1.00	0.00
ATOM	3624	CD2	LEU	A	741	13.977	-8.382	-5.600	1.00	0.00
ATOM	3625	HN	LEU	A	741	9.403	-7.768	-3.547	1.00	0.00

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ATOM	3626	HA	LEU A 741	10.356	-10.270	-4.395	1.00	0.00
ATOM	3627	IHB	LEU A 741	11.950	-7.704	-3.927	1.00	0.00
ATOM	3628	2HB	LEU A 741	11.179	-8.174	-5.445	1.00	0.00
ATOM	3629	HG	LEU A 741	13.455	-9.667	-4.062	1.00	0.00
ATOM	3630	IHD1	LEU A 741	11.955	-10.224	-6.671	1.00	0.00
ATOM	3631	2HD1	LEU A 741	12.094	-11.290	-5.273	1.00	0.00
ATOM	3632	3HD1	LEU A 741	13.521	-10.937	-6.280	1.00	0.00
ATOM	3633	IHD2	LEU A 741	14.269	-7.596	-4.904	1.00	0.00
ATOM	3634	2HD2	LEU A 741	13.557	-7.908	-6.487	1.00	0.00
ATOM	3635	3HD2	LEU A 741	14.872	-8.941	-5.873	1.00	0.00
ATOM	3636	N	ASP A 742	11.534	-9.248	-1.511	1.00	0.00
ATOM	3637	CA	ASP A 742	12.265	-9.803	-0.414	1.00	0.00
ATOM	3638	C	ASP A 742	11.571	-11.053	0.018	1.00	0.00
ATOM	3639	O	ASP A 742	10.347	-11.162	-0.050	1.00	0.00
ATOM	3640	CB	ASP A 742	12.541	-8.820	0.746	1.00	0.00
ATOM	3641	CG	ASP A 742	11.249	-8.276	1.322	1.00	0.00
ATOM	3642	OD1	ASP A 742	10.245	-9.033	1.325	1.00	0.00
ATOM	3643	OD2	ASP A 742	11.246	-7.093	1.757	1.00	0.00
ATOM	3644	HN	ASP A 742	11.134	-8.333	-1.460	1.00	0.00
ATOM	3645	HA	ASP A 742	13.209	-10.156	-0.828	1.00	0.00
ATOM	3646	IHB	ASP A 742	13.139	-7.982	0.386	1.00	0.00
ATOM	3647	2HB	ASP A 742	13.086	-9.330	1.540	1.00	0.00
ATOM	3648	N	LYS A 743	12.368	-12.049	0.448	1.00	0.00
ATOM	3649	CA	LYS A 743	11.832	-13.346	0.724	1.00	0.00
ATOM	3650	C	LYS A 743	10.692	-13.275	1.663	1.00	0.00
ATOM	3651	O	LYS A 743	9.628	-13.837	1.400	1.00	0.00
ATOM	3652	CB	LYS A 743	12.806	-14.309	1.412	1.00	0.00
ATOM	3653	CG	LYS A 743	12.044	-15.542	1.902	1.00	0.00
ATOM	3654	CD	LYS A 743	12.883	-16.607	2.605	1.00	0.00
ATOM	3655	CE	LYS A 743	12.022	-17.662	3.304	1.00	0.00
ATOM	3656	NZ	LYS A 743	11.056	-16.998	4.210	1.00	0.00
ATOM	3657	HN	LYS A 743	13.345	-11.880	0.575	1.00	0.00
ATOM	3658	HA	LYS A 743	11.525	-13.758	-0.236	1.00	0.00
ATOM	3659	IHB	LYS A 743	13.284	-13.811	2.255	1.00	0.00
ATOM	3660	2HB	LYS A 743	13.583	-14.611	0.709	1.00	0.00
ATOM	3661	IHG	LYS A 743	11.560	-16.005	1.044	1.00	0.00
ATOM	3662	2HG	LYS A 743	11.272	-15.210	2.594	1.00	0.00
ATOM	3663	IHD	LYS A 743	13.523	-16.124	3.344	1.00	0.00
ATOM	3664	2HD	LYS A 743	13.520	-17.098	1.870	1.00	0.00
ATOM	3665	IHE	LYS A 743	12.645	-18.329	3.899	1.00	0.00
ATOM	3666	2HE	LYS A 743	11.460	-18.241	2.571	1.00	0.00
ATOM	3667	IHZ	LYS A 743	10.178	-16.794	3.691	1.00	0.00
ATOM	3668	2HZ	LYS A 743	11.465	-16.109	4.561	1.00	0.00
ATOM	3669	3HZ	LYS A 743	10.847	-17.625	5.013	1.00	0.00
ATOM	3670	N	THR A 744	10.866	-12.578	2.792	1.00	0.00
ATOM	3671	CA	THR A 744	9.773	-12.650	3.697	1.00	0.00
ATOM	3672	C	THR A 744	9.253	-11.262	3.862	1.00	0.00
ATOM	3673	O	THR A 744	9.960	-10.390	4.369	1.00	0.00
ATOM	3674	CB	THR A 744	10.206	-13.141	5.048	1.00	0.00

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ATOM 3675	OG1 THR A 744	11.103	-14.232	4.899	1.00	0.00
ATOM 3676	CG2 THR A 744	8.960	-13.680	5.773	1.00	0.00
ATOM 3677	HN THR A 744	11.693	-12.052	2.981	1.00	0.00
ATOM 3678	HA THR A 744	9.043	-13.332	3.261	1.00	0.00
ATOM 3679	HB THR A 744	10.718	-12.349	5.594	1.00	0.00
ATOM 3680	HG1 THR A 744	11.846	-13.909	4.407	1.00	0.00
ATOM 3681	IHG2 THR A 744	8.820	-14.740	5.563	1.00	0.00
ATOM 3682	2HG2 THR A 744	8.069	-13.150	5.436	1.00	0.00
ATOM 3683	3HG2 THR A 744	9.071	-13.562	6.851	1.00	0.00
ATOM 3684	N MET A 745	8.018	-10.964	3.408	1.00	0.00
ATOM 3685	CA MET A 745	7.428	-9.642	3.726	1.00	0.00
ATOM 3686	C MET A 745	5.989	-9.601	3.232	1.00	0.00
ATOM 3687	O MET A 745	5.055	-9.884	3.973	1.00	0.00
ATOM 3688	CB MET A 745	8.233	-8.382	3.310	1.00	0.00
ATOM 3689	CG MET A 745	7.813	-7.093	4.023	1.00	0.00
ATOM 3690	SD MET A 745	9.021	-5.787	3.661	1.00	0.00
ATOM 3691	CE MET A 745	7.992	-4.302	3.617	1.00	0.00
ATOM 3692	HN MET A 745	7.516	-11.616	2.840	1.00	0.00
ATOM 3693	HA MET A 745	7.362	-9.591	4.801	1.00	0.00
ATOM 3694	1HB MET A 745	8.199	-8.227	2.245	1.00	0.00
ATOM 3695	2HB MET A 745	9.288	-8.489	3.533	1.00	0.00
ATOM 3696	1HG MET A 745	7.795	-7.286	5.094	1.00	0.00
ATOM 3697	2HG MET A 745	6.810	-6.798	3.719	1.00	0.00
ATOM 3698	1HE MET A 745	8.417	-3.530	4.257	1.00	0.00
ATOM 3699	2HE MET A 745	6.972	-4.501	3.945	1.00	0.00
ATOM 3700	3HE MET A 745	7.986	-3.875	2.615	1.00	0.00
ATOM 3701	N SER A 746	5.851	-9.230	1.946	1.00	0.00
ATOM 3702	CA SER A 746	4.516	-9.190	1.377	1.00	0.00
ATOM 3703	C SER A 746	4.071	-10.623	1.276	1.00	0.00
ATOM 3704	O SER A 746	4.874	-11.495	0.961	1.00	0.00
ATOM 3705	CB SER A 746	4.501	-8.593	-0.037	1.00	0.00
ATOM 3706	OG SER A 746	3.188	-8.162	-0.377	1.00	0.00
ATOM 3707	HN SER A 746	6.665	-9.030	1.391	1.00	0.00
ATOM 3708	HA SER A 746	3.877	-8.626	2.057	1.00	0.00
ATOM 3709	1HB SER A 746	4.846	-9.345	-0.755	1.00	0.00
ATOM 3710	2HB SER A 746	5.187	-7.749	-0.090	1.00	0.00
ATOM 3711	HG SER A 746	3.159	-7.827	-1.275	1.00	0.00
ATOM 3712	N ILE A 747	2.778	-10.859	1.568	1.00	0.00
ATOM 3713	CA ILE A 747	2.333	-12.194	1.377	1.00	0.00
ATOM 3714	C ILE A 747	2.368	-12.310	-0.104	1.00	0.00
ATOM 3715	O ILE A 747	1.618	-11.654	-0.825	1.00	0.00
ATOM 3716	CB ILE A 747	0.939	-12.479	1.863	1.00	0.00
ATOM 3717	CG1 ILE A 747	0.778	-12.082	3.341	1.00	0.00
ATOM 3718	CG2 ILE A 747	0.700	-13.986	1.658	1.00	0.00
ATOM 3719	CD1 ILE A 747	0.813	-10.575	3.581	1.00	0.00
ATOM 3720	HN ILE A 747	2.179	-10.147	1.933	1.00	0.00
ATOM 3721	HA ILE A 747	3.042	-12.826	1.911	1.00	0.00
ATOM 3722	HB ILE A 747	0.211	-11.897	1.297	1.00	0.00
ATOM 3723	1HG2 ILE A 747	1.303	-14.570	2.353	1.00	0.00

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ATOM	3724	2HG2	ILE	A	747	0.978	-14.277	0.645	1.00	0.00
ATOM	3725	3HG2	ILE	A	747	-0.348	-14.228	1.835	1.00	0.00
ATOM	3726	1HG1	ILE	A	747	1.579	-12.545	3.916	1.00	0.00
ATOM	3727	2HG1	ILE	A	747	-0.173	-12.471	3.704	1.00	0.00
ATOM	3728	1HD1	ILE	A	747	0.129	-10.061	2.906	1.00	0.00
ATOM	3729	2HD1	ILE	A	747	1.816	-10.189	3.403	1.00	0.00
ATOM	3730	3HD1	ILE	A	747	0.510	-10.350	4.604	1.00	0.00
ATOM	3731	N	GLU	A	748	3.284	-13.156	-0.596	1.00	0.00
ATOM	3732	CA	GLU	A	748	3.436	-13.371	-2.000	1.00	0.00
ATOM	3733	C	GLU	A	748	2.141	-13.951	-2.449	1.00	0.00
ATOM	3734	O	GLU	A	748	1.764	-13.859	-3.616	1.00	0.00
ATOM	3735	CB	GLU	A	748	4.568	-14.372	-2.304	1.00	0.00
ATOM	3736	CG	GLU	A	748	4.775	-14.670	-3.789	1.00	0.00
ATOM	3737	CD	GLU	A	748	3.903	-15.864	-4.150	1.00	0.00
ATOM	3738	OE1	GLU	A	748	3.323	-16.474	-3.212	1.00	0.00
ATOM	3739	OE2	GLU	A	748	3.813	-16.188	-5.363	1.00	0.00
ATOM	3740	HN	GLU	A	748	3.877	-13.651	0.039	1.00	0.00
ATOM	3741	HA	GLU	A	748	3.656	-12.402	-2.448	1.00	0.00
ATOM	3742	1HB	GLU	A	748	4.346	-15.308	-1.793	1.00	0.00
ATOM	3743	2HB	GLU	A	748	5.497	-13.973	-1.900	1.00	0.00
ATOM	3744	1HG	GLU	A	748	5.819	-14.911	-3.990	1.00	0.00
ATOM	3745	2HG	GLU	A	748	4.484	-13.813	-4.397	1.00	0.00
ATOM	3746	N	PHE	A	749	1.432	-14.561	-1.486	1.00	0.00
ATOM	3747	CA	PHE	A	749	0.228	-15.295	-1.685	1.00	0.00
ATOM	3748	C	PHE	A	749	-1.022	-14.586	-2.108	1.00	0.00
ATOM	3749	O	PHE	A	749	-1.822	-15.245	-2.771	1.00	0.00
ATOM	3750	CB	PHE	A	749	-0.049	-16.229	-0.502	1.00	0.00
ATOM	3751	CG	PHE	A	749	1.105	-17.172	-0.580	1.00	0.00
ATOM	3752	CD1	PHE	A	749	1.105	-18.179	-1.517	1.00	0.00
ATOM	3753	CD2	PHE	A	749	2.252	-16.944	0.145	1.00	0.00
ATOM	3754	CE1	PHE	A	749	2.221	-18.959	-1.716	1.00	0.00
ATOM	3755	CE2	PHE	A	749	3.369	-17.725	-0.043	1.00	0.00
ATOM	3756	CZ	PHE	A	749	3.358	-18.730	-0.980	1.00	0.00
ATOM	3757	HN	PHE	A	749	1.779	-14.494	-0.552	1.00	0.00
ATOM	3758	HA	PHE	A	749	0.350	-15.868	-2.604	1.00	0.00
ATOM	3759	1HB	PHE	A	749	-0.995	-16.757	-0.614	1.00	0.00
ATOM	3760	2HB	PHE	A	749	-0.054	-15.693	0.447	1.00	0.00
ATOM	3761	HD1	PHE	A	749	0.216	-18.361	-2.104	1.00	0.00
ATOM	3762	HD2	PHE	A	749	2.276	-16.143	0.869	1.00	0.00
ATOM	3763	HE1	PHE	A	749	2.203	-19.750	-2.450	1.00	0.00
ATOM	3764	HE2	PHE	A	749	4.256	-17.548	0.547	1.00	0.00
ATOM	3765	HZ	PHE	A	749	4.237	-19.337	-1.137	1.00	0.00
ATOM	3766	N	PRO	A	750	-1.315	-13.342	-1.805	1.00	0.00
ATOM	3767	CA	PRO	A	750	-2.560	-12.833	-2.313	1.00	0.00
ATOM	3768	C	PRO	A	750	-2.536	-12.817	-3.807	1.00	0.00
ATOM	3769	O	PRO	A	750	-1.746	-12.081	-4.395	1.00	0.00
ATOM	3770	CB	PRO	A	750	-2.791	-11.502	-1.606	1.00	0.00
ATOM	3771	CG	PRO	A	750	-2.100	-11.720	-0.244	1.00	0.00
ATOM	3772	CD	PRO	A	750	-0.975	-12.738	-0.529	1.00	0.00

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ATOM	3773	IHD	PRO A 750	-0.006	-12.243	-0.593	1.00	0.00
ATOM	3774	2HD	PRO A 750	-0.931	-13.501	0.248	1.00	0.00
ATOM	3775	HA	PRO A 750	-3.366	-13.534	-2.096	1.00	0.00
ATOM	3776	IHB	PRO A 750	-3.854	-11.293	-1.486	1.00	0.00
ATOM	3777	2HB	PRO A 750	-2.341	-10.675	-2.155	1.00	0.00
ATOM	3778	IHG	PRO A 750	-1.692	-10.785	0.139	1.00	0.00
ATOM	3779	2HG	PRO A 750	-2.803	-12.112	0.491	1.00	0.00
ATOM	3780	N	GLU A 751	-3.415	-13.633	-4.421	1.00	0.00
ATOM	3781	CA	GLU A 751	-3.460	-13.836	-5.840	1.00	0.00
ATOM	3782	C	GLU A 751	-3.919	-12.660	-6.642	1.00	0.00
ATOM	3783	O	GLU A 751	-3.277	-12.291	-7.623	1.00	0.00
ATOM	3784	CB	GLU A 751	-4.349	-15.034	-6.212	1.00	0.00
ATOM	3785	CG	GLU A 751	-5.788	-14.904	-5.711	1.00	0.00
ATOM	3786	CD	GLU A 751	-6.544	-16.157	-6.130	1.00	0.00
ATOM	3787	OE1	GLU A 751	-6.025	-17.274	-5.868	1.00	0.00
ATOM	3788	OE2	GLU A 751	-7.649	-16.014	-6.717	1.00	0.00
ATOM	3789	HN	GLU A 751	-4.073	-14.126	-3.853	1.00	0.00
ATOM	3790	HA	GLU A 751	-2.436	-14.006	-6.171	1.00	0.00
ATOM	3791	IHB	GLU A 751	-3.912	-15.937	-5.789	1.00	0.00
ATOM	3792	2HB	GLU A 751	-4.364	-15.135	-7.296	1.00	0.00
ATOM	3793	IHG	GLU A 751	-6.269	-14.030	-6.150	1.00	0.00
ATOM	3794	2HG	GLU A 751	-5.810	-14.815	-4.625	1.00	0.00
ATOM	3795	N	MET A 752	-5.033	-12.022	-6.240	1.00	0.00
ATOM	3796	CA	MET A 752	-5.558	-10.951	-7.036	1.00	0.00
ATOM	3797	C	MET A 752	-4.576	-9.828	-7.065	1.00	0.00
ATOM	3798	O	MET A 752	-4.358	-9.205	-8.103	1.00	0.00
ATOM	3799	CB	MET A 752	-6.887	-10.401	-6.498	1.00	0.00
ATOM	3800	CG	MET A 752	-7.528	-9.365	-7.423	1.00	0.00
ATOM	3801	SD	MET A 752	-8.234	-10.030	-8.960	1.00	0.00
ATOM	3802	CE	MET A 752	-8.804	-8.414	-9.560	1.00	0.00
ATOM	3803	HN	MET A 752	-5.491	-12.294	-5.393	1.00	0.00
ATOM	3804	HA	MET A 752	-5.697	-11.348	-8.041	1.00	0.00
ATOM	3805	IHB	MET A 752	-6.710	-9.942	-5.526	1.00	0.00
ATOM	3806	2HB	MET A 752	-7.582	-11.229	-6.364	1.00	0.00
ATOM	3807	IHG	MET A 752	-6.772	-8.630	-7.698	1.00	0.00
ATOM	3808	2HG	MET A 752	-8.329	-8.863	-6.881	1.00	0.00
ATOM	3809	IHE	MET A 752	-7.986	-7.695	-9.501	1.00	0.00
ATOM	3810	2HE	MET A 752	-9.627	-8.057	-8.941	1.00	0.00
ATOM	3811	3HE	MET A 752	-9.121	-8.495	-10.600	1.00	0.00
ATOM	3812	N	LEU A 753	-3.980	-9.571	-5.881	1.00	0.00
ATOM	3813	CA	LEU A 753	-3.011	-8.486	-5.797	1.00	0.00
ATOM	3814	C	LEU A 753	-1.796	-8.816	-6.679	1.00	0.00
ATOM	3815	O	LEU A 753	-1.275	-8.016	-7.411	1.00	0.00
ATOM	3816	CB	LEU A 753	-2.612	-8.246	-4.332	1.00	0.00
ATOM	3817	CG	LEU A 753	-1.716	-7.009	-4.115	1.00	0.00
ATOM	3818	CD1	LEU A 753	-2.411	-5.703	-4.529	1.00	0.00
ATOM	3819	CD2	LEU A 753	-1.262	-6.929	-2.652	1.00	0.00
ATOM	3820	HN	LEU A 753	-4.193	-10.142	-5.091	1.00	0.00
ATOM	3821	HA	LEU A 753	-3.510	-7.604	-6.201	1.00	0.00

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ATOM	3822	1HB	LEU	A	753	-2.102	-9.133	-3.950	1.00	0.00
ATOM	3823	2HB	LEU	A	753	-3.513	-8.138	-3.727	1.00	0.00
ATOM	3824	HG	LEU	A	753	-0.817	-7.118	-4.725	1.00	0.00
ATOM	3825	1HD1	LEU	A	753	-2.614	-5.679	-5.599	1.00	0.00
ATOM	3826	2HD1	LEU	A	753	-1.782	-4.841	-4.304	1.00	0.00
ATOM	3827	3HD1	LEU	A	753	-3.356	-5.572	-4.002	1.00	0.00
ATOM	3828	1HD2	LEU	A	753	-2.112	-6.817	-1.977	1.00	0.00
ATOM	3829	2HD2	LEU	A	753	-0.590	-6.087	-2.490	1.00	0.00
ATOM	3830	3HD2	LEU	A	753	-0.728	-7.835	-2.364	1.00	0.00
ATOM	3831	N	ALA	A	754	-1.355	-10.050	-6.651	1.00	0.00
ATOM	3832	CA	ALA	A	754	-0.204	-10.417	-7.422	1.00	0.00
ATOM	3833	C	ALA	A	754	-0.537	-10.216	-8.862	1.00	0.00
ATOM	3834	O	ALA	A	754	0.294	-9.759	-9.649	1.00	0.00
ATOM	3835	CB	ALA	A	754	0.178	-11.896	-7.250	1.00	0.00
ATOM	3836	HN	ALA	A	754	-1.817	-10.738	-6.092	1.00	0.00
ATOM	3837	HA	ALA	A	754	0.613	-9.777	-7.089	1.00	0.00
ATOM	3838	1HB	ALA	A	754	-0.640	-12.544	-7.564	1.00	0.00
ATOM	3839	2HB	ALA	A	754	0.394	-12.110	-6.203	1.00	0.00
ATOM	3840	3HB	ALA	A	754	1.050	-12.133	-7.859	1.00	0.00
ATOM	3841	N	GLU	A	755	-1.786	-10.545	-9.230	1.00	0.00
ATOM	3842	CA	GLU	A	755	-2.225	-10.455	-10.588	1.00	0.00
ATOM	3843	C	GLU	A	755	-2.065	-9.055	-11.070	1.00	0.00
ATOM	3844	O	GLU	A	755	-1.477	-8.828	-12.127	1.00	0.00
ATOM	3845	CB	GLU	A	755	-3.715	-10.810	-10.727	1.00	0.00
ATOM	3846	CG	GLU	A	755	-4.273	-10.739	-12.149	1.00	0.00
ATOM	3847	CD	GLU	A	755	-5.752	-11.092	-12.056	1.00	0.00
ATOM	3848	OE1	GLU	A	755	-6.066	-12.306	-11.925	1.00	0.00
ATOM	3849	OE2	GLU	A	755	-6.587	-10.150	-12.100	1.00	0.00
ATOM	3850	HN	GLU	A	755	-2.427	-10.864	-8.532	1.00	0.00
ATOM	3851	HA	GLU	A	755	-1.614	-11.147	-11.167	1.00	0.00
ATOM	3852	1HB	GLU	A	755	-4.288	-10.128	-10.101	1.00	0.00
ATOM	3853	2HB	GLU	A	755	-3.860	-11.823	-10.353	1.00	0.00
ATOM	3854	1HG	GLU	A	755	-3.767	-11.451	-12.801	1.00	0.00
ATOM	3855	2HG	GLU	A	755	-4.161	-9.736	-12.561	1.00	0.00
ATOM	3856	N	ILE	A	756	-2.558	-8.063	-10.300	1.00	0.00
ATOM	3857	CA	ILE	A	756	-2.405	-6.729	-10.798	1.00	0.00
ATOM	3858	C	ILE	A	756	-0.951	-6.435	-10.893	1.00	0.00
ATOM	3859	O	ILE	A	756	-0.505	-5.902	-11.910	1.00	0.00
ATOM	3860	CB	ILE	A	756	-3.029	-5.638	-9.952	1.00	0.00
ATOM	3861	CG1	ILE	A	756	-2.921	-4.241	-10.627	1.00	0.00
ATOM	3862	CG2	ILE	A	756	-2.437	-5.706	-8.536	1.00	0.00
ATOM	3863	CD1	ILE	A	756	-1.513	-3.634	-10.808	1.00	0.00
ATOM	3864	HN	ILE	A	756	-3.006	-8.250	-9.427	1.00	0.00
ATOM	3865	HA	ILE	A	756	-2.860	-6.726	-11.788	1.00	0.00
ATOM	3866	HB	ILE	A	756	-4.110	-5.774	-9.909	1.00	0.00
ATOM	3867	1HG2	ILE	A	756	-1.356	-5.563	-8.563	1.00	0.00
ATOM	3868	2HG2	ILE	A	756	-2.637	-6.680	-8.090	1.00	0.00
ATOM	3869	3HG2	ILE	A	756	-2.864	-4.922	-7.911	1.00	0.00
ATOM	3870	1HG1	ILE	A	756	-3.504	-3.542	-10.031	1.00	0.00

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ATOM	3871	2HG1	ILE A 756	-3.374	-4.317	-11.613	1.00	0.00
ATOM	3872	1HD1	ILE A 756	-1.016	-4.066	-11.676	1.00	0.00
ATOM	3873	2HD1	ILE A 756	-0.898	-3.840	-9.931	1.00	0.00
ATOM	3874	3HD1	ILE A 756	-1.584	-2.557	-10.961	1.00	0.00
ATOM	3875	N	ILE A 757	-0.175	-6.762	-9.850	1.00	0.00
ATOM	3876	CA	ILE A 757	1.184	-6.312	-9.796	1.00	0.00
ATOM	3877	C	ILE A 757	1.931	-6.758	-11.008	1.00	0.00
ATOM	3878	O	ILE A 757	2.694	-5.986	-11.586	1.00	0.00
ATOM	3879	CB	ILE A 757	1.925	-6.851	-8.613	1.00	0.00
ATOM	3880	CG1	ILE A 757	1.289	-6.331	-7.315	1.00	0.00
ATOM	3881	CG2	ILE A 757	3.410	-6.491	-8.781	1.00	0.00
ATOM	3882	CD1	ILE A 757	1.268	-4.806	-7.228	1.00	0.00
ATOM	3883	HN	ILE A 757	-0.547	-7.322	-9.109	1.00	0.00
ATOM	3884	HA	ILE A 757	1.151	-5.224	-9.755	1.00	0.00
ATOM	3885	HB	ILE A 757	1.805	-7.933	-8.555	1.00	0.00
ATOM	3886	1HG2	ILE A 757	3.519	-5.482	-9.180	1.00	0.00
ATOM	3887	2HG2	ILE A 757	3.889	-7.181	-9.475	1.00	0.00
ATOM	3888	3HG2	ILE A 757	3.917	-6.529	-7.817	1.00	0.00
ATOM	3889	1HG1	ILE A 757	1.849	-6.724	-6.468	1.00	0.00
ATOM	3890	2HG1	ILE A 757	0.267	-6.701	-7.252	1.00	0.00
ATOM	3891	1HD1	ILE A 757	0.559	-4.389	-7.943	1.00	0.00
ATOM	3892	2HD1	ILE A 757	2.254	-4.402	-7.456	1.00	0.00
ATOM	3893	3HD1	ILE A 757	0.965	-4.490	-6.230	1.00	0.00
ATOM	3894	N	THR A 758	1.699	-8.009	-11.440	1.00	0.00
ATOM	3895	CA	THR A 758	2.403	-8.548	-12.565	1.00	0.00
ATOM	3896	C	THR A 758	2.097	-7.753	-13.792	1.00	0.00
ATOM	3897	O	THR A 758	2.966	-7.545	-14.637	1.00	0.00
ATOM	3898	CB	THR A 758	2.045	-9.979	-12.854	1.00	0.00
ATOM	3899	OG1	THR A 758	2.968	-10.535	-13.779	1.00	0.00
ATOM	3900	CG2	THR A 758	0.620	-10.034	-13.435	1.00	0.00
ATOM	3901	HN	THR A 758	1.023	-8.573	-10.967	1.00	0.00
ATOM	3902	HA	THR A 758	3.465	-8.468	-12.334	1.00	0.00
ATOM	3903	HB	THR A 758	2.079	-10.570	-11.939	1.00	0.00
ATOM	3904	HG1	THR A 758	3.149	-9.862	-14.421	1.00	0.00
ATOM	3905	1HG2	THR A 758	0.650	-10.130	-14.520	1.00	0.00
ATOM	3906	2HG2	THR A 758	0.079	-9.120	-13.192	1.00	0.00
ATOM	3907	3HG2	THR A 758	0.084	-10.895	-13.035	1.00	0.00
ATOM	3908	N	ASN A 759	0.852	-7.259	-13.912	1.00	0.00
ATOM	3909	CA	ASN A 759	0.449	-6.558	-15.094	1.00	0.00
ATOM	3910	C	ASN A 759	1.381	-5.433	-15.388	1.00	0.00
ATOM	3911	O	ASN A 759	1.869	-5.304	-16.509	1.00	0.00
ATOM	3912	CB	ASN A 759	-0.951	-5.941	-14.956	1.00	0.00
ATOM	3913	CG	ASN A 759	-1.259	-5.187	-16.241	1.00	0.00
ATOM	3914	OD1	ASN A 759	-1.632	-4.013	-16.206	1.00	0.00
ATOM	3915	ND2	ASN A 759	-1.094	-5.868	-17.405	1.00	0.00
ATOM	3916	HN	ASN A 759	0.199	-7.383	-13.165	1.00	0.00
ATOM	3917	HA	ASN A 759	0.464	-7.282	-15.909	1.00	0.00
ATOM	3918	1HB	ASN A 759	-0.983	-5.249	-14.115	1.00	0.00
ATOM	3919	2HB	ASN A 759	-1.700	-6.719	-14.806	1.00	0.00

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ATOM	3920	IHD2 ASN A 759	-0.784	-6.819	-17.383	1.00	0.00
ATOM	3921	2HD2 ASN A 759	-1.278	-5.437	-18.288	1.00	0.00
ATOM	3922	N GLN A 760	1.663	-4.583	-14.389	1.00	0.00
ATOM	3923	CA GLN A 760	2.499	-3.460	-14.673	1.00	0.00
ATOM	3924	C GLN A 760	3.920	-3.842	-14.935	1.00	0.00
ATOM	3925	O GLN A 760	4.581	-3.218	-15.763	1.00	0.00
ATOM	3926	CB GLN A 760	2.341	-2.318	-13.653	1.00	0.00
ATOM	3927	CG GLN A 760	0.911	-1.764	-13.764	1.00	0.00
ATOM	3928	CD GLN A 760	0.769	-0.440	-13.032	1.00	0.00
ATOM	3929	OE1 GLN A 760	1.510	0.510	-13.277	1.00	0.00
ATOM	3930	NE2 GLN A 760	-0.221	-0.373	-12.102	1.00	0.00
ATOM	3931	HN GLN A 760	1.298	-4.733	-13.470	1.00	0.00
ATOM	3932	HA GLN A 760	2.225	-3.112	-15.669	1.00	0.00
ATOM	3933	1HB GLN A 760	3.065	-1.530	-13.860	1.00	0.00
ATOM	3934	2HB GLN A 760	2.521	-2.690	-12.645	1.00	0.00
ATOM	3935	1HG GLN A 760	0.207	-2.474	-13.330	1.00	0.00
ATOM	3936	2HG GLN A 760	0.659	-1.606	-14.812	1.00	0.00
ATOM	3937	1HE2 GLN A 760	-0.702	-1.206	-11.828	1.00	0.00
ATOM	3938	2HE2 GLN A 760	-0.480	0.497	-11.683	1.00	0.00
ATOM	3939	N ILE A 761	4.442	-4.879	-14.248	1.00	0.00
ATOM	3940	CA ILE A 761	5.781	-5.292	-14.553	1.00	0.00
ATOM	3941	C ILE A 761	5.742	-6.011	-15.908	1.00	0.00
ATOM	3942	1OCT ILE A 761	5.322	-5.360	-16.902	1.00	0.00
ATOM	3943	CB ILE A 761	6.385	-6.218	-13.530	1.00	0.00
ATOM	3944	CG1 ILE A 761	7.830	-6.571	-13.928	1.00	0.00
ATOM	3945	CG2 ILE A 761	5.457	-7.428	-13.332	1.00	0.00
ATOM	3946	CD1 ILE A 761	8.597	-7.355	-12.864	1.00	0.00
ATOM	3947	2OCT ILE A 761	6.129	-7.209	-15.978	1.00	0.00
ATOM	3948	HN ILE A 761	3.908	-5.347	-13.544	1.00	0.00
ATOM	3949	HA ILE A 761	6.375	-4.381	-14.624	1.00	0.00
ATOM	3950	HB ILE A 761	6.414	-5.651	-12.601	1.00	0.00
ATOM	3951	1HG2 ILE A 761	4.449	-7.102	-13.075	1.00	0.00
ATOM	3952	2HG2 ILE A 761	5.825	-8.056	-12.520	1.00	0.00
ATOM	3953	3HG2 ILE A 761	5.399	-8.013	-14.250	1.00	0.00
ATOM	3954	1HG1 ILE A 761	8.369	-5.647	-14.132	1.00	0.00
ATOM	3955	2HG1 ILE A 761	7.804	-7.162	-14.842	1.00	0.00
ATOM	3956	1HD1 ILE A 761	8.098	-8.299	-12.647	1.00	0.00
ATOM	3957	2HD1 ILE A 761	8.649	-6.781	-11.939	1.00	0.00
ATOM	3958	3HD1 ILE A 761	9.604	-7.578	-13.214	1.00	0.00
ATOM	3959	HCT ILE A 761	5.361	-4.423	-16.765	1.00	0.00
ATOM	3960	O HOH W 516	-9.097	2.914	0.913	1.00	0.00
ATOM	3961	1H HOH W 516	-8.853	3.396	0.115	1.00	0.00
ATOM	3962	2H HOH W 516	-8.335	2.330	1.052	1.00	0.00
ATOM	3963	NA+ CIP C 206	6.097	8.962	-3.974	1.00	0.00
ATOM	3964	NA+ CIP C 157	-9.340	-4.397	-27.602	1.00	0.00
ATOM	3965	NA+ CIP C 105	-8.364	-4.063	14.059	1.00	0.00
ATOM	3966	NA+ CIP C 184	-23.434	28.968	-12.650	1.00	0.00
ATOM	3967	NA+ CIP C 202	3.261	11.659	-12.120	1.00	0.00
ATOM	3968	NA+ CIP C 166	-15.650	5.434	-32.841	1.00	0.00

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ATOM	3969	NA+	CIP C 234	-7.350	-13.381	-10.083	1.00	0.00
ATOM	3970	NA+	CIP C 120	9.673	4.279	-1.053	1.00	0.00
ATOM	3971	CL-	CIM C 58	-20.663	-6.966	-18.429	1.00	0.00
ATOM	3972	NA+	CIP C 167	-16.694	-0.528	-26.996	1.00	0.00
ATOM	3973	CL-	CIM C 174	-24.680	17.196	-19.047	1.00	0.00
ATOM	3974	NA+	CIP C 16	-22.819	13.330	-4.433	1.00	0.00
ATOM	3975	NA+	CIP C 227	1.631	-16.295	-6.675	1.00	0.00
ATOM	3976	NA+	CIP C 221	11.345	-4.726	2.532	1.00	0.00
ATOM	3977	CL-	CIM C 93	-13.515	6.310	6.654	1.00	0.00
ATOM	3978	CL-	CIM C 160	-10.213	-4.624	-36.213	1.00	0.00
ATOM	3979	CL-	CIM C 173	-24.595	17.570	-9.392	1.00	0.00
ATOM	3980	CL-	CIM C 55	-18.222	-8.698	-11.429	1.00	0.00
ATOM	3981	CL-	CIM C 183	-15.467	17.246	-10.379	1.00	0.00

END

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Fig 13

REMARK 1 grfromer modeller, no optimisation july 15 1998

ATOM	1	N	GLN	1	1	31.226	-1.970	94.273	1.00	5.90
ATOM	2	CA	GLN	1	1	32.061	-3.185	94.135	1.00	5.90
ATOM	3	C	GLN	1	1	33.238	-2.949	93.251	1.00	5.90
ATOM	4	O	GLN	1	1	33.964	-1.969	93.402	1.00	5.90
ATOM	5	CB	GLN	1	1	31.246	-4.344	93.534	1.00	5.90
ATOM	6	CG	GLN	1	1	30.248	-4.977	94.504	1.00	5.90
ATOM	7	CD	GLN	1	1	31.030	-5.896	95.434	1.00	5.90
ATOM	8	OE1	GLN	1	1	30.460	-6.569	96.291	1.00	5.90
ATOM	9	NE2	GLN	1	1	32.378	-5.931	95.256	1.00	5.90
ATOM	10	N	LEU	1	2	33.462	-3.888	92.314	1.00	0.97
ATOM	11	CA	LEU	1	2	34.556	-3.825	91.394	1.00	0.97
ATOM	12	C	LEU	1	2	34.400	-2.709	90.407	1.00	0.97
ATOM	13	O	LEU	1	2	35.388	-2.108	89.988	1.00	0.97
ATOM	14	CB	LEU	1	2	34.752	-5.124	90.594	1.00	0.97
ATOM	15	CG	LEU	1	2	35.203	-6.310	91.465	1.00	0.97
ATOM	16	CD1	LEU	1	2	35.397	-7.582	90.624	1.00	0.97
ATOM	17	CD2	LEU	1	2	36.445	-5.948	92.295	1.00	0.97
ATOM	18	N	THR	1	3	33.154	-2.414	89.990	1.00	4.97
ATOM	19	CA	THR	1	3	32.946	-1.389	89.006	1.00	4.97
ATOM	20	C	THR	1	3	33.539	-0.098	89.475	1.00	4.97
ATOM	21	O	THR	1	3	33.281	0.370	90.583	1.00	4.97
ATOM	22	CB	THR	1	3	31.496	-1.151	88.687	1.00	4.97
ATOM	23	OG1	THR	1	3	31.375	-0.248	87.598	1.00	4.97
ATOM	24	CG2	THR	1	3	30.792	-0.588	89.932	1.00	4.97
ATOM	25	N	PRO	1	4	34.334	0.496	88.629	1.00	1.53
ATOM	26	CA	PRO	1	4	34.970	1.734	88.985	1.00	1.53
ATOM	27	C	PRO	1	4	33.953	2.822	89.105	1.00	1.53
ATOM	28	O	PRO	1	4	32.935	2.768	88.416	1.00	1.53
ATOM	29	CB	PRO	1	4	36.021	1.984	87.906	1.00	1.53
ATOM	30	CG	PRO	1	4	36.397	0.567	87.435	1.00	1.53
ATOM	31	CD	PRO	1	4	35.129	-0.270	87.682	1.00	1.53
ATOM	32	N	THR	1	5	34.221	3.822	89.966	1.00	4.74
ATOM	33	CA	THR	1	5	33.280	4.873	90.217	1.00	4.74
ATOM	34	C	THR	1	5	32.996	5.653	88.973	1.00	4.74
ATOM	35	O	THR	1	5	31.839	5.946	88.679	1.00	4.74
ATOM	36	CB	THR	1	5	33.749	5.833	91.276	1.00	4.74
ATOM	37	OG1	THR	1	5	32.717	6.755	91.592	1.00	4.74
ATOM	38	CG2	THR	1	5	35.000	6.575	90.777	1.00	4.74
ATOM	39	N	LEU	1	6	34.042	5.976	88.189	1.00	0.89
ATOM	40	CA	LEU	1	6	33.888	6.778	87.008	1.00	0.89
ATOM	41	C	LEU	1	6	33.005	6.068	86.029	1.00	0.89
ATOM	42	O	LEU	1	6	32.203	6.696	85.338	1.00	0.89
ATOM	43	CB	LEU	1	6	35.231	7.060	86.306	1.00	0.89
ATOM	44	CG	LEU	1	6	35.101	7.915	85.031	1.00	0.89
ATOM	45	CD1	LEU	1	6	34.528	9.306	85.351	1.00	0.89
ATOM	46	CD2	LEU	1	6	36.436	7.988	84.273	1.00	0.89
ATOM	47	N	VAL	1	7	33.146	4.733	85.934	1.00	0.63
ATOM	48	CA	VAL	1	7	32.354	3.959	85.021	1.00	0.63

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ATOM	49	C	VAL	1	7	30.930	4.080	85.438	1.00	0.63
ATOM	50	O	VAL	1	7	30.032	4.219	84.610	1.00	0.63
ATOM	51	CB	VAL	1	7	32.646	2.485	85.082	1.00	0.63
ATOM	52	CG1	VAL	1	7	31.739	1.778	84.061	1.00	0.63
ATOM	53	CG2	VAL	1	7	34.150	2.232	84.893	1.00	0.63
ATOM	54	N	SER	1	8	30.698	4.024	86.760	1.00	0.66
ATOM	55	CA	SER	1	8	29.369	4.077	87.284	1.00	0.66
ATOM	56	C	SER	1	8	28.753	5.387	86.910	1.00	0.66
ATOM	57	O	SER	1	8	27.579	5.432	86.546	1.00	0.66
ATOM	58	CB	SER	1	8	29.331	3.967	88.819	1.00	0.66
ATOM	59	OG	SER	1	8	29.819	2.698	89.229	1.00	0.66
ATOM	60	N	LEU	1	9	29.523	6.497	86.978	1.00	8.73
ATOM	61	CA	LEU	1	9	28.901	7.750	86.646	1.00	8.73
ATOM	62	C	LEU	1	9	28.462	7.675	85.232	1.00	8.73
ATOM	63	O	LEU	1	9	27.335	8.038	84.904	1.00	8.73
ATOM	64	CB	LEU	1	9	29.780	9.012	86.517	1.00	8.73
ATOM	65	CG	LEU	1	9	30.572	9.500	87.724	1.00	8.73
ATOM	66	CD1	LEU	1	9	29.685	9.772	88.945	1.00	8.73
ATOM	67	CD2	LEU	1	9	31.763	8.586	87.961	1.00	8.73
ATOM	68	N	LEU	1	10	29.363	7.182	84.363	1.00	1.17
ATOM	69	CA	LEU	1	10	29.124	7.190	82.952	1.00	1.17
ATOM	70	C	LEU	1	10	27.867	6.438	82.663	1.00	1.17
ATOM	71	O	LEU	1	10	27.061	6.863	81.837	1.00	1.17
ATOM	72	CB	LEU	1	10	30.291	6.589	82.144	1.00	1.17
ATOM	73	CG	LEU	1	10	31.600	7.406	82.258	1.00	1.17
ATOM	74	CD1	LEU	1	10	32.739	6.781	81.435	1.00	1.17
ATOM	75	CD2	LEU	1	10	31.372	8.887	81.913	1.00	1.17
ATOM	76	N	GLU	1	11	27.653	5.307	83.355	1.00	3.68
ATOM	77	CA	GLU	1	11	26.453	4.545	83.160	1.00	3.68
ATOM	78	C	GLU	1	11	25.296	5.429	83.496	1.00	3.68
ATOM	79	O	GLU	1	11	24.319	5.514	82.752	1.00	3.68
ATOM	80	CB	GLU	1	11	26.364	3.363	84.145	1.00	3.68
ATOM	81	CG	GLU	1	11	27.158	2.110	83.772	1.00	3.68
ATOM	82	CD	GLU	1	11	26.140	1.007	83.512	1.00	3.68
ATOM	83	OE1	GLU	1	11	25.188	0.896	84.330	1.00	3.68
ATOM	84	OE2	GLU	1	11	26.293	0.260	82.511	1.00	3.68
ATOM	85	N	VAL	1	12	25.395	6.135	84.635	1.00	0.75
ATOM	86	CA	VAL	1	12	24.309	6.939	85.107	1.00	0.75
ATOM	87	C	VAL	1	12	23.970	8.054	84.169	1.00	0.75
ATOM	88	O	VAL	1	12	22.797	8.283	83.880	1.00	0.75
ATOM	89	CB	VAL	1	12	24.598	7.561	86.442	1.00	0.75
ATOM	90	CG1	VAL	1	12	23.394	8.424	86.854	1.00	0.75
ATOM	91	CG2	VAL	1	12	24.934	6.439	87.440	1.00	0.75
ATOM	92	N	ILE	1	13	24.984	8.784	83.664	1.00	4.56
ATOM	93	CA	ILE	1	13	24.694	9.920	82.836	1.00	4.56
ATOM	94	C	ILE	1	13	24.234	9.610	81.445	1.00	4.56
ATOM	95	O	ILE	1	13	23.698	10.497	80.784	1.00	4.56
ATOM	96	CB	ILE	1	13	25.744	11.011	82.766	1.00	4.56
ATOM	97	CG1	ILE	1	13	27.064	10.605	82.098	1.00	4.56

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ATOM	98	CG2	ILE	1	13	25.959	11.490	84.213	1.00	4.56
ATOM	99	CD1	ILE	1	13	28.035	9.910	83.035	1.00	4.56
ATOM	100	N	GLU	1	14	24.471	8.384	80.928	1.00	2.30
ATOM	101	CA	GLU	1	14	24.078	8.151	79.566	1.00	2.30
ATOM	102	C	GLU	1	14	22.611	8.405	79.384	1.00	2.30
ATOM	103	O	GLU	1	14	21.774	8.069	80.220	1.00	2.30
ATOM	104	CB	GLU	1	14	24.485	6.783	78.994	1.00	2.30
ATOM	105	CG	GLU	1	14	24.341	6.743	77.471	1.00	2.30
ATOM	106	CD	GLU	1	14	25.404	5.808	76.924	1.00	2.30
ATOM	107	OE1	GLU	1	14	26.589	6.006	77.303	1.00	2.30
ATOM	108	OE2	GLU	1	14	25.060	4.899	76.122	1.00	2.30
ATOM	109	N	PRO	1	15	22.304	9.030	78.278	1.00	6.71
ATOM	110	CA	PRO	1	15	20.949	9.443	78.025	1.00	6.71
ATOM	111	C	PRO	1	15	20.014	8.313	77.771	1.00	6.71
ATOM	112	O	PRO	1	15	20.454	7.242	77.356	1.00	6.71
ATOM	113	CB	PRO	1	15	21.022	10.438	76.870	1.00	6.71
ATOM	114	CG	PRO	1	15	22.432	11.038	76.998	1.00	6.71
ATOM	115	CD	PRO	1	15	23.264	9.918	77.643	1.00	6.71
ATOM	116	N	GLU	1	16	18.712	8.539	78.032	1.00	3.50
ATOM	117	CA	GLU	1	16	17.726	7.533	77.798	1.00	3.50
ATOM	118	C	GLU	1	16	17.577	7.447	76.316	1.00	3.50
ATOM	119	O	GLU	1	16	18.023	8.329	75.584	1.00	3.50
ATOM	120	CB	GLU	1	16	16.348	7.856	78.404	1.00	3.50
ATOM	121	CG	GLU	1	16	15.723	9.143	77.862	1.00	3.50
ATOM	122	CD	GLU	1	16	14.375	9.333	78.542	1.00	3.50
ATOM	123	OE1	GLU	1	16	14.007	8.465	79.378	1.00	3.50
ATOM	124	OE2	GLU	1	16	13.695	10.348	78.235	1.00	3.50
ATOM	125	N	VAL	1	17	16.953	6.359	75.831	1.00	1.33
ATOM	126	CA	VAL	1	17	16.815	6.185	74.417	1.00	1.33
ATOM	127	C	VAL	1	17	16.046	7.322	73.826	1.00	1.33
ATOM	128	O	VAL	1	17	15.108	7.846	74.423	1.00	1.33
ATOM	129	CB	VAL	1	17	16.115	4.914	74.029	1.00	1.33
ATOM	130	CG1	VAL	1	17	15.809	4.956	72.526	1.00	1.33
ATOM	131	CG2	VAL	1	17	17.015	3.732	74.408	1.00	1.33
ATOM	132	N	LEU	1	18	16.453	7.724	72.607	1.00	6.49
ATOM	133	CA	LEU	1	18	15.863	8.817	71.889	1.00	6.49
ATOM	134	C	LEU	1	18	15.010	8.266	70.788	1.00	6.49
ATOM	135	O	LEU	1	18	15.418	7.345	70.083	1.00	6.49
ATOM	136	CB	LEU	1	18	16.940	9.683	71.217	1.00	6.49
ATOM	137	CG	LEU	1	18	16.413	10.883	70.418	1.00	6.49
ATOM	138	CD1	LEU	1	18	15.769	11.940	71.329	1.00	6.49
ATOM	139	CD2	LEU	1	18	17.523	11.442	69.514	1.00	6.49
ATOM	140	N	TYR	1	19	13.795	8.830	70.609	1.00	0.75
ATOM	141	CA	TYR	1	19	12.907	8.372	69.575	1.00	0.75
ATOM	142	C	TYR	1	19	12.967	9.322	68.419	1.00	0.75
ATOM	143	O	TYR	1	19	13.101	10.533	68.592	1.00	0.75
ATOM	144	CB	TYR	1	19	11.432	8.284	70.007	1.00	0.75
ATOM	145	CG	TYR	1	19	11.317	7.194	71.016	1.00	0.75
ATOM	146	CD1	TYR	1	19	11.565	7.440	72.347	1.00	0.75

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ATOM	147	CD2 TYR 1	19	10.970	5.920	70.627	1.00	0.75
ATOM	148	CE1 TYR 1	19	11.468	6.431	73.276	1.00	0.75
ATOM	149	CE2 TYR 1	19	10.874	4.907	71.552	1.00	0.75
ATOM	150	CZ TYR 1	19	11.125	5.162	72.878	1.00	0.75
ATOM	151	OH TYR 1	19	11.032	4.124	73.830	1.00	0.75
ATOM	152	N ALA 1	20	12.923	8.766	67.192	1.00	1.03
ATOM	153	CA ALA 1	20	12.957	9.542	65.982	1.00	1.03
ATOM	154	C ALA 1	20	11.661	10.258	65.768	1.00	1.03
ATOM	155	O ALA 1	20	11.626	11.345	65.191	1.00	1.03
ATOM	156	CB ALA 1	20	13.237	8.691	64.730	1.00	1.03
ATOM	157	N GLY 1	21	10.549	9.642	66.210	1.00	0.75
ATOM	158	CA GLY 1	21	9.268	10.244	66.005	1.00	0.75
ATOM	159	C GLY 1	21	8.897	10.016	64.574	1.00	0.75
ATOM	160	O GLY 1	21	8.194	10.836	63.983	1.00	0.75
ATOM	161	N TYR 1	22	9.368	8.905	63.959	1.00	4.21
ATOM	162	CA TYR 1	22	9.008	8.766	62.577	1.00	4.21
ATOM	163	C TYR 1	22	7.659	8.129	62.432	1.00	4.21
ATOM	164	O TYR 1	22	7.187	7.412	63.313	1.00	4.21
ATOM	165	CB TYR 1	22	10.036	8.080	61.636	1.00	4.21
ATOM	166	CG TYR 1	22	9.989	6.587	61.596	1.00	4.21
ATOM	167	CD1 TYR 1	22	8.946	5.944	60.960	1.00	4.21
ATOM	168	CD2 TYR 1	22	11.165	5.887	61.738	1.00	4.21
ATOM	169	CE1 TYR 1	22	9.008	4.616	60.613	1.00	4.21
ATOM	170	CE2 TYR 1	22	11.255	4.573	61.345	1.00	4.21
ATOM	171	CZ TYR 1	22	10.174	3.924	60.806	1.00	4.21
ATOM	172	OH TYR 1	22	10.274	2.570	60.421	1.00	4.21
ATOM	173	N ASP 1	23	6.996	8.403	61.290	1.00	3.58
ATOM	174	CA ASP 1	23	5.649	7.950	61.068	1.00	3.58
ATOM	175	C ASP 1	23	5.491	6.457	61.014	1.00	3.58
ATOM	176	O ASP 1	23	4.768	5.874	61.823	1.00	3.58
ATOM	177	CB ASP 1	23	5.060	8.515	59.762	1.00	3.58
ATOM	178	CG ASP 1	23	3.559	8.254	59.744	1.00	3.58
ATOM	179	OD1 ASP 1	23	3.041	7.660	60.727	1.00	3.58
ATOM	180	OD2 ASP 1	23	2.909	8.650	58.740	1.00	3.58
ATOM	181	N SER 1	24	6.185	5.797	60.069	1.00	3.81
ATOM	182	CA SER 1	24	6.117	4.371	59.899	1.00	3.81
ATOM	183	C SER 1	24	4.843	3.956	59.222	1.00	3.81
ATOM	184	O SER 1	24	4.821	2.977	58.478	1.00	3.81
ATOM	185	CB SER 1	24	6.208	3.608	61.231	1.00	3.81
ATOM	186	OG SER 1	24	6.138	2.209	60.997	1.00	3.81
ATOM	187	N SER 1	25	3.760	4.735	59.402	1.00	3.40
ATOM	188	CA SER 1	25	2.488	4.381	58.834	1.00	3.40
ATOM	189	C SER 1	25	2.578	4.438	57.345	1.00	3.40
ATOM	190	O SER 1	25	1.996	3.609	56.647	1.00	3.40
ATOM	191	CB SER 1	25	1.358	5.334	59.260	1.00	3.40
ATOM	192	OG SER 1	25	0.131	4.932	58.670	1.00	3.40
ATOM	193	N VAL 1	26	3.332	5.425	56.826	1.00	1.09
ATOM	194	CA VAL 1	26	3.411	5.643	55.409	1.00	1.09
ATOM	195	C VAL 1	26	4.639	4.982	54.864	1.00	1.09

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ATOM	196	O	VAL 1 26	5.579	4.677	55.597	1.00	1.09
ATOM	197	CB	VAL 1 26	3.478	7.107	55.066	1.00	1.09
ATOM	198	CG1	VAL 1 26	3.569	7.286	53.541	1.00	1.09
ATOM	199	CG2	VAL 1 26	2.258	7.800	55.694	1.00	1.09
ATOM	200	N	PRO 1 27	4.631	4.714	53.582	1.00	1.62
ATOM	201	CA	PRO 1 27	5.779	4.108	52.974	1.00	1.62
ATOM	202	C	PRO 1 27	6.940	5.046	53.001	1.00	1.62
ATOM	203	O	PRO 1 27	6.802	6.193	52.577	1.00	1.62
ATOM	204	CB	PRO 1 27	5.336	3.662	51.583	1.00	1.62
ATOM	205	CG	PRO 1 27	3.831	3.388	51.767	1.00	1.62
ATOM	206	CD	PRO 1 27	3.401	4.330	52.906	1.00	1.62
ATOM	207	N	ASP 1 28	8.104	4.559	53.467	1.00	1.30
ATOM	208	CA	ASP 1 28	9.254	5.398	53.617	1.00	1.30
ATOM	209	C	ASP 1 28	9.928	5.629	52.304	1.00	1.30
ATOM	210	O	ASP 1 28	10.293	4.688	51.600	1.00	1.30
ATOM	211	CB	ASP 1 28	10.315	4.781	54.543	1.00	1.30
ATOM	212	CG	ASP 1 28	9.737	4.660	55.947	1.00	1.30
ATOM	213	OD1	ASP 1 28	8.605	5.166	56.170	1.00	1.30
ATOM	214	OD2	ASP 1 28	10.423	4.057	56.815	1.00	1.30
ATOM	215	N	SER 1 29	10.124	6.911	51.948	1.00	3.54
ATOM	216	CA	SER 1 29	10.824	7.216	50.739	1.00	3.54
ATOM	217	C	SER 1 29	12.225	7.538	51.142	1.00	3.54
ATOM	218	O	SER 1 29	12.521	7.686	52.327	1.00	3.54
ATOM	219	CB	SER 1 29	10.246	8.412	49.973	1.00	3.54
ATOM	220	OG	SER 1 29	11.001	8.632	48.793	1.00	3.54
ATOM	221	N	THR 1 30	13.138	7.644	50.160	1.00	4.86
ATOM	222	CA	THR 1 30	14.509	7.906	50.481	1.00	4.86
ATOM	223	C	THR 1 30	14.641	9.237	51.156	1.00	4.86
ATOM	224	O	THR 1 30	15.323	9.357	52.173	1.00	4.86
ATOM	225	CB	THR 1 30	15.399	7.895	49.269	1.00	4.86
ATOM	226	OG1	THR 1 30	16.754	8.080	49.653	1.00	4.86
ATOM	227	CG2	THR 1 30	14.956	9.001	48.295	1.00	4.86
ATOM	228	N	TRP 1 31	13.976	10.275	50.616	1.00	6.14
ATOM	229	CA	TRP 1 31	14.080	11.589	51.186	1.00	6.14
ATOM	230	C	TRP 1 31	13.464	11.621	52.544	1.00	6.14
ATOM	231	O	TRP 1 31	14.005	12.236	53.461	1.00	6.14
ATOM	232	CB	TRP 1 31	13.359	12.670	50.367	1.00	6.14
ATOM	233	CG	TRP 1 31	11.901	12.359	50.163	1.00	6.14
ATOM	234	CD1	TRP 1 31	11.320	11.152	49.924	1.00	6.14
ATOM	235	CD2	TRP 1 31	10.830	13.306	50.286	1.00	6.14
ATOM	236	NE1	TRP 1 31	9.956	11.290	49.846	1.00	6.14
ATOM	237	CE2	TRP 1 31	9.639	12.612	50.074	1.00	6.14
ATOM	238	CE3	TRP 1 31	10.836	14.642	50.560	1.00	6.14
ATOM	239	CZ2	TRP 1 31	8.433	13.248	50.122	1.00	6.14
ATOM	240	CZ3	TRP 1 31	9.619	15.283	50.606	1.00	6.14
ATOM	241	CH2	TRP 1 31	8.440	14.600	50.387	1.00	6.14
ATOM	242	N	ARG 1 32	12.303	10.961	52.705	1.00	4.31
ATOM	243	CA	ARG 1 32	11.616	10.989	53.964	1.00	4.31
ATOM	244	C	ARG 1 32	12.464	10.336	55.006	1.00	4.31

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ATOM	245	O	ARG	1	32	12.542	10.805	56.141	1.00	4.31
ATOM	246	CB	ARG	1	32	10.270	10.243	53.942	1.00	4.31
ATOM	247	CG	ARG	1	32	9.191	10.930	53.104	1.00	4.31
ATOM	248	CD	ARG	1	32	7.797	10.331	53.305	1.00	4.31
ATOM	249	NE	ARG	1	32	7.321	10.755	54.653	1.00	4.31
ATOM	250	CZ	ARG	1	32	6.177	10.226	55.177	1.00	4.31
ATOM	251	NH1	ARG	1	32	5.742	10.626	56.408	1.00	4.31
ATOM	252	NH2	ARG	1	32	5.469	9.295	54.473	1.00	4.31
ATOM	253	N	ILE	1	33	13.125	9.224	54.644	1.00	3.71
ATOM	254	CA	ILE	1	33	13.940	8.530	55.594	1.00	3.71
ATOM	255	C	ILE	1	33	15.061	9.402	56.059	1.00	3.71
ATOM	256	O	ILE	1	33	15.351	9.472	57.252	1.00	3.71
ATOM	257	CB	ILE	1	33	14.560	7.284	55.032	1.00	3.71
ATOM	258	CG1	ILE	1	33	13.474	6.250	54.703	1.00	3.71
ATOM	259	CG2	ILE	1	33	15.600	6.777	56.045	1.00	3.71
ATOM	260	CD1	ILE	1	33	12.707	5.788	55.940	1.00	3.71
ATOM	261	N	MET	1	34	15.725	10.105	55.129	1.00	6.71
ATOM	262	CA	MET	1	34	16.838	10.910	55.535	1.00	6.71
ATOM	263	C	MET	1	34	16.356	12.005	56.428	1.00	6.71
ATOM	264	O	MET	1	34	17.008	12.349	57.413	1.00	6.71
ATOM	265	CB	MET	1	34	17.596	11.530	54.353	1.00	6.71
ATOM	266	CG	MET	1	34	18.982	12.038	54.748	1.00	6.71
ATOM	267	SD	MET	1	34	20.190	10.734	55.128	1.00	6.71
ATOM	268	CE	MET	1	34	21.536	11.890	55.515	1.00	6.71
ATOM	269	N	THR	1	35	15.182	12.578	56.104	1.00	0.49
ATOM	270	CA	THR	1	35	14.647	13.643	56.897	1.00	0.49
ATOM	271	C	THR	1	35	14.395	13.141	58.285	1.00	0.49
ATOM	272	O	THR	1	35	14.699	13.826	59.260	1.00	0.49
ATOM	273	CB	THR	1	35	13.344	14.164	56.367	1.00	0.49
ATOM	274	OG1	THR	1	35	13.515	14.665	55.049	1.00	0.49
ATOM	275	CG2	THR	1	35	12.845	15.282	57.299	1.00	0.49
ATOM	276	N	THR	1	36	13.835	11.922	58.418	1.00	4.72
ATOM	277	CA	THR	1	36	13.543	11.426	59.732	1.00	4.72
ATOM	278	C	THR	1	36	14.811	11.197	60.490	1.00	4.72
ATOM	279	O	THR	1	36	14.868	11.419	61.698	1.00	4.72
ATOM	280	CB	THR	1	36	12.757	10.144	59.749	1.00	4.72
ATOM	281	OG1	THR	1	36	12.240	9.916	61.052	1.00	4.72
ATOM	282	CG2	THR	1	36	13.674	8.976	59.355	1.00	4.72
ATOM	283	N	LEU	1	37	15.865	10.722	59.805	1.00	6.67
ATOM	284	CA	LEU	1	37	17.095	10.476	60.496	1.00	6.67
ATOM	285	C	LEU	1	37	17.709	11.770	60.945	1.00	6.67
ATOM	286	O	LEU	1	37	18.377	11.827	61.976	1.00	6.67
ATOM	287	CB	LEU	1	37	18.104	9.650	59.689	1.00	6.67
ATOM	288	CG	LEU	1	37	19.264	9.170	60.574	1.00	6.67
ATOM	289	CD1	LEU	1	37	18.732	8.452	61.824	1.00	6.67
ATOM	290	CD2	LEU	1	37	20.215	8.261	59.788	1.00	6.67
ATOM	291	N	ASN	1	38	17.520	12.851	60.164	1.00	0.62
ATOM	292	CA	ASN	1	38	18.044	14.132	60.547	1.00	0.62
ATOM	293	C	ASN	1	38	17.355	14.597	61.793	1.00	0.62

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ATOM	294	O	ASN	1	38	17.978	15.197	62.668	1.00	0.62
ATOM	295	CB	ASN	1	38	17.840	15.217	59.474	1.00	0.62
ATOM	296	CG	ASN	1	38	18.787	14.931	58.315	1.00	0.62
ATOM	297	OD1	ASN	1	38	19.823	14.291	58.486	1.00	0.62
ATOM	298	ND2	ASN	1	38	18.427	15.428	57.101	1.00	0.62
ATOM	299	N	MET	1	39	16.036	14.337	61.896	1.00	3.81
ATOM	300	CA	MET	1	39	15.265	14.746	63.037	1.00	3.81
ATOM	301	C	MET	1	39	15.797	14.033	64.238	1.00	3.81
ATOM	302	O	MET	1	39	15.937	14.618	65.312	1.00	3.81
ATOM	303	CB	MET	1	39	13.779	14.373	62.907	1.00	3.81
ATOM	304	CG	MET	1	39	13.070	15.075	61.746	1.00	3.81
ATOM	305	SD	MET	1	39	11.311	14.649	61.572	1.00	3.81
ATOM	306	CE	MET	1	39	11.071	15.588	60.036	1.00	3.81
ATOM	307	N	LEU	1	40	16.109	12.735	64.081	1.00	0.61
ATOM	308	CA	LEU	1	40	16.635	11.963	65.166	1.00	0.61
ATOM	309	C	LEU	1	40	17.956	12.559	65.555	1.00	0.61
ATOM	310	O	LEU	1	40	18.264	12.708	66.737	1.00	0.61
ATOM	311	CB	LEU	1	40	16.868	10.496	64.762	1.00	0.61
ATOM	312	CG	LEU	1	40	17.439	9.607	65.880	1.00	0.61
ATOM	313	CD1	LEU	1	40	16.465	9.504	67.066	1.00	0.61
ATOM	314	CD2	LEU	1	40	17.853	8.232	65.332	1.00	0.61
ATOM	315	N	GLY	1	41	18.762	12.947	64.550	1.00	0.41
ATOM	316	CA	GLY	1	41	20.063	13.501	64.797	1.00	0.41
ATOM	317	C	GLY	1	41	19.947	14.758	65.600	1.00	0.41
ATOM	318	O	GLY	1	41	20.773	15.023	66.472	1.00	0.41
ATOM	319	N	GLY	1	42	18.926	15.584	65.309	1.00	0.36
ATOM	320	CA	GLY	1	42	18.765	16.812	66.031	1.00	0.36
ATOM	321	C	GLY	1	42	18.514	16.504	67.473	1.00	0.36
ATOM	322	O	GLY	1	42	19.052	17.165	68.359	1.00	0.36
ATOM	323	N	ARG	1	43	17.667	15.491	67.742	1.00	3.86
ATOM	324	CA	ARG	1	43	17.347	15.134	69.095	1.00	3.86
ATOM	325	C	ARG	1	43	18.549	14.575	69.790	1.00	3.86
ATOM	326	O	ARG	1	43	18.742	14.794	70.983	1.00	3.86
ATOM	327	CB	ARG	1	43	16.243	14.074	69.213	1.00	3.86
ATOM	328	CG	ARG	1	43	14.859	14.528	68.756	1.00	3.86
ATOM	329	CD	ARG	1	43	13.772	13.521	69.131	1.00	3.86
ATOM	330	NE	ARG	1	43	12.525	13.909	68.420	1.00	3.86
ATOM	331	CZ	ARG	1	43	12.362	13.517	67.124	1.00	3.86
ATOM	332	NH1	ARG	1	43	11.193	13.774	66.469	1.00	3.86
ATOM	333	NH2	ARG	1	43	13.380	12.867	66.488	1.00	3.86
ATOM	334	N	GLN	1	44	19.371	13.792	69.069	1.00	1.14
ATOM	335	CA	GLN	1	44	20.545	13.211	69.655	1.00	1.14
ATOM	336	C	GLN	1	44	21.563	14.265	69.967	1.00	1.14
ATOM	337	O	GLN	1	44	22.303	14.153	70.944	1.00	1.14
ATOM	338	CB	GLN	1	44	21.202	12.148	68.759	1.00	1.14
ATOM	339	CG	GLN	1	44	20.322	10.909	68.574	1.00	1.14
ATOM	340	CD	GLN	1	44	21.060	9.924	67.679	1.00	1.14
ATOM	341	OE1	GLN	1	44	20.499	9.396	66.720	1.00	1.14
ATOM	342	NE2	GLN	1	44	22.351	9.655	68.008	1.00	1.14

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ATOM	343	N	VAL	1	45	21.640	15.316	69.129	1.00	0.68
ATOM	344	CA	VAL	1	45	22.607	16.356	69.340	1.00	0.68
ATOM	345	C	VAL	1	45	22.347	17.012	70.657	1.00	0.68
ATOM	346	O	VAL	1	45	23.276	17.273	71.419	1.00	0.68
ATOM	347	CB	VAL	1	45	22.551	17.427	68.290	1.00	0.68
ATOM	348	CG1	VAL	1	45	23.548	18.534	68.669	1.00	0.68
ATOM	349	CG2	VAL	1	45	22.829	16.787	66.919	1.00	0.68
ATOM	350	N	ILE	1	46	21.066	17.292	70.968	1.00	3.68
ATOM	351	CA	ILE	1	46	20.767	17.932	72.216	1.00	3.68
ATOM	352	C	ILE	1	46	21.144	16.999	73.323	1.00	3.68
ATOM	353	O	ILE	1	46	21.656	17.416	74.360	1.00	3.68
ATOM	354	CB	ILE	1	46	19.320	18.308	72.383	1.00	3.68
ATOM	355	CG1	ILE	1	46	19.163	19.287	73.559	1.00	3.68
ATOM	356	CG2	ILE	1	46	18.487	17.028	72.547	1.00	3.68
ATOM	357	CD1	ILE	1	46	17.789	19.952	73.617	1.00	3.68
ATOM	358	N	ALA	1	47	20.910	15.691	73.123	1.00	0.54
ATOM	359	CA	ALA	1	47	21.221	14.727	74.136	1.00	0.54
ATOM	360	C	ALA	1	47	22.695	14.748	74.397	1.00	0.54
ATOM	361	O	ALA	1	47	23.130	14.677	75.546	1.00	0.54
ATOM	362	CB	ALA	1	47	20.845	13.293	73.726	1.00	0.54
ATOM	363	N	ALA	1	48	23.505	14.854	73.327	1.00	0.69
ATOM	364	CA	ALA	1	48	24.934	14.846	73.450	1.00	0.69
ATOM	365	C	ALA	1	48	25.414	16.025	74.239	1.00	0.69
ATOM	366	O	ALA	1	48	26.303	15.890	75.078	1.00	0.69
ATOM	367	CB	ALA	1	48	25.648	14.887	72.089	1.00	0.69
ATOM	368	N	VAL	1	49	24.846	17.222	73.992	1.00	4.14
ATOM	369	CA	VAL	1	49	25.308	18.380	74.705	1.00	4.14
ATOM	370	C	VAL	1	49	24.997	18.224	76.160	1.00	4.14
ATOM	371	O	VAL	1	49	25.816	18.556	77.015	1.00	4.14
ATOM	372	CB	VAL	1	49	24.685	19.680	74.258	1.00	4.14
ATOM	373	CG1	VAL	1	49	25.020	19.902	72.779	1.00	4.14
ATOM	374	CG2	VAL	1	49	23.180	19.682	74.561	1.00	4.14
ATOM	375	N	LYS	1	50	23.797	17.703	76.478	1.00	4.12
ATOM	376	CA	LYS	1	50	23.385	17.556	77.843	1.00	4.12
ATOM	377	C	LYS	1	50	24.303	16.597	78.529	1.00	4.12
ATOM	378	O	LYS	1	50	24.723	16.823	79.663	1.00	4.12
ATOM	379	CB	LYS	1	50	21.956	17.000	77.969	1.00	4.12
ATOM	380	CG	LYS	1	50	20.885	17.949	77.427	1.00	4.12
ATOM	381	CD	LYS	1	50	19.523	17.283	77.219	1.00	4.12
ATOM	382	CE	LYS	1	50	18.819	16.903	78.523	1.00	4.12
ATOM	383	NZ	LYS	1	50	18.315	18.118	79.200	1.00	4.12
ATOM	384	N	TRP	1	51	24.653	15.500	77.835	1.00	1.08
ATOM	385	CA	TRP	1	51	25.499	14.479	78.378	1.00	1.08
ATOM	386	C	TRP	1	51	26.840	15.056	78.713	1.00	1.08
ATOM	387	O	TRP	1	51	27.404	14.777	79.769	1.00	1.08
ATOM	388	CB	TRP	1	51	25.696	13.328	77.372	1.00	1.08
ATOM	389	CG	TRP	1	51	26.619	12.207	77.794	1.00	1.08
ATOM	390	CD1	TRP	1	51	26.426	11.208	78.703	1.00	1.08
ATOM	391	CD2	TRP	1	51	27.845	11.903	77.112	1.00	1.08

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ATOM	392	NE1 TRP	1	51	27.477	10.322	78.658	1.00	1.08
ATOM	393	CE2 TRP	1	51	28.351	10.731	77.673	1.00	1.08
ATOM	394	CE3 TRP	1	51	28.486	12.539	76.089	1.00	1.08
ATOM	395	CZ2 TRP	1	51	29.515	10.176	77.220	1.00	1.08
ATOM	396	CZ3 TRP	1	51	29.659	11.977	75.634	1.00	1.08
ATOM	397	CH2 TRP	1	51	30.163	10.818	76.187	1.00	1.08
ATOM	398	N ALA	1	52	27.369	15.915	77.827	1.00	0.96
ATOM	399	CA ALA	1	52	28.672	16.497	78.001	1.00	0.96
ATOM	400	C ALA	1	52	28.739	17.346	79.234	1.00	0.96
ATOM	401	O ALA	1	52	29.788	17.447	79.869	1.00	0.96
ATOM	402	CB ALA	1	52	29.092	17.377	76.811	1.00	0.96
ATOM	403	N LYS	1	53	27.624	18.005	79.593	1.00	1.49
ATOM	404	CA LYS	1	53	27.607	18.862	80.744	1.00	1.49
ATOM	405	C LYS	1	53	27.885	18.038	81.967	1.00	1.49
ATOM	406	O LYS	1	53	28.537	18.496	82.902	1.00	1.49
ATOM	407	CB LYS	1	53	26.241	19.541	80.934	1.00	1.49
ATOM	408	CG LYS	1	53	25.853	20.448	79.763	1.00	1.49
ATOM	409	CD LYS	1	53	24.376	20.846	79.760	1.00	1.49
ATOM	410	CE LYS	1	53	23.985	21.753	78.592	1.00	1.49
ATOM	411	NZ LYS	1	53	22.544	22.086	78.671	1.00	1.49
ATOM	412	N ALA	1	54	27.331	16.813	82.003	1.00	1.47
ATOM	413	CA ALA	1	54	27.477	15.863	83.072	1.00	1.47
ATOM	414	C ALA	1	54	28.807	15.162	83.114	1.00	1.47
ATOM	415	O ALA	1	54	29.223	14.688	84.171	1.00	1.47
ATOM	416	CB ALA	1	54	26.400	14.766	83.028	1.00	1.47
ATOM	417	N ILE	1	55	29.487	15.027	81.957	1.00	4.27
ATOM	418	CA ILE	1	55	30.697	14.250	81.896	1.00	4.27
ATOM	419	C ILE	1	55	31.835	14.871	82.643	1.00	4.27
ATOM	420	O ILE	1	55	32.224	16.013	82.407	1.00	4.27
ATOM	421	CB ILE	1	55	31.139	13.951	80.492	1.00	4.27
ATOM	422	CG1 ILE	1	55	32.287	12.928	80.492	1.00	4.27
ATOM	423	CG2 ILE	1	55	31.470	15.278	79.796	1.00	4.27
ATOM	424	CD1 ILE	1	55	32.586	12.351	79.109	1.00	4.27
ATOM	425	N PRO	1	56	32.400	14.113	83.548	1.00	6.47
ATOM	426	CA PRO	1	56	33.455	14.586	84.395	1.00	6.47
ATOM	427	C PRO	1	56	34.624	15.142	83.639	1.00	6.47
ATOM	428	O PRO	1	56	35.175	14.461	82.775	1.00	6.47
ATOM	429	CB PRO	1	56	33.793	13.420	85.332	1.00	6.47
ATOM	430	CG PRO	1	56	33.206	12.179	84.629	1.00	6.47
ATOM	431	CD PRO	1	56	32.028	12.733	83.810	1.00	6.47
ATOM	432	N GLY	1	57	35.005	16.395	83.964	1.00	0.90
ATOM	433	CA GLY	1	57	36.155	17.046	83.406	1.00	0.90
ATOM	434	C GLY	1	57	35.842	17.885	82.201	1.00	0.90
ATOM	435	O GLY	1	57	36.558	18.839	81.906	1.00	0.90
ATOM	436	N PHE	1	58	34.753	17.572	81.480	1.00	1.63
ATOM	437	CA PHE	1	58	34.449	18.259	80.254	1.00	1.63
ATOM	438	C PHE	1	58	34.130	19.708	80.487	1.00	1.63
ATOM	439	O PHE	1	58	34.602	20.583	79.763	1.00	1.63
ATOM	440	CB PHE	1	58	33.255	17.606	79.532	1.00	1.63

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ATOM	441	CG	PHE	1	58	33.258	17.977	78.087	1.00	1.63
ATOM	442	CD1	PHE	1	58	34.096	17.320	77.213	1.00	1.63
ATOM	443	CD2	PHE	1	58	32.309	18.831	77.576	1.00	1.63
ATOM	444	CE1	PHE	1	58	34.027	17.553	75.860	1.00	1.63
ATOM	445	CE2	PHE	1	58	32.233	19.067	76.223	1.00	1.63
ATOM	446	CZ	PHE	1	58	33.094	18.430	75.363	1.00	1.63
ATOM	447	N	ARG	1	59	33.345	20.002	81.538	1.00	3.96
ATOM	448	CA	ARG	1	59	32.897	21.339	81.821	1.00	3.96
ATOM	449	C	ARG	1	59	34.060	22.230	82.134	1.00	3.96
ATOM	450	O	ARG	1	59	33.975	23.446	81.976	1.00	3.96
ATOM	451	CB	ARG	1	59	31.901	21.413	82.993	1.00	3.96
ATOM	452	CG	ARG	1	59	32.454	20.929	84.335	1.00	3.96
ATOM	453	CD	ARG	1	59	31.399	20.919	85.444	1.00	3.96
ATOM	454	NE	ARG	1	59	32.051	20.436	86.693	1.00	3.96
ATOM	455	CZ	ARG	1	59	32.659	21.326	87.530	1.00	3.96
ATOM	456	NH1	ARG	1	59	33.256	20.887	88.677	1.00	3.96
ATOM	457	NH2	ARG	1	59	32.665	22.656	87.224	1.00	3.96
ATOM	458	N	ASN	1	60	35.160	21.640	82.632	1.00	1.96
ATOM	459	CA	ASN	1	60	36.355	22.344	83.008	1.00	1.96
ATOM	460	C	ASN	1	60	37.037	22.967	81.824	1.00	1.96
ATOM	461	O	ASN	1	60	37.734	23.971	81.961	1.00	1.96
ATOM	462	CB	ASN	1	60	37.373	21.425	83.699	1.00	1.96
ATOM	463	CG	ASN	1	60	36.744	20.971	85.008	1.00	1.96
ATOM	464	OD1	ASN	1	60	37.173	19.989	85.611	1.00	1.96
ATOM	465	ND2	ASN	1	60	35.687	21.700	85.455	1.00	1.96
ATOM	466	N	LEU	1	61	36.887	22.352	80.636	1.00	3.77
ATOM	467	CA	LEU	1	61	37.464	22.809	79.400	1.00	3.77
ATOM	468	C	LEU	1	61	36.970	24.195	79.135	1.00	3.77
ATOM	469	O	LEU	1	61	35.922	24.604	79.629	1.00	3.77
ATOM	470	CB	LEU	1	61	36.933	22.006	78.192	1.00	3.77
ATOM	471	CG	LEU	1	61	37.348	20.524	78.084	1.00	3.77
ATOM	472	CD1	LEU	1	61	38.702	20.360	77.389	1.00	3.77
ATOM	473	CD2	LEU	1	61	37.318	19.825	79.450	1.00	3.77
ATOM	474	N	HIS	1	62	37.728	24.956	78.323	1.00	0.83
ATOM	475	CA	HIS	1	62	37.312	26.273	77.944	1.00	0.83
ATOM	476	C	HIS	1	62	36.042	26.055	77.181	1.00	0.83
ATOM	477	O	HIS	1	62	35.859	25.014	76.553	1.00	0.83
ATOM	478	CB	HIS	1	62	38.329	26.959	77.014	1.00	0.83
ATOM	479	CG	HIS	1	62	38.028	28.396	76.709	1.00	0.83
ATOM	480	ND1	HIS	1	62	37.075	28.811	75.807	1.00	0.83
ATOM	481	CD2	HIS	1	62	38.621	29.530	77.172	1.00	0.83
ATOM	482	CE1	HIS	1	62	37.135	30.166	75.770	1.00	0.83
ATOM	483	NE2	HIS	1	62	38.059	30.648	76.582	1.00	0.83
ATOM	484	N	LEU	1	63	35.124	27.040	77.217	1.00	6.44
ATOM	485	CA	LEU	1	63	33.841	26.895	76.589	1.00	6.44
ATOM	486	C	LEU	1	63	34.012	26.678	75.119	1.00	6.44
ATOM	487	O	LEU	1	63	33.338	25.838	74.524	1.00	6.44
ATOM	488	CB	LEU	1	63	32.960	28.144	76.769	1.00	6.44
ATOM	489	CG	LEU	1	63	31.576	28.033	76.105	1.00	6.44

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ATOM	490	CD1 LEU 1 63	30.730	26.927	76.756	1.00	6.44
ATOM	491	CD2 LEU 1 63	30.858	29.392	76.080	1.00	6.44
ATOM	492	N ASP 1 64	34.939	27.426	74.496	1.00	0.59
ATOM	493	CA ASP 1 64	35.142	27.315	73.083	1.00	0.59
ATOM	494	C ASP 1 64	35.587	25.925	72.762	1.00	0.59
ATOM	495	O ASP 1 64	35.194	25.356	71.746	1.00	0.59
ATOM	496	CB ASP 1 64	36.215	28.286	72.561	1.00	0.59
ATOM	497	CG ASP 1 64	35.652	29.697	72.655	1.00	0.59
ATOM	498	OD1 ASP 1 64	34.419	29.830	72.879	1.00	0.59
ATOM	499	OD2 ASP 1 64	36.446	30.663	72.499	1.00	0.59
ATOM	500	N ASP 1 65	36.439	25.343	73.622	1.00	2.31
ATOM	501	CA ASP 1 65	36.945	24.022	73.393	1.00	2.31
ATOM	502	C ASP 1 65	35.824	23.033	73.448	1.00	2.31
ATOM	503	O ASP 1 65	35.732	22.133	72.615	1.00	2.31
ATOM	504	CB ASP 1 65	37.961	23.605	74.466	1.00	2.31
ATOM	505	CG ASP 1 65	39.139	24.565	74.380	1.00	2.31
ATOM	506	OD1 ASP 1 65	39.973	24.559	75.321	1.00	2.31
ATOM	507	OD2 ASP 1 65	39.216	25.329	73.383	1.00	2.31
ATOM	508	N GLN 1 66	34.923	23.176	74.437	1.00	4.28
ATOM	509	CA GLN 1 66	33.871	22.214	74.544	1.00	4.28
ATOM	510	C GLN 1 66	32.997	22.275	73.331	1.00	4.28
ATOM	511	O GLN 1 66	32.573	21.241	72.818	1.00	4.28
ATOM	512	CB GLN 1 66	33.060	22.315	75.850	1.00	4.28
ATOM	513	CG GLN 1 66	32.355	23.643	76.091	1.00	4.28
ATOM	514	CD GLN 1 66	31.667	23.538	77.446	1.00	4.28
ATOM	515	OE1 GLN 1 66	31.207	24.530	78.008	1.00	4.28
ATOM	516	NE2 GLN 1 66	31.603	22.296	77.997	1.00	4.28
ATOM	517	N MET 1 67	32.721	23.488	72.819	1.00	3.13
ATOM	518	CA MET 1 67	31.898	23.612	71.650	1.00	3.13
ATOM	519	C MET 1 67	32.571	22.973	70.468	1.00	3.13
ATOM	520	O MET 1 67	31.939	22.233	69.715	1.00	3.13
ATOM	521	CB MET 1 67	31.607	25.077	71.280	1.00	3.13
ATOM	522	CG MET 1 67	30.664	25.228	70.084	1.00	3.13
ATOM	523	SD MET 1 67	30.294	26.948	69.626	1.00	3.13
ATOM	524	CE MET 1 67	31.963	27.311	69.009	1.00	3.13
ATOM	525	N THR 1 68	33.886	23.223	70.288	1.00	5.42
ATOM	526	CA THR 1 68	34.602	22.693	69.158	1.00	5.42
ATOM	527	C THR 1 68	34.617	21.202	69.180	1.00	5.42
ATOM	528	O THR 1 68	34.468	20.547	68.153	1.00	5.42
ATOM	529	CB THR 1 68	36.045	23.110	69.088	1.00	5.42
ATOM	530	OG1 THR 1 68	36.730	22.735	70.274	1.00	5.42
ATOM	531	CG2 THR 1 68	36.138	24.620	68.855	1.00	5.42
ATOM	532	N LEU 1 69	34.805	20.625	70.369	1.00	4.63
ATOM	533	CA LEU 1 69	34.932	19.209	70.528	1.00	4.63
ATOM	534	C LEU 1 69	33.649	18.522	70.135	1.00	4.63
ATOM	535	O LEU 1 69	33.668	17.458	69.515	1.00	4.63
ATOM	536	CB LEU 1 69	35.364	18.942	71.982	1.00	4.63
ATOM	537	CG LEU 1 69	35.680	17.500	72.368	1.00	4.63
ATOM	538	CD1 LEU 1 69	36.393	17.456	73.731	1.00	4.63

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ATOM	539	CD2 LEU	1	69	34.402	16.660	72.377	1.00	4.63
ATOM	540	N LEU	1	70	32.491	19.117	70.484	1.00	3.55
ATOM	541	CA LEU	1	70	31.209	18.564	70.139	1.00	3.55
ATOM	542	C LEU	1	70	31.023	18.656	68.654	1.00	3.55
ATOM	543	O LEU	1	70	30.531	17.729	68.011	1.00	3.55
ATOM	544	CB LEU	1	70	30.063	19.334	70.829	1.00	3.55
ATOM	545	CG LEU	1	70	28.646	18.719	70.748	1.00	3.55
ATOM	546	CD1 LEU	1	70	27.651	19.623	71.485	1.00	3.55
ATOM	547	CD2 LEU	1	70	28.175	18.417	69.314	1.00	3.55
ATOM	548	N GLN	1	71	31.417	19.794	68.065	1.00	3.95
ATOM	549	CA GLN	1	71	31.204	20.011	66.669	1.00	3.95
ATOM	550	C GLN	1	71	32.006	19.031	65.867	1.00	3.95
ATOM	551	O GLN	1	71	31.579	18.612	64.791	1.00	3.95
ATOM	552	CB GLN	1	71	31.568	21.451	66.279	1.00	3.95
ATOM	553	CG GLN	1	71	30.966	21.902	64.956	1.00	3.95
ATOM	554	CD GLN	1	71	30.911	23.421	65.006	1.00	3.95
ATOM	555	OE1 GLN	1	71	31.916	24.103	65.206	1.00	3.95
ATOM	556	NE2 GLN	1	71	29.677	23.971	64.852	1.00	3.95
ATOM	557	N TYR	1	72	33.225	18.690	66.340	1.00	4.09
ATOM	558	CA TYR	1	72	34.080	17.754	65.656	1.00	4.09
ATOM	559	C TYR	1	72	33.570	16.343	65.724	1.00	4.09
ATOM	560	O TYR	1	72	33.602	15.594	64.749	1.00	4.09
ATOM	561	CB TYR	1	72	35.523	17.725	66.214	1.00	4.09
ATOM	562	CG TYR	1	72	36.110	19.104	66.193	1.00	4.09
ATOM	563	CD1 TYR	1	72	36.146	19.840	65.034	1.00	4.09
ATOM	564	CD2 TYR	1	72	36.860	19.556	67.257	1.00	4.09
ATOM	565	CE1 TYR	1	72	36.796	21.046	64.957	1.00	4.09
ATOM	566	CE2 TYR	1	72	37.529	20.759	67.192	1.00	4.09
ATOM	567	CZ TYR	1	72	37.486	21.514	66.044	1.00	4.09
ATOM	568	OH TYR	1	72	38.169	22.746	65.962	1.00	4.09
ATOM	569	N SER	1	73	33.144	15.947	66.930	1.00	1.90
ATOM	570	CA SER	1	73	32.739	14.620	67.315	1.00	1.90
ATOM	571	C SER	1	73	31.344	14.111	67.096	1.00	1.90
ATOM	572	O SER	1	73	31.133	12.901	67.159	1.00	1.90
ATOM	573	CB SER	1	73	33.055	14.338	68.794	1.00	1.90
ATOM	574	OG SER	1	73	32.243	15.147	69.631	1.00	1.90
ATOM	575	N TRP	1	74	30.348	14.988	66.875	1.00	1.47
ATOM	576	CA TRP	1	74	28.973	14.557	66.922	1.00	1.47
ATOM	577	C TRP	1	74	28.678	13.369	66.047	1.00	1.47
ATOM	578	O TRP	1	74	28.008	12.436	66.488	1.00	1.47
ATOM	579	CB TRP	1	74	27.998	15.678	66.520	1.00	1.47
ATOM	580	CG TRP	1	74	28.085	16.095	65.072	1.00	1.47
ATOM	581	CD1 TRP	1	74	28.924	16.982	64.464	1.00	1.47
ATOM	582	CD2 TRP	1	74	27.155	15.661	64.068	1.00	1.47
ATOM	583	NE1 TRP	1	74	28.588	17.113	63.137	1.00	1.47
ATOM	584	CE2 TRP	1	74	27.496	16.310	62.882	1.00	1.47
ATOM	585	CE3 TRP	1	74	26.098	14.800	64.134	1.00	1.47
ATOM	586	CZ2 TRP	1	74	26.783	16.102	61.737	1.00	1.47
ATOM	587	CZ3 TRP	1	74	25.382	14.591	62.977	1.00	1.47

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ATOM	588	CH2 TRP	1	74	25.719	15.230	61.801	1.00	1.47
ATOM	589	N MET	1	75	29.179	13.348	64.799	1.00	8.65
ATOM	590	CA MET	1	75	28.914	12.245	63.909	1.00	8.65
ATOM	591	C MET	1	75	29.449	10.969	64.476	1.00	8.65
ATOM	592	O MET	1	75	28.795	9.928	64.442	1.00	8.65
ATOM	593	CB MET	1	75	29.654	12.355	62.562	1.00	8.65
ATOM	594	CG MET	1	75	29.113	13.388	61.582	1.00	8.65
ATOM	595	SD MET	1	75	27.569	12.911	60.754	1.00	8.65
ATOM	596	CE MET	1	75	27.660	14.291	59.579	1.00	8.65
ATOM	597	N PHE	1	76	30.680	11.037	65.002	1.00	6.18
ATOM	598	CA PHE	1	76	31.420	9.914	65.494	1.00	6.18
ATOM	599	C PHE	1	76	30.657	9.318	66.645	1.00	6.18
ATOM	600	O PHE	1	76	30.457	8.106	66.712	1.00	6.18
ATOM	601	CB PHE	1	76	32.777	10.430	66.015	1.00	6.18
ATOM	602	CG PHE	1	76	33.873	9.429	65.892	1.00	6.18
ATOM	603	CD1 PHE	1	76	34.022	8.395	66.780	1.00	6.18
ATOM	604	CD2 PHE	1	76	34.898	9.693	65.013	1.00	6.18
ATOM	605	CE1 PHE	1	76	35.157	7.616	66.761	1.00	6.18
ATOM	606	CE2 PHE	1	76	36.038	8.926	54.993	1.00	6.18
ATOM	607	CZ PHE	1	76	36.175	7.890	65.882	1.00	6.18
ATOM	608	N LEU	1	77	30.188	10.172	67.576	1.00	0.90
ATOM	609	CA LEU	1	77	29.472	9.716	68.736	1.00	0.90
ATOM	610	C LEU	1	77	28.177	9.076	68.347	1.00	0.90
ATOM	611	O LEU	1	77	27.792	8.046	68.902	1.00	0.90
ATOM	612	CB LEU	1	77	29.124	10.853	69.712	1.00	0.90
ATOM	613	CG LEU	1	77	30.343	11.484	70.408	1.00	0.90
ATOM	614	CD1 LEU	1	77	29.906	12.608	71.360	1.00	0.90
ATOM	615	CD2 LEU	1	77	31.201	10.420	71.112	1.00	0.90
ATOM	616	N MET	1	78	27.461	9.682	67.385	1.00	3.39
ATOM	617	CA MET	1	78	26.169	9.206	66.980	1.00	3.39
ATOM	618	C MET	1	78	26.256	7.850	66.344	1.00	3.39
ATOM	619	O MET	1	78	25.462	6.962	66.650	1.00	3.39
ATOM	620	CB MET	1	78	25.521	10.127	65.931	1.00	3.39
ATOM	621	CG MET	1	78	25.394	11.589	66.368	1.00	3.39
ATOM	622	SD MET	1	78	24.325	11.892	67.804	1.00	3.39
ATOM	623	CE MET	1	78	24.452	13.702	67.722	1.00	3.39
ATOM	624	N ALA	1	79	27.226	7.663	65.428	1.00	1.42
ATOM	625	CA ALA	1	79	27.373	6.418	64.725	1.00	1.42
ATOM	626	C ALA	1	79	27.784	5.339	65.684	1.00	1.42
ATOM	627	O ALA	1	79	27.378	4.183	65.554	1.00	1.42
ATOM	628	CB ALA	1	79	28.436	6.484	63.613	1.00	1.42
ATOM	629	N PHE	1	80	28.630	5.701	66.665	1.00	4.87
ATOM	630	CA PHE	1	80	29.131	4.776	67.643	1.00	4.87
ATOM	631	C PHE	1	80	27.961	4.289	68.446	1.00	4.87
ATOM	632	O PHE	1	80	27.832	3.097	68.731	1.00	4.87
ATOM	633	CB PHE	1	80	30.128	5.481	68.591	1.00	4.87
ATOM	634	CG PHE	1	80	31.005	4.494	69.285	1.00	4.87
ATOM	635	CD1 PHE	1	80	30.669	3.929	70.489	1.00	4.87
ATOM	636	CD2 PHE	1	80	32.240	4.204	68.766	1.00	4.87

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ATOM	637	CE1 PHE	1	80	31.541	3.085	71.140	1.00	4.87
ATOM	638	CE2 PHE	1	80	33.110	3.357	69.408	1.00	4.87
ATOM	639	CZ PHE	1	80	32.767	2.789	70.604	1.00	4.87
ATOM	640	N ALA	1	81	27.061	5.221	68.816	1.00	0.63
ATOM	641	CA ALA	1	81	25.899	4.891	69.593	1.00	0.63
ATOM	642	C ALA	1	81	25.013	3.977	68.800	1.00	0.63
ATOM	643	O ALA	1	81	24.439	3.030	69.337	1.00	0.63
ATOM	644	CB ALA	1	81	25.065	6.128	69.966	1.00	0.63
ATOM	645	N LEU	1	82	24.889	4.247	67.486	1.00	4.41
ATOM	646	CA LEU	1	82	24.068	3.458	66.610	1.00	4.41
ATOM	647	C LEU	1	82	24.616	2.070	66.661	1.00	4.41
ATOM	648	O LEU	1	82	23.873	1.092	66.763	1.00	4.41
ATOM	649	CB LEU	1	82	24.174	3.949	65.147	1.00	4.41
ATOM	650	CG LEU	1	82	23.343	3.203	64.072	1.00	4.41
ATOM	651	CD1 LEU	1	82	23.781	1.752	63.854	1.00	4.41
ATOM	652	CD2 LEU	1	82	21.840	3.322	64.339	1.00	4.41
ATOM	653	N GLY	1	83	25.956	1.959	66.610	1.00	0.71
ATOM	654	CA GLY	1	83	26.551	0.656	66.624	1.00	0.71
ATOM	655	C GLY	1	83	26.209	-0.053	67.891	1.00	0.71
ATOM	656	O GLY	1	83	25.846	-1.230	67.875	1.00	0.71
ATOM	657	N TRP	1	84	26.312	0.647	69.036	1.00	5.43
ATOM	658	CA TRP	1	84	26.070	-0.084	70.238	1.00	5.43
ATOM	659	C TRP	1	84	24.644	-0.492	70.371	1.00	5.43
ATOM	660	O TRP	1	84	24.377	-1.570	70.885	1.00	5.43
ATOM	661	CB TRP	1	84	26.530	0.587	71.534	1.00	5.43
ATOM	662	CG TRP	1	84	26.714	-0.487	72.576	1.00	5.43
ATOM	663	CD1 TRP	1	84	27.620	-1.503	72.549	1.00	5.43
ATOM	664	CD2 TRP	1	84	25.993	-0.628	73.804	1.00	5.43
ATOM	665	NE1 TRP	1	84	27.490	-2.282	73.667	1.00	5.43
ATOM	666	CE2 TRP	1	84	26.489	-1.762	74.449	1.00	5.43
ATOM	667	CE3 TRP	1	84	25.004	0.121	74.350	1.00	5.43
ATOM	668	CZ2 TRP	1	84	25.993	-2.175	75.648	1.00	5.43
ATOM	669	CZ3 TRP	1	84	24.521	-0.293	75.566	1.00	5.43
ATOM	670	CH2 TRP	1	84	24.986	-1.424	76.197	1.00	5.43
ATOM	671	N ARG	1	85	23.680	0.347	69.945	1.00	7.10
ATOM	672	CA ARG	1	85	22.302	-0.062	70.044	1.00	7.10
ATOM	673	C ARG	1	85	21.943	-1.219	69.137	1.00	7.10
ATOM	674	O ARG	1	85	21.117	-2.053	69.506	1.00	7.10
ATOM	675	CB ARG	1	85	21.334	1.119	69.846	1.00	7.10
ATOM	676	CG ARG	1	85	21.549	1.909	68.557	1.00	7.10
ATOM	677	CD ARG	1	85	20.961	3.320	68.634	1.00	7.10
ATOM	678	NE ARG	1	85	21.336	4.032	67.380	1.00	7.10
ATOM	679	CZ ARG	1	85	21.148	5.380	67.289	1.00	7.10
ATOM	680	NH1 ARG	1	85	20.612	6.062	68.343	1.00	7.10
ATOM	681	NH2 ARG	1	85	21.491	6.044	66.147	1.00	7.10
ATOM	682	N SER	1	86	22.527	-1.297	67.919	1.00	4.93
ATOM	683	CA SER	1	86	22.239	-2.347	66.954	1.00	4.93
ATOM	684	C SER	1	86	22.731	-3.699	67.418	1.00	4.93
ATOM	685	O SER	1	86	22.118	-4.736	67.201	1.00	4.93

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ATOM	686	CB	SER 1	86	22.780	-2.038	65.543	1.00	4.93
ATOM	687	OG	SER 1	86	24.177	-1.799	65.572	1.00	4.93
ATOM	688	N	TYR 1	87	23.740	-3.599	68.271	1.00	5.71
ATOM	689	CA	TYR 1	87	24.722	-4.268	69.053	1.00	5.71
ATOM	690	C	TYR 1	87	23.797	-4.370	70.201	1.00	5.71
ATOM	691	O	TYR 1	87	22.949	-3.542	70.391	1.00	5.71
ATOM	692	CB	TYR 1	87	25.916	-3.424	69.523	1.00	5.71
ATOM	693	CG	TYR 1	87	26.607	-4.240	70.565	1.00	5.71
ATOM	694	CD1	TYR 1	87	27.507	-5.222	70.215	1.00	5.71
ATOM	695	CD2	TYR 1	87	26.295	-4.074	71.895	1.00	5.71
ATOM	696	CE1	TYR 1	87	28.105	-6.003	71.177	1.00	5.71
ATOM	697	CE2	TYR 1	87	26.876	-4.864	72.860	1.00	5.71
ATOM	698	CZ	TYR 1	87	27.793	-5.821	72.503	1.00	5.71
ATOM	699	OH	TYR 1	87	28.403	-6.622	73.491	1.00	5.71
ATOM	700	N	ARG 1	88	23.651	-5.475	70.882	1.00	11.72
ATOM	701	CA	ARG 1	88	22.545	-6.028	71.589	1.00	11.72
ATOM	702	C	ARG 1	88	21.089	-5.674	71.453	1.00	11.72
ATOM	703	O	ARG 1	88	20.291	-6.542	71.804	1.00	11.72
ATOM	704	CB	ARG 1	88	22.920	-5.950	73.084	1.00	11.72
ATOM	705	CG	ARG 1	88	21.818	-5.469	74.021	1.00	11.72
ATOM	706	CD	ARG 1	88	22.173	-5.588	75.505	1.00	11.72
ATOM	707	NE	ARG 1	88	23.480	-4.919	75.748	1.00	11.72
ATOM	708	CZ	ARG 1	88	24.070	-5.048	76.973	1.00	11.72
ATOM	709	NH1	ARG 1	88	23.453	-5.777	77.949	1.00	11.72
ATOM	710	NH2	ARG 1	88	25.274	-4.457	77.226	1.00	11.72
ATOM	711	N	GLN 1	89	20.621	-4.489	71.058	1.00	4.60
ATOM	712	CA	GLN 1	89	19.203	-4.505	70.793	1.00	4.60
ATOM	713	C	GLN 1	89	18.855	-5.524	69.711	1.00	4.60
ATOM	714	O	GLN 1	89	17.867	-6.245	69.854	1.00	4.60
ATOM	715	CB	GLN 1	89	18.679	-3.141	70.312	1.00	4.60
ATOM	716	CG	GLN 1	89	18.840	-2.013	71.336	1.00	4.60
ATOM	717	CD	GLN 1	89	17.787	-2.169	72.427	1.00	4.60
ATOM	718	OE1	GLN 1	89	17.342	-1.180	73.008	1.00	4.60
ATOM	719	NE2	GLN 1	89	17.378	-3.431	72.722	1.00	4.60
ATOM	720	N	SER 1	90	19.645	-5.639	68.610	1.00	2.81
ATOM	721	CA	SER 1	90	19.280	-6.556	67.551	1.00	2.81
ATOM	722	C	SER 1	90	20.424	-7.420	67.087	1.00	2.81
ATOM	723	O	SER 1	90	20.424	-7.886	65.947	1.00	2.81
ATOM	724	CB	SER 1	90	18.752	-5.830	66.302	1.00	2.81
ATOM	725	OG	SER 1	90	19.785	-5.049	65.718	1.00	2.81
ATOM	726	N	SER 1	91	21.429	-7.669	67.951	1.00	3.74
ATOM	727	CA	SER 1	91	22.507	-8.560	67.595	1.00	3.74
ATOM	728	C	SER 1	91	23.278	-8.110	66.390	1.00	3.74
ATOM	729	O	SER 1	91	23.876	-8.922	65.683	1.00	3.74
ATOM	730	CB	SER 1	91	22.028	-9.999	67.336	1.00	3.74
ATOM	731	OG	SER 1	91	21.476	-10.550	68.522	1.00	3.74
ATOM	732	N	ALA 1	92	23.308	-6.789	66.147	1.00	1.75
ATOM	733	CA	ALA 1	92	24.041	-6.197	65.060	1.00	1.75
ATOM	734	C	ALA 1	92	23.484	-6.566	63.718	1.00	1.75

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ATOM	735	O	ALA	1	92	24.097	-6.277	62.691	1.00	1.75
ATOM	736	CB	ALA	1	92	25.531	-6.580	65.070	1.00	1.75
ATOM	737	N	ASN	1	93	22.299	-7.204	63.703	1.00	1.99
ATOM	738	CA	ASN	1	93	21.631	-7.643	62.505	1.00	1.99
ATOM	739	C	ASN	1	93	21.009	-6.533	61.709	1.00	1.99
ATOM	740	O	ASN	1	93	20.905	-6.627	60.485	1.00	1.99
ATOM	741	CB	ASN	1	93	20.515	-8.661	62.794	1.00	1.99
ATOM	742	CG	ASN	1	93	21.168	-9.945	63.287	1.00	1.99
ATOM	743	OD1	ASN	1	93	20.496	-10.843	63.792	1.00	1.99
ATOM	744	ND2	ASN	1	93	22.517	-10.033	63.144	1.00	1.99
ATOM	745	N	LEU	1	94	20.521	-5.479	62.390	1.00	0.96
ATOM	746	CA	LEU	1	94	19.880	-4.388	61.710	1.00	0.96
ATOM	747	C	LEU	1	94	20.429	-3.134	62.313	1.00	0.96
ATOM	748	O	LEU	1	94	21.133	-3.185	63.320	1.00	0.96
ATOM	749	CB	LEU	1	94	18.355	-4.359	61.899	1.00	0.96
ATOM	750	CG	LEU	1	94	17.639	-5.581	61.295	1.00	0.96
ATOM	751	CD1	LEU	1	94	16.120	-5.501	61.511	1.00	0.96
ATOM	752	CD2	LEU	1	94	18.023	-5.780	59.820	1.00	0.96
ATOM	753	N	LEU	1	95	20.147	-1.967	61.693	1.00	3.62
ATOM	754	CA	LEU	1	95	20.646	-0.735	62.243	1.00	3.62
ATOM	755	C	LEU	1	95	19.565	-0.166	63.102	1.00	3.62
ATOM	756	O	LEU	1	95	18.527	0.265	62.603	1.00	3.62
ATOM	757	CB	LEU	1	95	20.954	0.327	61.172	1.00	3.62
ATOM	758	CG	LEU	1	95	22.168	0.034	60.269	1.00	3.62
ATOM	759	CD1	LEU	1	95	23.490	0.393	60.953	1.00	3.62
ATOM	760	CD2	LEU	1	95	22.162	-1.420	59.788	1.00	3.62
ATOM	761	N	CYS	1	96	19.764	-0.139	64.433	1.00	4.51
ATOM	762	CA	CYS	1	96	18.683	0.408	65.190	1.00	4.51
ATOM	763	C	CYS	1	96	18.976	1.828	65.556	1.00	4.51
ATOM	764	O	CYS	1	96	19.596	2.141	66.571	1.00	4.51
ATOM	765	CB	CYS	1	96	18.219	-0.417	66.413	1.00	4.51
ATOM	766	SG	CYS	1	96	19.291	-0.380	67.867	1.00	4.51
ATOM	767	N	PHE	1	97	18.527	2.749	64.686	1.00	0.88
ATOM	768	CA	PHE	1	97	18.736	4.145	64.915	1.00	0.88
ATOM	769	C	PHE	1	97	17.946	4.578	66.113	1.00	0.88
ATOM	770	O	PHE	1	97	18.428	5.352	66.938	1.00	0.88
ATOM	771	CB	PHE	1	97	18.340	5.023	63.714	1.00	0.88
ATOM	772	CG	PHE	1	97	19.305	4.748	62.607	1.00	0.88
ATOM	773	CD1	PHE	1	97	19.077	3.728	61.712	1.00	0.88
ATOM	774	CD2	PHE	1	97	20.453	5.497	62.477	1.00	0.88
ATOM	775	CE1	PHE	1	97	19.966	3.474	60.695	1.00	0.88
ATOM	776	CE2	PHE	1	97	21.350	5.242	61.466	1.00	0.88
ATOM	777	CZ	PHE	1	97	21.104	4.233	60.568	1.00	0.88
ATOM	778	N	ALA	1	98	16.694	4.094	66.232	1.00	0.99
ATOM	779	CA	ALA	1	98	15.862	4.421	67.357	1.00	0.99
ATOM	780	C	ALA	1	98	14.863	3.309	67.454	1.00	0.99
ATOM	781	O	ALA	1	98	14.773	2.480	66.551	1.00	0.99
ATOM	782	CB	ALA	1	98	15.081	5.735	67.181	1.00	0.99
ATOM	783	N	PRO	1	99	14.113	3.239	68.522	1.00	1.69

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ATOM	784	CA	PRO	1	99	13.143	2.183	68.629	1.00	1.69
ATOM	785	C	PRO	1	99	12.092	2.311	67.572	1.00	1.69
ATOM	786	O	PRO	1	99	11.548	1.296	67.140	1.00	1.69
ATOM	787	CB	PRO	1	99	12.632	2.242	70.066	1.00	1.69
ATOM	788	CG	PRO	1	99	13.837	2.804	70.847	1.00	1.69
ATOM	789	CD	PRO	1	99	14.591	3.674	69.824	1.00	1.69
ATOM	790	N	ASP	1	100	11.757	3.555	67.192	1.00	1.75
ATOM	791	CA	ASP	1	100	10.802	3.836	66.160	1.00	1.75
ATOM	792	C	ASP	1	100	11.387	3.687	64.790	1.00	1.75
ATOM	793	O	ASP	1	100	10.637	3.615	63.820	1.00	1.75
ATOM	794	CB	ASP	1	100	10.150	5.228	66.271	1.00	1.75
ATOM	795	CG	ASP	1	100	11.209	6.304	66.121	1.00	1.75
ATOM	796	OD1	ASP	1	100	12.253	6.218	66.820	1.00	1.75
ATOM	797	OD2	ASP	1	100	10.985	7.228	65.295	1.00	1.75
ATOM	798	N	LEU	1	101	12.732	3.746	64.662	1.00	1.92
ATOM	799	CA	LEU	1	101	13.358	3.662	63.368	1.00	1.92
ATOM	800	C	LEU	1	101	14.440	2.619	63.354	1.00	1.92
ATOM	801	O	LEU	1	101	15.581	2.886	63.732	1.00	1.92
ATOM	802	CB	LEU	1	101	13.994	5.010	62.969	1.00	1.92
ATOM	803	CG	LEU	1	101	14.853	5.009	61.688	1.00	1.92
ATOM	804	CD1	LEU	1	101	14.049	4.622	60.438	1.00	1.92
ATOM	805	CD2	LEU	1	101	15.571	6.358	61.523	1.00	1.92
ATOM	806	N	ILE	1	102	14.113	1.399	62.879	1.00	3.39
ATOM	807	CA	ILE	1	102	15.094	0.355	62.783	1.00	3.39
ATOM	808	C	ILE	1	102	15.201	0.038	61.323	1.00	3.39
ATOM	809	O	ILE	1	102	14.186	-0.155	60.656	1.00	3.39
ATOM	810	CB	ILE	1	102	14.709	-0.926	63.477	1.00	3.39
ATOM	811	CG1	ILE	1	102	14.529	-0.719	64.991	1.00	3.39
ATOM	812	CG2	ILE	1	102	15.774	-1.979	63.134	1.00	3.39
ATOM	813	CD1	ILE	1	102	13.243	0.008	65.374	1.00	3.39
ATOM	814	N	ILE	1	103	16.436	-0.029	60.779	1.00	4.51
ATOM	815	CA	ILE	1	103	16.560	-0.283	59.374	1.00	4.51
ATOM	816	C	ILE	1	103	17.129	-1.634	59.093	1.00	4.51
ATOM	817	O	ILE	1	103	18.055	-2.108	59.748	1.00	4.51
ATOM	818	CB	ILE	1	103	17.407	0.716	58.636	1.00	4.51
ATOM	819	CG1	ILE	1	103	18.857	0.673	59.134	1.00	4.51
ATOM	820	CG2	ILE	1	103	16.744	2.096	58.778	1.00	4.51
ATOM	821	CD1	ILE	1	103	19.831	1.443	58.243	1.00	4.51
ATOM	822	N	ASN	1	104	16.548	-2.265	58.062	1.00	4.77
ATOM	823	CA	ASN	1	104	16.843	-3.577	57.583	1.00	4.77
ATOM	824	C	ASN	1	104	17.201	-3.356	56.144	1.00	4.77
ATOM	825	O	ASN	1	104	16.881	-2.306	55.592	1.00	4.77
ATOM	826	CB	ASN	1	104	15.562	-4.421	57.659	1.00	4.77
ATOM	827	CG	ASN	1	104	15.739	-5.726	56.930	1.00	4.77
ATOM	828	OD1	ASN	1	104	15.674	-5.768	55.703	1.00	4.77
ATOM	829	ND2	ASN	1	104	15.945	-6.822	57.703	1.00	4.77
ATOM	830	N	GLU	1	105	17.855	-4.338	55.489	1.00	6.85
ATOM	831	CA	GLU	1	105	18.307	-4.145	54.137	1.00	6.85
ATOM	832	C	GLU	1	105	17.168	-3.846	53.217	1.00	6.85

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ATOM	833	O	GLU	1	105	17.317	-3.074	52.273	1.00	6.85
ATOM	834	CB	GLU	1	105	19.109	-5.319	53.541	1.00	6.85
ATOM	835	CG	GLU	1	105	18.321	-6.616	53.372	1.00	6.85
ATOM	836	CD	GLU	1	105	18.211	-7.282	54.738	1.00	6.85
ATOM	837	OE1	GLU	1	105	18.830	-6.762	55.704	1.00	6.85
ATOM	838	OE2	GLU	1	105	17.507	-8.323	54.832	1.00	6.85
ATOM	839	N	GLN	1	106	15.987	-4.435	53.465	1.00	3.68
ATOM	840	CA	GLN	1	106	14.888	-4.206	52.576	1.00	3.68
ATOM	841	C	GLN	1	106	14.583	-2.741	52.519	1.00	3.68
ATOM	842	O	GLN	1	106	14.276	-2.208	51.456	1.00	3.68
ATOM	843	CB	GLN	1	106	13.615	-4.962	52.999	1.00	3.68
ATOM	844	CG	GLN	1	106	13.061	-4.546	54.363	1.00	3.68
ATOM	845	CD	GLN	1	106	11.816	-5.379	54.632	1.00	3.68
ATOM	846	OE1	GLN	1	106	11.323	-6.085	53.753	1.00	3.68
ATOM	847	NE2	GLN	1	106	11.294	-5.300	55.885	1.00	3.68
ATOM	848	N	ARG	1	107	14.651	-2.051	53.670	1.00	6.71
ATOM	849	CA	ARG	1	107	14.369	-0.647	53.733	1.00	6.71
ATOM	850	C	ARG	1	107	15.397	0.257	53.114	1.00	6.71
ATOM	851	O	ARG	1	107	15.080	1.401	52.795	1.00	6.71
ATOM	852	CB	ARG	1	107	13.931	-0.177	55.129	1.00	6.71
ATOM	853	CG	ARG	1	107	14.838	-0.579	56.282	1.00	6.71
ATOM	854	CD	ARG	1	107	14.205	-0.220	57.627	1.00	6.71
ATOM	855	NE	ARG	1	107	12.773	-0.633	57.597	1.00	6.71
ATOM	856	CZ	ARG	1	107	11.801	0.262	57.252	1.00	6.71
ATOM	857	NH1	ARG	1	107	10.493	-0.128	57.243	1.00	6.71
ATOM	858	NH2	ARG	1	107	12.132	1.546	56.924	1.00	6.71
ATOM	859	N	MET	1	108	16.669	-0.171	52.971	1.00	7.61
ATOM	860	CA	MET	1	108	17.574	0.739	52.321	1.00	7.61
ATOM	861	C	MET	1	108	17.626	0.489	50.841	1.00	7.61
ATOM	862	O	MET	1	108	18.500	-0.215	50.338	1.00	7.61
ATOM	863	CB	MET	1	108	19.014	0.755	52.878	1.00	7.61
ATOM	864	CG	MET	1	108	19.680	-0.604	53.099	1.00	7.61
ATOM	865	SD	MET	1	108	19.434	-1.350	54.736	1.00	7.61
ATOM	866	CE	MET	1	108	20.502	-0.222	55.677	1.00	7.61
ATOM	867	N	THR	1	109	16.653	1.068	50.106	1.00	5.21
ATOM	868	CA	THR	1	109	16.574	0.937	48.678	1.00	5.21
ATOM	869	C	THR	1	109	17.645	1.713	47.974	1.00	5.21
ATOM	870	O	THR	1	109	18.330	1.188	47.097	1.00	5.21
ATOM	871	CB	THR	1	109	15.263	1.422	48.132	1.00	5.21
ATOM	872	OG1	THR	1	109	15.110	2.810	48.390	1.00	5.21
ATOM	873	CG2	THR	1	109	14.127	0.631	48.802	1.00	5.21
ATOM	874	N	LEU	1	110	17.835	2.987	48.372	1.00	6.15
ATOM	875	CA	LEU	1	110	18.754	3.865	47.704	1.00	6.15
ATOM	876	C	LEU	1	110	20.118	3.254	47.804	1.00	6.15
ATOM	877	O	LEU	1	110	20.606	2.945	48.890	1.00	6.15
ATOM	878	CB	LEU	1	110	18.716	5.280	48.323	1.00	6.15
ATOM	879	CG	LEU	1	110	19.494	6.380	47.577	1.00	6.15
ATOM	880	CD1	LEU	1	110	21.006	6.245	47.767	1.00	6.15
ATOM	881	CD2	LEU	1	110	19.081	6.446	46.098	1.00	6.15

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ATOM	882 N PRO 1 111	20.729	3.040	46.668	1.00	5.04
ATOM	883 CA PRO 1 111	22.012	2.390	46.633	1.00	5.04
ATOM	884 C PRO 1 111	23.112	3.146	47.305	1.00	5.04
ATOM	885 O PRO 1 111	23.973	2.516	47.918	1.00	5.04
ATOM	886 CB PRO 1 111	22.274	2.068	45.164	1.00	5.04
ATOM	887 CG PRO 1 111	20.859	1.908	44.576	1.00	5.04
ATOM	888 CD PRO 1 111	19.973	2.815	45.447	1.00	5.04
ATOM	889 N CYS 1 112	23.121	4.484	47.192	1.00	0.66
ATOM	890 CA CYS 1 112	24.142	5.271	47.817	1.00	0.66
ATOM	891 C CYS 1 112	23.989	5.156	49.297	1.00	0.66
ATOM	892 O CYS 1 112	24.966	4.996	50.028	1.00	0.66
ATOM	893 CB CYS 1 112	24.043	6.765	47.466	1.00	0.66
ATOM	894 SG CYS 1 112	24.332	7.087	45.700	1.00	0.66
ATOM	895 N MET 1 113	22.733	5.242	49.769	1.00	3.18
ATOM	896 CA MET 1 113	22.433	5.193	51.167	1.00	3.18
ATOM	897 C MET 1 113	22.748	3.849	51.740	1.00	3.18
ATOM	898 O MET 1 113	23.314	3.754	52.829	1.00	3.18
ATOM	899 CB MET 1 113	20.949	5.478	51.457	1.00	3.18
ATOM	900 CG MET 1 113	20.599	5.458	52.946	1.00	3.18
ATOM	901 SD MET 1 113	18.849	5.795	53.310	1.00	3.18
ATOM	902 CE MET 1 113	18.935	7.557	52.885	1.00	3.18
ATOM	903 N TYR 1 114	22.391	2.751	51.045	1.00	7.80
ATOM	904 CA TYR 1 114	22.695	1.531	51.725	1.00	7.80
ATOM	905 C TYR 1 114	24.163	1.278	51.734	1.00	7.80
ATOM	906 O TYR 1 114	24.678	0.611	52.629	1.00	7.80
ATOM	907 CB TYR 1 114	21.893	0.261	51.375	1.00	7.80
ATOM	908 CG TYR 1 114	22.306	-0.518	50.184	1.00	7.80
ATOM	909 CD1 TYR 1 114	21.577	-0.433	49.024	1.00	7.80
ATOM	910 CD2 TYR 1 114	23.153	-1.587	50.369	1.00	7.80
ATOM	911 CE1 TYR 1 114	21.679	-1.424	48.077	1.00	7.80
ATOM	912 CE2 TYR 1 114	23.282	-2.562	49.412	1.00	7.80
ATOM	913 CZ TYR 1 114	22.517	-2.496	48.275	1.00	7.80
ATOM	914 OH TYR 1 114	22.572	-3.541	47.330	1.00	7.80
ATOM	915 N ASP 1 115	24.887	1.809	50.735	1.00	4.14
ATOM	916 CA ASP 1 115	26.308	1.631	50.732	1.00	4.14
ATOM	917 C ASP 1 115	26.814	2.261	51.992	1.00	4.14
ATOM	918 O ASP 1 115	27.707	1.733	52.653	1.00	4.14
ATOM	919 CB ASP 1 115	26.993	2.331	49.545	1.00	4.14
ATOM	920 CG ASP 1 115	28.461	1.929	49.534	1.00	4.14
ATOM	921 OD1 ASP 1 115	29.180	2.348	48.588	1.00	4.14
ATOM	922 OD2 ASP 1 115	28.882	1.193	50.466	1.00	4.14
ATOM	923 N GLN 1 116	26.238	3.421	52.360	1.00	2.66
ATOM	924 CA GLN 1 116	26.637	4.121	53.546	1.00	2.66
ATOM	925 C GLN 1 116	26.311	3.286	54.750	1.00	2.66
ATOM	926 O GLN 1 116	27.085	3.237	55.705	1.00	2.66
ATOM	927 CB GLN 1 116	25.934	5.487	53.680	1.00	2.66
ATOM	928 CG GLN 1 116	26.323	6.282	54.928	1.00	2.66
ATOM	929 CD GLN 1 116	25.405	5.871	56.069	1.00	2.66
ATOM	930 OE1 GLN 1 116	25.635	6.236	57.220	1.00	2.66

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ATOM	931	NE2	GLN	1	116	24.330	5.104	55.745	1.00	2.66
ATOM	932	N	CYS	1	117	25.151	2.600	54.731	1.00	0.90
ATOM	933	CA	CYS	1	117	24.729	1.792	55.843	1.00	0.90
ATOM	934	C	CYS	1	117	25.679	0.662	56.073	1.00	0.90
ATOM	935	O	CYS	1	117	25.979	0.312	57.214	1.00	0.90
ATOM	936	CB	CYS	1	117	23.328	1.185	55.654	1.00	0.90
ATOM	937	SG	CYS	1	117	22.022	2.449	55.682	1.00	0.90
ATOM	938	N	LYS	1	118	26.185	0.063	54.982	1.00	4.62
ATOM	939	CA	LYS	1	118	27.083	-1.046	55.097	1.00	4.62
ATOM	940	C	LYS	1	118	28.284	-0.562	55.835	1.00	4.62
ATOM	941	O	LYS	1	118	28.868	-1.283	56.642	1.00	4.62
ATOM	942	CB	LYS	1	118	27.556	-1.566	53.728	1.00	4.62
ATOM	943	CG	LYS	1	118	28.508	-2.760	53.815	1.00	4.62
ATOM	944	CD	LYS	1	118	28.748	-3.443	52.467	1.00	4.62
ATOM	945	CE	LYS	1	118	27.506	-4.136	51.901	1.00	4.62
ATOM	946	NZ	LYS	1	118	27.821	-4.746	50.590	1.00	4.62
ATOM	947	N	HIS	1	119	28.687	0.687	55.551	1.00	4.28
ATOM	948	CA	HIS	1	119	29.831	1.283	56.167	1.00	4.28
ATOM	949	C	HIS	1	119	29.583	1.420	57.639	1.00	4.28
ATOM	950	O	HIS	1	119	30.446	1.079	58.448	1.00	4.28
ATOM	951	CB	HIS	1	119	30.108	2.673	55.569	1.00	4.28
ATOM	952	CG	HIS	1	119	31.467	3.225	55.867	1.00	4.28
ATOM	953	ND1	HIS	1	119	32.643	2.608	55.502	1.00	4.28
ATOM	954	CD2	HIS	1	119	31.824	4.440	56.364	1.00	4.28
ATOM	955	CE1	HIS	1	119	33.647	3.468	55.803	1.00	4.28
ATOM	956	NE2	HIS	1	119	33.197	4.595	56.325	1.00	4.28
ATOM	957	N	MET	1	120	28.391	1.912	58.045	1.00	7.65
ATOM	958	CA	MET	1	120	28.194	2.013	59.463	1.00	7.65
ATOM	959	C	MET	1	120	28.060	0.670	60.109	1.00	7.65
ATOM	960	O	MET	1	120	28.397	0.505	61.278	1.00	7.65
ATOM	961	CB	MET	1	120	27.096	2.955	60.020	1.00	7.65
ATOM	962	CG	MET	1	120	25.636	2.694	59.675	1.00	7.65
ATOM	963	SD	MET	1	120	25.017	3.639	58.262	1.00	7.65
ATOM	964	CE	MET	1	120	23.295	3.110	58.489	1.00	7.65
ATOM	965	N	LEU	1	121	27.592	-0.333	59.348	1.00	7.58
ATOM	966	CA	LEU	1	121	27.347	-1.667	59.827	1.00	7.58
ATOM	967	C	LEU	1	121	28.611	-2.254	60.386	1.00	7.58
ATOM	968	O	LEU	1	121	28.573	-3.128	61.250	1.00	7.58
ATOM	969	CB	LEU	1	121	26.815	-2.579	58.700	1.00	7.58
ATOM	970	CG	LEU	1	121	26.520	-4.042	59.093	1.00	7.58
ATOM	971	CD1	LEU	1	121	27.803	-4.867	59.280	1.00	7.58
ATOM	972	CD2	LEU	1	121	25.582	-4.108	60.309	1.00	7.58
ATOM	973	N	TYR	1	122	29.777	-1.785	59.913	1.00	0.69
ATOM	974	CA	TYR	1	122	31.023	-2.339	60.358	1.00	0.69
ATOM	975	C	TYR	1	122	31.168	-2.246	61.850	1.00	0.69
ATOM	976	O	TYR	1	122	31.742	-3.141	62.468	1.00	0.69
ATOM	977	CB	TYR	1	122	32.243	-1.652	59.722	1.00	0.69
ATOM	978	CG	TYR	1	122	32.225	-1.982	58.269	1.00	0.69
ATOM	979	CD1	TYR	1	122	32.714	-3.189	57.823	1.00	0.69

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ATOM	980	CD2 TYR	1	122	31.727	-1.087	57.351	1.00	0.69
ATOM	981	CE1 TYR	1	122	32.699	-3.501	56.484	1.00	0.69
ATOM	982	CE2 TYR	1	122	31.710	-1.392	56.010	1.00	0.69
ATOM	983	CZ TYR	1	122	32.195	-2.602	55.575	1.00	0.69
ATOM	984	OH TYR	1	122	32.176	-2.919	54.201	1.00	0.69
ATOM	985	N VAL	1	123	30.676	-1.160	62.477	1.00	3.47
ATOM	986	CA VAL	1	123	30.837	-1.018	63.900	1.00	3.47
ATOM	987	C VAL	1	123	30.149	-2.098	64.691	1.00	3.47
ATOM	988	O VAL	1	123	30.777	-2.759	65.515	1.00	3.47
ATOM	989	CB VAL	1	123	30.340	0.309	64.404	1.00	3.47
ATOM	990	CG1 VAL	1	123	31.208	1.416	63.783	1.00	3.47
ATOM	991	CG2 VAL	1	123	28.844	0.445	64.075	1.00	3.47
ATOM	992	N SER	1	124	28.854	-2.356	64.434	1.00	0.91
ATOM	993	CA SER	1	124	28.133	-3.337	65.201	1.00	0.91
ATOM	994	C SER	1	124	28.804	-4.660	65.027	1.00	0.91
ATOM	995	O SER	1	124	28.880	-5.461	65.958	1.00	0.91
ATOM	996	CB SER	1	124	26.677	-3.501	64.737	1.00	0.91
ATOM	997	OG SER	1	124	26.642	-4.017	63.415	1.00	0.91
ATOM	998	N SER	1	125	29.311	-4.921	63.812	1.00	3.19
ATOM	999	CA SER	1	125	29.950	-6.171	63.518	1.00	3.19
ATOM	1000	C SER	1	125	31.149	-6.353	64.395	1.00	3.19
ATOM	1001	O SER	1	125	31.382	-7.440	64.920	1.00	3.19
ATOM	1002	CB SER	1	125	30.432	-6.263	62.061	1.00	3.19
ATOM	1003	OG SER	1	125	29.321	-6.233	61.178	1.00	3.19
ATOM	1004	N GLU	1	126	31.954	-5.289	64.570	1.00	3.11
ATOM	1005	CA GLU	1	126	33.127	-5.381	65.392	1.00	3.11
ATOM	1006	C GLU	1	126	32.716	-5.589	66.813	1.00	3.11
ATOM	1007	O GLU	1	126	33.373	-6.320	67.553	1.00	3.11
ATOM	1008	CB GLU	1	126	34.006	-4.119	65.341	1.00	3.11
ATOM	1009	CG GLU	1	126	34.707	-3.940	63.994	1.00	3.11
ATOM	1010	CD GLU	1	126	35.640	-5.129	63.802	1.00	3.11
ATOM	1011	OE1 GLU	1	126	35.848	-5.885	64.788	1.00	3.11
ATOM	1012	OE2 GLU	1	126	36.156	-5.297	62.665	1.00	3.11
ATOM	1013	N LEU	1	127	31.616	-4.934	67.235	1.00	3.70
ATOM	1014	CA LEU	1	127	31.166	-5.078	68.587	1.00	3.70
ATOM	1015	C LEU	1	127	30.795	-6.497	68.858	1.00	3.70
ATOM	1016	O LEU	1	127	31.127	-7.029	69.915	1.00	3.70
ATOM	1017	CB LEU	1	127	29.962	-4.186	68.948	1.00	3.70
ATOM	1018	CG LEU	1	127	30.327	-2.724	69.279	1.00	3.70
ATOM	1019	CD1 LEU	1	127	31.093	-2.640	70.609	1.00	3.70
ATOM	1020	CD2 LEU	1	127	31.083	-2.036	68.136	1.00	3.70
ATOM	1021	N HIS	1	128	30.097	-7.152	67.913	1.00	3.09
ATOM	1022	CA HIS	1	128	29.723	-8.521	68.119	1.00	3.09
ATOM	1023	C HIS	1	128	30.943	-9.388	68.199	1.00	3.09
ATOM	1024	O HIS	1	128	31.056	-10.246	69.074	1.00	3.09
ATOM	1025	CB HIS	1	128	28.840	-9.071	66.986	1.00	3.09
ATOM	1026	CG HIS	1	128	28.369	-10.473	67.237	1.00	3.09
ATOM	1027	ND1 HIS	1	128	27.246	-10.789	67.969	1.00	3.09
ATOM	1028	CD2 HIS	1	128	28.898	-11.662	66.836	1.00	3.09

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ATOM 1029	CE1 HIS 1 128	27.151 -12.143 67.975 1.00 3.09
ATOM 1030	NE2 HIS 1 128	28.131 -12.716 67.300 1.00 3.09
ATOM 1031	N ARG 1 129	31.906 -9.176 67.286 1.00 3.04
ATOM 1032	CA ARG 1 129	33.067 -10.023 67.264 1.00 3.04
ATOM 1033	C ARG 1 129	33.843 -9.890 68.540 1.00 3.04
ATOM 1034	O ARG 1 129	34.161 -10.882 69.195 1.00 3.04
ATOM 1035	CB ARG 1 129	34.023 -9.667 66.112 1.00 3.04
ATOM 1036	CG ARG 1 129	35.201 -10.632 65.965 1.00 3.04
ATOM 1037	CD ARG 1 129	36.150 -10.270 64.821 1.00 3.04
ATOM 1038	NE ARG 1 129	37.233 -11.294 64.801 1.00 3.04
ATOM 1039	CZ ARG 1 129	38.348 -11.132 65.570 1.00 3.04
ATOM 1040	NH1 ARG 1 129	39.335 -12.075 65.547 1.00 3.04
ATOM 1041	NH2 ARG 1 129	38.478 -10.029 66.365 1.00 3.04
ATOM 1042	N LEU 1 130	34.148 -8.638 68.924 1.00 1.27
ATOM 1043	CA LEU 1 130	34.912 -8.315 70.098 1.00 1.27
ATOM 1044	C LEU 1 130	34.140 -8.585 71.349 1.00 1.27
ATOM 1045	O LEU 1 130	34.726 -8.841 72.402 1.00 1.27
ATOM 1046	CB LEU 1 130	35.349 -6.840 70.154 1.00 1.27
ATOM 1047	CG LEU 1 130	36.357 -6.449 69.058 1.00 1.27
ATOM 1048	CD1 LEU 1 130	36.756 -4.967 69.166 1.00 1.27
ATOM 1049	CD2 LEU 1 130	37.568 -7.395 69.056 1.00 1.27
ATOM 1050	N GLN 1 131	32.800 -8.512 71.280 1.00 3.66
ATOM 1051	CA GLN 1 131	32.028 -8.721 72.465 1.00 3.66
ATOM 1052	C GLN 1 131	32.351 -7.633 73.444 1.00 3.66
ATOM 1053	O GLN 1 131	32.692 -7.886 74.598 1.00 3.66
ATOM 1054	CB GLN 1 131	32.317 -10.086 73.107 1.00 3.66
ATOM 1055	CG GLN 1 131	31.424 -10.404 74.298 1.00 3.66
ATOM 1056	CD GLN 1 131	31.824 -11.775 74.824 1.00 3.66
ATOM 1057	OE1 GLN 1 131	32.705 -12.433 74.273 1.00 3.66
ATOM 1058	NE2 GLN 1 131	31.157 -12.222 75.922 1.00 3.66
ATOM 1059	N VAL 1 132	32.242 -6.372 72.973 1.00 1.28
ATOM 1060	CA VAL 1 132	32.502 -5.198 73.762 1.00 1.28
ATOM 1061	C VAL 1 132	31.545 -5.125 74.907 1.00 1.28
ATOM 1062	O VAL 1 132	30.359 -5.417 74.766 1.00 1.28
ATOM 1063	CB VAL 1 132	32.332 -3.926 72.979 1.00 1.28
ATOM 1064	CG1 VAL 1 132	32.333 -2.726 73.943 1.00 1.28
ATOM 1065	CG2 VAL 1 132	33.438 -3.871 71.912 1.00 1.28
ATOM 1066	N SER 1 133	32.065 -4.719 76.083 1.00 3.60
ATOM 1067	CA SER 1 133	31.288 -4.615 77.284 1.00 3.60
ATOM 1068	C SER 1 133	30.703 -3.246 77.382 1.00 3.60
ATOM 1069	O SER 1 133	31.171 -2.297 76.754 1.00 3.60
ATOM 1070	CB SER 1 133	32.135 -4.715 78.559 1.00 3.60
ATOM 1071	OG SER 1 133	33.062 -5.779 78.468 1.00 3.60
ATOM 1072	N TYR 1 134	29.669 -3.112 78.231 1.00 3.87
ATOM 1073	CA TYR 1 134	29.038 -1.843 78.423 1.00 3.87
ATOM 1074	C TYR 1 134	30.064 -0.924 79.016 1.00 3.87
ATOM 1075	O TYR 1 134	30.149 0.244 78.643 1.00 3.87
ATOM 1076	CB TYR 1 134	27.849 -1.915 79.396 1.00 3.87
ATOM 1077	CG TYR 1 134	27.208 -0.571 79.429 1.00 3.87

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ATOM 1078	CD1 TYR 1 134	27.732	0.446	80.191	1.00	3.87
ATOM 1079	CD2 TYR 1 134	26.052	-0.339	78.721	1.00	3.87
ATOM 1080	CE1 TYR 1 134	27.105	1.667	80.243	1.00	3.87
ATOM 1081	CE2 TYR 1 134	25.432	0.887	78.753	1.00	3.87
ATOM 1082	CZ TYR 1 134	25.961	1.896	79.520	1.00	3.87
ATOM 1083	OH TYR 1 134	25.333	3.159	79.566	1.00	3.87
ATOM 1084	N GLU 1 135	30.883	-1.434	79.957	1.00	5.78
ATOM 1085	CA GLU 1 135	31.859	-0.601	80.599	1.00	5.78
ATOM 1086	C GLU 1 135	32.885	-0.112	79.621	1.00	5.78
ATOM 1087	O GLU 1 135	33.347	1.025	79.700	1.00	5.78
ATOM 1088	CB GLU 1 135	32.589	-1.300	81.763	1.00	5.78
ATOM 1089	CG GLU 1 135	33.356	-2.570	81.385	1.00	5.78
ATOM 1090	CD GLU 1 135	32.391	-3.750	81.391	1.00	5.78
ATOM 1091	OE1 GLU 1 135	31.166	-3.532	81.582	1.00	5.78
ATOM 1092	OE2 GLU 1 135	32.875	-4.896	81.197	1.00	5.78
ATOM 1093	N GLU 1 136	33.286	-0.980	78.682	1.00	3.49
ATOM 1094	CA GLU 1 136	34.276	-0.676	77.692	1.00	3.49
ATOM 1095	C GLU 1 136	33.736	0.366	76.745	1.00	3.49
ATOM 1096	O GLU 1 136	34.420	1.323	76.380	1.00	3.49
ATOM 1097	CB GLU 1 136	34.580	-1.976	76.932	1.00	3.49
ATOM 1098	CG GLU 1 136	36.007	-2.148	76.438	1.00	3.49
ATOM 1099	CD GLU 1 136	36.196	-3.653	76.286	1.00	3.49
ATOM 1100	OE1 GLU 1 136	35.422	-4.270	75.507	1.00	3.49
ATOM 1101	OE2 GLU 1 136	37.102	-4.210	76.963	1.00	3.49
ATOM 1102	N TYR 1 137	32.459	0.208	76.351	1.00	1.07
ATOM 1103	CA TYR 1 137	31.774	1.072	75.425	1.00	1.07
ATOM 1104	C TYR 1 137	31.710	2.476	75.955	1.00	1.07
ATOM 1105	O TYR 1 137	31.964	3.439	75.229	1.00	1.07
ATOM 1106	CB TYR 1 137	30.329	0.568	75.207	1.00	1.07
ATOM 1107	CG TYR 1 137	29.561	1.518	74.358	1.00	1.07
ATOM 1108	CD1 TYR 1 137	29.695	1.512	72.990	1.00	1.07
ATOM 1109	CD2 TYR 1 137	28.597	2.314	74.931	1.00	1.07
ATOM 1110	CE1 TYR 1 137	28.904	2.320	72.209	1.00	1.07
ATOM 1111	CE2 TYR 1 137	27.814	3.134	74.155	1.00	1.07
ATOM 1112	CZ TYR 1 137	27.974	3.144	72.791	1.00	1.07
ATOM 1113	OH TYR 1 137	27.165	3.979	71.990	1.00	1.07
ATOM 1114	N LEU 1 138	31.391	2.624	77.254	1.00	1.14
ATOM 1115	CA LEU 1 138	31.235	3.929	77.836	1.00	1.14
ATOM 1116	C LEU 1 138	32.502	4.725	77.769	1.00	1.14
ATOM 1117	O LEU 1 138	32.474	5.919	77.474	1.00	1.14
ATOM 1118	CB LEU 1 138	30.862	3.910	79.328	1.00	1.14
ATOM 1119	CG LEU 1 138	29.457	3.381	79.651	1.00	1.14
ATOM 1120	CD1 LEU 1 138	29.143	3.587	81.143	1.00	1.14
ATOM 1121	CD2 LEU 1 138	28.393	3.991	78.723	1.00	1.14
ATOM 1122	N CYS 1 139	33.645	4.088	78.084	1.00	1.03
ATOM 1123	CA CYS 1 139	34.923	4.743	78.092	1.00	1.03
ATOM 1124	C CYS 1 139	35.315	5.115	76.696	1.00	1.03
ATOM 1125	O CYS 1 139	35.836	6.200	76.445	1.00	1.03
ATOM 1126	CB CYS 1 139	36.025	3.817	78.627	1.00	1.03

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ATOM	1127	SG	CYS	1	139	35.597	3.111	80.246	1.00	1.03
ATOM	1128	N	MET	1	140	35.070	4.209	75.735	1.00	1.00
ATOM	1129	CA	MET	1	140	35.468	4.495	74.387	1.00	1.00
ATOM	1130	C	MET	1	140	34.720	5.683	73.874	1.00	1.00
ATOM	1131	O	MET	1	140	35.275	6.502	73.150	1.00	1.00
ATOM	1132	CB	MET	1	140	35.236	3.338	73.402	1.00	1.00
ATOM	1133	CG	MET	1	140	36.172	2.154	73.642	1.00	1.00
ATOM	1134	SD	MET	1	140	35.935	0.762	72.499	1.00	1.00
ATOM	1135	CE	MET	1	140	36.614	1.644	71.064	1.00	1.00
ATOM	1136	N	LYS	1	141	33.440	5.821	74.255	1.00	8.36
ATOM	1137	CA	LYS	1	141	32.600	6.896	73.798	1.00	8.36
ATOM	1138	C	LYS	1	141	33.239	8.207	74.142	1.00	8.36
ATOM	1139	O	LYS	1	141	33.265	9.126	73.324	1.00	8.36
ATOM	1140	CB	LYS	1	141	31.266	6.892	74.563	1.00	8.36
ATOM	1141	CG	LYS	1	141	30.210	5.896	74.094	1.00	8.36
ATOM	1142	CD	LYS	1	141	29.337	6.420	72.957	1.00	8.36
ATOM	1143	CE	LYS	1	141	28.021	7.015	73.475	1.00	8.36
ATOM	1144	NZ	LYS	1	141	28.282	7.977	74.575	1.00	8.36
ATOM	1145	N	THR	1	142	33.757	8.333	75.380	1.00	4.68
ATOM	1146	CA	THR	1	142	34.342	9.572	75.806	1.00	4.68
ATOM	1147	C	THR	1	142	35.582	9.858	75.018	1.00	4.68
ATOM	1148	O	THR	1	142	35.838	10.999	74.639	1.00	4.68
ATOM	1149	CB	THR	1	142	34.699	9.614	77.266	1.00	4.68
ATOM	1150	OG1	THR	1	142	34.996	10.947	77.652	1.00	4.68
ATOM	1151	CG2	THR	1	142	35.920	8.717	77.518	1.00	4.68
ATOM	1152	N	LEU	1	143	36.380	8.813	74.733	1.00	1.09
ATOM	1153	CA	LEU	1	143	37.596	8.982	73.995	1.00	1.09
ATOM	1154	C	LEU	1	143	37.268	9.518	72.634	1.00	1.09
ATOM	1155	O	LEU	1	143	38.052	10.264	72.047	1.00	1.09
ATOM	1156	CB	LEU	1	143	38.401	7.680	73.834	1.00	1.09
ATOM	1157	CG	LEU	1	143	39.033	7.181	75.150	1.00	1.09
ATOM	1158	CD1	LEU	1	143	39.825	5.882	74.932	1.00	1.09
ATOM	1159	CD2	LEU	1	143	39.883	8.279	75.812	1.00	1.09
ATOM	1160	N	LEU	1	144	36.107	9.127	72.080	1.00	4.43
ATOM	1161	CA	LEU	1	144	35.669	9.620	70.802	1.00	4.43
ATOM	1162	C	LEU	1	144	35.448	11.105	70.850	1.00	4.43
ATOM	1163	O	LEU	1	144	35.804	11.807	69.905	1.00	4.43
ATOM	1164	CB	LEU	1	144	34.345	8.988	70.331	1.00	4.43
ATOM	1165	CG	LEU	1	144	34.469	7.624	69.623	1.00	4.43
ATOM	1166	CD1	LEU	1	144	35.238	6.580	70.428	1.00	4.43
ATOM	1167	CD2	LEU	1	144	33.083	7.095	69.244	1.00	4.43
ATOM	1168	N	LEU	1	145	34.859	11.633	71.947	1.00	7.68
ATOM	1169	CA	LEU	1	145	34.649	13.060	72.019	1.00	7.68
ATOM	1170	C	LEU	1	145	35.968	13.755	71.901	1.00	7.68
ATOM	1171	O	LEU	1	145	36.092	14.810	71.286	1.00	7.68
ATOM	1172	CB	LEU	1	145	34.168	13.631	73.373	1.00	7.68
ATOM	1173	CG	LEU	1	145	32.665	13.714	73.671	1.00	7.68
ATOM	1174	CD1	LEU	1	145	31.946	14.615	72.655	1.00	7.68
ATOM	1175	CD2	LEU	1	145	32.028	12.343	73.869	1.00	7.68

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ATOM 1176 N LEU 1 146	36.964	13.187	72.583	1.00	2.09
ATOM 1177 CA LEU 1 146	38.313	13.644	72.745	1.00	2.09
ATOM 1178 C LEU 1 146	39.224	13.344	71.590	1.00	2.09
ATOM 1179 O LEU 1 146	40.428	13.562	71.694	1.00	2.09
ATOM 1180 CB LEU 1 146	38.957	13.045	74.006	1.00	2.09
ATOM 1181 CG LEU 1 146	38.174	13.370	75.294	1.00	2.09
ATOM 1182 CD1 LEU 1 146	38.845	12.755	76.532	1.00	2.09
ATOM 1183 CD2 LEU 1 146	37.921	14.879	75.436	1.00	2.09
ATOM 1184 N SER 1 147	38.702	12.687	70.541	1.00	1.91
ATOM 1185 CA SER 1 147	39.438	12.173	69.420	1.00	1.91
ATOM 1186 C SER 1 147	40.101	13.132	68.468	1.00	1.91
ATOM 1187 O SER 1 147	41.080	12.752	67.830	1.00	1.91
ATOM 1188 CB SER 1 147	38.556	11.238	68.576	1.00	1.91
ATOM 1189 OG SER 1 147	39.322	10.657	67.535	1.00	1.91
ATOM 1190 N SER 1 148	39.570	14.355	68.262	1.00	1.23
ATOM 1191 CA SER 1 148	40.202	15.238	67.315	1.00	1.23
ATOM 1192 C SER 1 148	40.247	16.631	67.864	1.00	1.23
ATOM 1193 O SER 1 148	39.362	17.032	68.619	1.00	1.23
ATOM 1194 CB SER 1 148	39.460	15.310	65.971	1.00	1.23
ATOM 1195 OG SER 1 148	39.439	14.026	65.364	1.00	1.23
ATOM 1196 N VAL 1 149	41.297	17.412	67.515	1.00	2.96
ATOM 1197 CA VAL 1 149	41.290	18.766	67.989	1.00	2.96
ATOM 1198 C VAL 1 149	41.865	19.635	66.902	1.00	2.96
ATOM 1199 O VAL 1 149	42.328	19.128	65.881	1.00	2.96
ATOM 1200 CB VAL 1 149	42.008	18.984	69.297	1.00	2.96
ATOM 1201 CG1 VAL 1 149	43.323	19.756	69.103	1.00	2.96
ATOM 1202 CG2 VAL 1 149	40.995	19.585	70.278	1.00	2.96
ATOM 1203 N PRO 1 150	41.840	20.932	67.070	1.00	1.47
ATOM 1204 CA PRO 1 150	42.293	21.827	66.038	1.00	1.47
ATOM 1205 C PRO 1 150	43.760	21.693	65.799	1.00	1.47
ATOM 1206 O PRO 1 150	44.470	21.226	66.687	1.00	1.47
ATOM 1207 CB PRO 1 150	41.879	23.223	66.496	1.00	1.47
ATOM 1208 CG PRO 1 150	40.654	22.967	67.394	1.00	1.47
ATOM 1209 CD PRO 1 150	40.887	21.561	67.969	1.00	1.47
ATOM 1210 N LYS 1 151	44.233	22.091	64.601	1.00	7.70
ATOM 1211 CA LYS 1 151	45.627	21.985	64.285	1.00	7.70
ATOM 1212 C LYS 1 151	46.373	22.845	65.252	1.00	7.70
ATOM 1213 O LYS 1 151	47.477	22.508	65.674	1.00	7.70
ATOM 1214 CB LYS 1 151	45.969	22.422	62.847	1.00	7.70
ATOM 1215 CG LYS 1 151	45.445	23.804	62.455	1.00	7.70
ATOM 1216 CD LYS 1 151	43.917	23.896	62.448	1.00	7.70
ATOM 1217 CE LYS 1 151	43.378	25.217	61.895	1.00	7.70
ATOM 1218 NZ LYS 1 151	43.413	25.197	60.415	1.00	7.70
ATOM 1219 N ASP 1 152	45.768	23.990	65.613	1.00	4.33
ATOM 1220 CA ASP 1 152	46.301	24.933	66.553	1.00	4.33
ATOM 1221 C ASP 1 152	46.338	24.294	67.911	1.00	4.33
ATOM 1222 O ASP 1 152	47.229	24.555	68.719	1.00	4.33
ATOM 1223 CB ASP 1 152	45.407	26.180	66.648	1.00	4.33
ATOM 1224 CG ASP 1 152	46.062	27.198	67.562	1.00	4.33

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ATOM	1225	OD1 ASP	1	152	47.234	26.977	67.967	1.00	4.33
ATOM	1226	OD2 ASP	1	152	45.394	28.222	67.868	1.00	4.33
ATOM	1227	N GLY	1	153	45.359	23.420	68.201	1.00	2.44
ATOM	1228	CA GLY	1	153	45.294	22.834	69.507	1.00	2.44
ATOM	1229	C GLY	1	153	44.183	23.547	70.208	1.00	2.44
ATOM	1230	O GLY	1	153	43.566	24.446	69.639	1.00	2.44
ATOM	1231	N LEU	1	154	43.904	23.152	71.467	1.00	1.42
ATOM	1232	CA LEU	1	154	42.822	23.715	72.225	1.00	1.42
ATOM	1233	C LEU	1	154	43.372	24.737	73.167	1.00	1.42
ATOM	1234	O LEU	1	154	44.554	24.721	73.504	1.00	1.42
ATOM	1235	CB LEU	1	154	42.091	22.689	73.118	1.00	1.42
ATOM	1236	CG LEU	1	154	41.267	21.609	72.388	1.00	1.42
ATOM	1237	CD1 LEU	1	154	40.595	20.649	73.387	1.00	1.42
ATOM	1238	CD2 LEU	1	154	40.227	22.221	71.435	1.00	1.42
ATOM	1239	N LYS	1	155	42.510	25.676	73.602	1.00	1.13
ATOM	1240	CA LYS	1	155	42.936	26.678	74.532	1.00	1.13
ATOM	1241	C LYS	1	155	43.307	25.989	75.804	1.00	1.13
ATOM	1242	O LYS	1	155	44.310	26.323	76.433	1.00	1.13
ATOM	1243	CB LYS	1	155	41.839	27.702	74.866	1.00	1.13
ATOM	1244	CG LYS	1	155	41.486	28.617	73.694	1.00	1.13
ATOM	1245	CD LYS	1	155	40.266	29.502	73.952	1.00	1.13
ATOM	1246	CE LYS	1	155	40.053	30.567	72.876	1.00	1.13
ATOM	1247	NZ LYS	1	155	38.923	31.447	73.249	1.00	1.13
ATOM	1248	N SER	1	156	42.498	24.996	76.214	1.00	4.74
ATOM	1249	CA SER	1	156	42.757	24.284	77.431	1.00	4.74
ATOM	1250	C SER	1	156	43.387	22.972	77.079	1.00	4.74
ATOM	1251	O SER	1	156	42.895	21.908	77.453	1.00	4.74
ATOM	1252	CB SER	1	156	41.469	24.009	78.225	1.00	4.74
ATOM	1253	OG SER	1	156	40.569	23.231	77.451	1.00	4.74
ATOM	1254	N GLN	1	157	44.525	23.021	76.362	1.00	1.05
ATOM	1255	CA GLN	1	157	45.170	21.820	75.920	1.00	1.05
ATOM	1256	C GLN	1	157	45.643	20.998	77.079	1.00	1.05
ATOM	1257	O GLN	1	157	45.504	19.776	77.075	1.00	1.05
ATOM	1258	CB GLN	1	157	46.381	22.086	75.010	1.00	1.05
ATOM	1259	CG GLN	1	157	46.956	20.810	74.392	1.00	1.05
ATOM	1260	CD GLN	1	157	45.943	20.286	73.381	1.00	1.05
ATOM	1261	OE1 GLN	1	157	45.030	21.000	72.969	1.00	1.05
ATOM	1262	NE2 GLN	1	157	46.106	19.000	72.967	1.00	1.05
ATOM	1263	N GLU	1	158	46.212	21.644	78.114	1.00	0.94
ATOM	1264	CA GLU	1	158	46.742	20.891	79.214	1.00	0.94
ATOM	1265	C GLU	1	158	45.659	20.120	79.899	1.00	0.94
ATOM	1266	O GLU	1	158	45.817	18.930	80.171	1.00	0.94
ATOM	1267	CB GLU	1	158	47.424	21.774	80.272	1.00	0.94
ATOM	1268	CG GLU	1	158	48.706	22.437	79.763	1.00	0.94
ATOM	1269	CD GLU	1	158	49.284	23.279	80.891	1.00	0.94
ATOM	1270	OE1 GLU	1	158	48.666	23.303	81.988	1.00	0.94
ATOM	1271	OE2 GLU	1	158	50.354	23.907	80.670	1.00	0.94
ATOM	1272	N LEU	1	159	44.516	20.771	80.183	1.00	6.51
ATOM	1273	CA LEU	1	159	43.458	20.081	80.860	1.00	6.51

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ATOM 1274 C LEU 1 159	42.923	19.004	79.972	1.00	6.51
ATOM 1275 O LEU 1 159	42.515	17.943	80.440	1.00	6.51
ATOM 1276 CB LEU 1 159	42.317	21.002	81.343	1.00	6.51
ATOM 1277 CG LEU 1 159	41.671	21.902	80.276	1.00	6.51
ATOM 1278 CD1 LEU 1 159	40.863	21.092	79.254	1.00	6.51
ATOM 1279 CD2 LEU 1 159	40.842	23.018	80.932	1.00	6.51
ATOM 1280 N PHE 1 160	42.914	19.254	78.652	1.00	0.70
ATOM 1281 CA PHE 1 160	42.424	18.300	77.701	1.00	0.70
ATOM 1282 C PHE 1 160	43.261	17.057	77.743	1.00	0.70
ATOM 1283 O PHE 1 160	42.737	15.943	77.743	1.00	0.70
ATOM 1284 CB PHE 1 160	42.463	18.878	76.274	1.00	0.70
ATOM 1285 CG PHE 1 160	42.008	17.861	75.284	1.00	0.70
ATOM 1286 CD1 PHE 1 160	40.669	17.641	75.049	1.00	0.70
ATOM 1287 CD2 PHE 1 160	42.936	17.229	74.489	1.00	0.70
ATOM 1288 CE1 PHE 1 160	40.265	16.779	74.055	1.00	0.70
ATOM 1289 CE2 PHE 1 160	42.539	16.371	73.492	1.00	0.70
ATOM 1290 CZ PHE 1 160	41.202	16.146	73.273	1.00	0.70
ATOM 1291 N ASP 1 161	44.595	17.217	77.804	1.00	2.07
ATOM 1292 CA ASP 1 161	45.471	16.080	77.802	1.00	2.07
ATOM 1293 C ASP 1 161	45.219	15.249	79.018	1.00	2.07
ATOM 1294 O ASP 1 161	45.138	14.024	78.939	1.00	2.07
ATOM 1295 CB ASP 1 161	46.959	16.474	77.823	1.00	2.07
ATOM 1296 CG ASP 1 161	47.307	17.100	76.480	1.00	2.07
ATOM 1297 OD1 ASP 1 161	48.432	17.656	76.361	1.00	2.07
ATOM 1298 OD2 ASP 1 161	46.453	17.035	75.556	1.00	2.07
ATOM 1299 N GLU 1 162	45.075	15.901	80.185	1.00	4.44
ATOM 1300 CA GLU 1 162	44.878	15.164	81.396	1.00	4.44
ATOM 1301 C GLU 1 162	43.575	14.430	81.337	1.00	4.44
ATOM 1302 O GLU 1 162	43.483	13.287	81.782	1.00	4.44
ATOM 1303 CB GLU 1 162	44.905	16.049	82.658	1.00	4.44
ATOM 1304 CG GLU 1 162	43.824	17.129	82.707	1.00	4.44
ATOM 1305 CD GLU 1 162	44.022	17.927	83.987	1.00	4.44
ATOM 1306 OE1 GLU 1 162	43.156	18.792	84.287	1.00	4.44
ATOM 1307 OE2 GLU 1 162	45.045	17.685	84.682	1.00	4.44
ATOM 1308 N ILE 1 163	42.528	15.062	80.774	1.00	0.97
ATOM 1309 CA ILE 1 163	41.251	14.412	80.717	1.00	0.97
ATOM 1310 C ILE 1 163	41.348	13.174	79.880	1.00	0.97
ATOM 1311 O ILE 1 163	40.853	12.117	80.271	1.00	0.97
ATOM 1312 CB ILE 1 163	40.184	15.272	80.104	1.00	0.97
ATOM 1313 CG1 ILE 1 163	39.978	16.548	80.936	1.00	0.97
ATOM 1314 CG2 ILE 1 163	38.913	14.418	79.955	1.00	0.97
ATOM 1315 CD1 ILE 1 163	39.125	17.603	80.233	1.00	0.97
ATOM 1316 N ARG 1 164	42.018	13.266	78.714	1.00	5.11
ATOM 1317 CA ARG 1 164	42.112	12.133	77.835	1.00	5.11
ATOM 1318 C ARG 1 164	42.798	11.013	78.542	1.00	5.11
ATOM 1319 O ARG 1 164	42.361	9.866	78.486	1.00	5.11
ATOM 1320 CB ARG 1 164	42.978	12.373	76.588	1.00	5.11
ATOM 1321 CG ARG 1 164	42.373	13.301	75.545	1.00	5.11
ATOM 1322 CD ARG 1 164	43.195	13.347	74.256	1.00	5.11

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ATOM	1323	NE	ARG	1	164	42.787	12.183	73.419	1.00	5.11
ATOM	1324	CZ	ARG	1	164	43.376	10.963	73.583	1.00	5.11
ATOM	1325	NH1	ARG	1	164	44.321	10.774	74.550	1.00	5.11
ATOM	1326	NH2	ARG	1	164	43.013	9.929	72.770	1.00	5.11
ATOM	1327	N	MET	1	165	43.897	11.331	79.244	1.00	5.20
ATOM	1328	CA	MET	1	165	44.683	10.329	79.900	1.00	5.20
ATOM	1329	C	MET	1	165	43.852	9.624	80.923	1.00	5.20
ATOM	1330	O	MET	1	165	43.925	8.404	81.056	1.00	5.20
ATOM	1331	CB	MET	1	165	45.916	10.942	80.591	1.00	5.20
ATOM	1332	CG	MET	1	165	46.814	9.941	81.318	1.00	5.20
ATOM	1333	SD	MET	1	165	46.178	9.395	82.929	1.00	5.20
ATOM	1334	CE	MET	1	165	47.681	8.484	83.384	1.00	5.20
ATOM	1335	N	THR	1	166	43.020	10.377	81.665	1.00	1.86
ATOM	1336	CA	THR	1	166	42.227	9.776	82.696	1.00	1.86
ATOM	1337	C	THR	1	166	41.281	8.781	82.099	1.00	1.86
ATOM	1338	O	THR	1	166	41.107	7.687	82.633	1.00	1.86
ATOM	1339	CB	THR	1	166	41.409	10.777	83.454	1.00	1.86
ATOM	1340	OG1	THR	1	166	42.256	11.741	84.062	1.00	1.86
ATOM	1341	CG2	THR	1	166	40.597	10.034	84.528	1.00	1.86
ATOM	1342	N	TYR	1	167	40.633	9.138	80.976	1.00	4.58
ATOM	1343	CA	TYR	1	167	39.712	8.236	80.346	1.00	4.58
ATOM	1344	C	TYR	1	167	40.375	7.041	79.745	1.00	4.58
ATOM	1345	O	TYR	1	167	39.795	5.956	79.725	1.00	4.58
ATOM	1346	CB	TYR	1	167	38.807	8.904	79.299	1.00	4.58
ATOM	1347	CG	TYR	1	167	37.739	9.600	80.072	1.00	4.58
ATOM	1348	CD1	TYR	1	167	37.899	10.876	80.557	1.00	4.58
ATOM	1349	CD2	TYR	1	167	36.585	8.922	80.383	1.00	4.58
ATOM	1350	CE1	TYR	1	167	36.903	11.471	81.298	1.00	4.58
ATOM	1351	CE2	TYR	1	167	35.584	9.512	81.117	1.00	4.58
ATOM	1352	CZ	TYR	1	167	35.741	10.796	81.571	1.00	4.58
ATOM	1353	OH	TYR	1	167	34.717	11.422	82.312	1.00	4.58
ATOM	1354	N	ILE	1	168	41.591	7.203	79.193	1.00	4.85
ATOM	1355	CA	ILE	1	168	42.252	6.046	78.673	1.00	4.85
ATOM	1356	C	ILE	1	168	42.607	5.114	79.792	1.00	4.85
ATOM	1357	O	ILE	1	168	42.560	3.896	79.634	1.00	4.85
ATOM	1358	CB	ILE	1	168	43.380	6.367	77.726	1.00	4.85
ATOM	1359	CG1	ILE	1	168	44.398	7.344	78.319	1.00	4.85
ATOM	1360	CG2	ILE	1	168	42.748	6.849	76.412	1.00	4.85
ATOM	1361	CD1	ILE	1	168	45.536	7.660	77.347	1.00	4.85
ATOM	1362	N	LYS	1	169	42.939	5.668	80.973	1.00	6.27
ATOM	1363	CA	LYS	1	169	43.238	4.856	82.121	1.00	6.27
ATOM	1364	C	LYS	1	169	41.992	4.099	82.471	1.00	6.27
ATOM	1365	O	LYS	1	169	42.035	2.915	82.795	1.00	6.27
ATOM	1366	CB	LYS	1	169	43.582	5.704	83.355	1.00	6.27
ATOM	1367	CG	LYS	1	169	44.715	6.703	83.123	1.00	6.27
ATOM	1368	CD	LYS	1	169	46.071	6.077	82.805	1.00	6.27
ATOM	1369	CE	LYS	1	169	46.877	5.725	84.055	1.00	6.27
ATOM	1370	NZ	LYS	1	169	48.286	5.481	83.687	1.00	6.27
ATOM	1371	N	GLU	1	170	40.842	4.792	82.393	1.00	3.71

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ATOM 1372 CA GLU 1 170	39.535	4.287	82.702	1.00	3.71
ATOM 1373 C GLU 1 170	39.184	3.129	81.813	1.00	3.71
ATOM 1374 O GLU 1 170	38.618	2.135	82.266	1.00	3.71
ATOM 1375 CB GLU 1 170	38.514	5.426	82.519	1.00	3.71
ATOM 1376 CG GLU 1 170	37.104	5.005	82.131	1.00	3.71
ATOM 1377 CD GLU 1 170	36.480	4.192	83.241	1.00	3.71
ATOM 1378 OE1 GLU 1 170	37.231	3.606	84.064	1.00	3.71
ATOM 1379 OE2 GLU 1 170	35.223	4.142	83.261	1.00	3.71
ATOM 1380 N LEU 1 171	39.525	3.226	80.517	1.00	0.72
ATOM 1381 CA LEU 1 171	39.238	2.176	79.584	1.00	0.72
ATOM 1382 C LEU 1 171	39.997	0.961	80.009	1.00	0.72
ATOM 1383 O LEU 1 171	39.512	-0.164	79.893	1.00	0.72
ATOM 1384 CB LEU 1 171	39.674	2.534	78.152	1.00	0.72
ATOM 1385 CG LEU 1 171	39.381	1.437	77.112	1.00	0.72
ATOM 1386 CD1 LEU 1 171	37.873	1.178	76.984	1.00	0.72
ATOM 1387 CD2 LEU 1 171	40.040	1.764	75.760	1.00	0.72
ATOM 1388 N GLY 1 172	41.229	1.159	80.511	1.00	0.34
ATOM 1389 CA GLY 1 172	42.030	0.051	80.940	1.00	0.34
ATOM 1390 C GLY 1 172	41.331	-0.658	82.061	1.00	0.34
ATOM 1391 O GLY 1 172	41.312	-1.888	82.100	1.00	0.34
ATOM 1392 N LYS 1 173	40.736	0.098	83.009	1.00	4.65
ATOM 1393 CA LYS 1 173	40.076	-0.530	84.122	1.00	4.65
ATOM 1394 C LYS 1 173	38.922	-1.329	83.607	1.00	4.65
ATOM 1395 O LYS 1 173	38.646	-2.427	84.081	1.00	4.65
ATOM 1396 CB LYS 1 173	39.408	0.418	85.140	1.00	4.65
ATOM 1397 CG LYS 1 173	40.289	1.453	85.840	1.00	4.65
ATOM 1398 CD LYS 1 173	40.465	2.734	85.030	1.00	4.65
ATOM 1399 CE LYS 1 173	41.022	3.903	85.841	1.00	4.65
ATOM 1400 NZ LYS 1 173	42.467	3.709	86.083	1.00	4.65
ATOM 1401 N ALA 1 174	38.194	-0.786	82.618	1.00	0.62
ATOM 1402 CA ALA 1 174	37.042	-1.476	82.119	1.00	0.62
ATOM 1403 C ALA 1 174	37.494	-2.785	81.562	1.00	0.62
ATOM 1404 O ALA 1 174	36.845	-3.812	81.751	1.00	0.62
ATOM 1405 CB ALA 1 174	36.331	-0.715	80.988	1.00	0.62
ATOM 1406 N ILE 1 175	38.640	-2.765	80.862	1.00	4.02
ATOM 1407 CA ILE 1 175	39.217	-3.929	80.253	1.00	4.02
ATOM 1408 C ILE 1 175	39.540	-4.928	81.321	1.00	4.02
ATOM 1409 O ILE 1 175	39.264	-6.119	81.178	1.00	4.02
ATOM 1410 CB ILE 1 175	40.539	-3.616	79.608	1.00	4.02
ATOM 1411 CG1 ILE 1 175	40.398	-2.574	78.486	1.00	4.02
ATOM 1412 CG2 ILE 1 175	41.172	-4.942	79.163	1.00	4.02
ATOM 1413 CD1 ILE 1 175	39.588	-3.060	77.292	1.00	4.02
ATOM 1414 N VAL 1 176	40.121	-4.453	82.440	1.00	1.20
ATOM 1415 CA VAL 1 176	40.587	-5.342	83.465	1.00	1.20
ATOM 1416 C VAL 1 176	39.463	-6.067	84.123	1.00	1.20
ATOM 1417 O VAL 1 176	39.662	-7.154	84.662	1.00	1.20
ATOM 1418 CB VAL 1 176	41.426	-4.700	84.542	1.00	1.20
ATOM 1419 CG1 VAL 1 176	42.626	-4.010	83.872	1.00	1.20
ATOM 1420 CG2 VAL 1 176	40.566	-3.806	85.444	1.00	1.20

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ATOM	1421	N	LYS	1	177	38.252	-5.483	84.122	1.00	9.34
ATOM	1422	CA	LYS	1	177	37.173	-6.140	84.794	1.00	9.34
ATOM	1423	C	LYS	1	177	36.987	-7.509	84.215	1.00	9.34
ATOM	1424	O	LYS	1	177	36.793	-8.474	84.950	1.00	9.34
ATOM	1425	CB	LYS	1	177	35.843	-5.372	84.655	1.00	9.34
ATOM	1426	CG	LYS	1	177	34.706	-5.886	85.546	1.00	9.34
ATOM	1427	CD	LYS	1	177	34.225	-7.301	85.213	1.00	9.34
ATOM	1428	CE	LYS	1	177	33.356	-7.371	83.955	1.00	9.34
ATOM	1429	NZ	LYS	1	177	34.185	-7.132	82.752	1.00	9.34
ATOM	1430	N	ARG	1	178	36.949	-7.602	82.876	1.00	6.15
ATOM	1431	CA	ARG	1	178	36.803	-8.830	82.146	1.00	6.15
ATOM	1432	C	ARG	1	178	38.089	-9.552	81.835	1.00	6.15
ATOM	1433	O	ARG	1	178	38.151	-10.779	81.870	1.00	6.15
ATOM	1434	CB	ARG	1	178	36.100	-8.536	80.816	1.00	6.15
ATOM	1435	CG	ARG	1	178	35.172	-9.641	80.330	1.00	6.15
ATOM	1436	CD	ARG	1	178	33.960	-9.792	81.253	1.00	6.15
ATOM	1437	NE	ARG	1	178	32.797	-10.215	80.427	1.00	6.15
ATOM	1438	CZ	ARG	1	178	31.923	-9.270	79.973	1.00	6.15
ATOM	1439	NH1	ARG	1	178	32.113	-7.958	80.297	1.00	6.15
ATOM	1440	NH2	ARG	1	178	30.855	-9.632	79.205	1.00	6.15
ATOM	1441	N	GLU	1	179	39.160	-8.795	81.512	1.00	5.83
ATOM	1442	CA	GLU	1	179	40.337	-9.414	80.964	1.00	5.83
ATOM	1443	C	GLU	1	179	41.421	-9.588	81.984	1.00	5.83
ATOM	1444	O	GLU	1	179	42.183	-8.665	82.267	1.00	5.83
ATOM	1445	CB	GLU	1	179	40.893	-8.582	79.801	1.00	5.83
ATOM	1446	CG	GLU	1	179	41.573	-9.440	78.749	1.00	5.83
ATOM	1447	CD	GLU	1	179	40.468	-10.276	78.116	1.00	5.83
ATOM	1448	OE1	GLU	1	179	39.682	-9.709	77.312	1.00	5.83
ATOM	1449	OE2	GLU	1	179	40.386	-11.492	78.438	1.00	5.83
ATOM	1450	N	GLY	1	180	41.525	-10.812	82.540	1.00	1.02
ATOM	1451	CA	GLY	1	180	42.476	-11.112	83.571	1.00	1.02
ATOM	1452	C	GLY	1	180	43.910	-11.102	83.135	1.00	1.02
ATOM	1453	O	GLY	1	180	44.758	-10.507	83.798	1.00	1.02
ATOM	1454	N	ASN	1	181	44.232	-11.755	82.001	1.00	3.29
ATOM	1455	CA	ASN	1	181	45.613	-11.860	81.628	1.00	3.29
ATOM	1456	C	ASN	1	181	46.206	-10.515	81.364	1.00	3.29
ATOM	1457	O	ASN	1	181	45.548	-9.582	80.907	1.00	3.29
ATOM	1458	CB	ASN	1	181	45.873	-12.755	80.400	1.00	3.29
ATOM	1459	CG	ASN	1	181	47.344	-13.150	80.358	1.00	3.29
ATOM	1460	OD1	ASN	1	181	48.113	-12.886	81.281	1.00	3.29
ATOM	1461	ND2	ASN	1	181	47.751	-13.816	79.244	1.00	3.29
ATOM	1462	N	SER	1	182	47.498	-10.375	81.696	1.00	0.74
ATOM	1463	CA	SER	1	182	48.172	-9.145	81.442	1.00	0.74
ATOM	1464	C	SER	1	182	48.248	-8.998	79.961	1.00	0.74
ATOM	1465	O	SER	1	182	48.082	-7.904	79.426	1.00	0.74
ATOM	1466	CB	SER	1	182	49.610	-9.127	81.988	1.00	0.74
ATOM	1467	OG	SER	1	182	50.400	-10.094	81.312	1.00	0.74
ATOM	1468	N	SER	1	183	48.541	-10.113	79.266	1.00	3.77
ATOM	1469	CA	SER	1	183	48.669	-10.105	77.840	1.00	3.77

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ATOM 1470 C SER 1 183	47.372 -9.935 77.115 1.00 3.77
ATOM 1471 O SER 1 183	47.274 -9.086 76.229 1.00 3.77
ATOM 1472 CB SER 1 183	49.314 -11.393 77.299 1.00 3.77
ATOM 1473 OG SER 1 183	50.645 -11.510 77.779 1.00 3.77
ATOM 1474 N GLN 1 184	46.325 -10.719 77.460 1.00 7.63
ATOM 1475 CA GLN 1 184	45.186 -10.561 76.607 1.00 7.63
ATOM 1476 C GLN 1 184	44.550 -9.246 76.903 1.00 7.63
ATOM 1477 O GLN 1 184	43.887 -8.663 76.050 1.00 7.63
ATOM 1478 CB GLN 1 184	44.127 -11.695 76.545 1.00 7.63
ATOM 1479 CG GLN 1 184	42.965 -11.733 77.535 1.00 7.63
ATOM 1480 CD GLN 1 184	43.429 -11.922 78.952 1.00 7.63
ATOM 1481 OE1 GLN 1 184	43.982 -10.984 79.514 1.00 7.63
ATOM 1482 NE2 GLN 1 184	43.165 -13.116 79.548 1.00 7.63
ATOM 1483 N ASN 1 185	44.715 -8.751 78.144 1.00 3.79
ATOM 1484 CA ASN 1 185	44.194 -7.463 78.495 1.00 3.79
ATOM 1485 C ASN 1 185	44.890 -6.451 77.637 1.00 3.79
ATOM 1486 O ASN 1 185	44.265 -5.531 77.111 1.00 3.79
ATOM 1487 CB ASN 1 185	44.483 -7.108 79.967 1.00 3.79
ATOM 1488 CG ASN 1 185	43.716 -5.849 80.347 1.00 3.79
ATOM 1489 OD1 ASN 1 185	42.795 -5.901 81.160 1.00 3.79
ATOM 1490 ND2 ASN 1 185	44.101 -4.687 79.754 1.00 3.79
ATOM 1491 N TRP 1 186	46.220 -6.603 77.477 1.00 3.97
ATOM 1492 CA TRP 1 186	46.982 -5.673 76.695 1.00 3.97
ATOM 1493 C TRP 1 186	46.541 -5.785 75.275 1.00 3.97
ATOM 1494 O TRP 1 186	46.382 -4.785 74.577 1.00 3.97
ATOM 1495 CB TRP 1 186	48.496 -5.939 76.727 1.00 3.97
ATOM 1496 CG TRP 1 186	49.305 -4.839 76.079 1.00 3.97
ATOM 1497 CD1 TRP 1 186	49.978 -3.811 76.672 1.00 3.97
ATOM 1498 CD2 TRP 1 186	49.426 -4.640 74.662 1.00 3.97
ATOM 1499 NE1 TRP 1 186	50.528 -2.994 75.713 1.00 3.97
ATOM 1500 CE2 TRP 1 186	50.192 -3.489 74.471 1.00 3.97
ATOM 1501 CE3 TRP 1 186	48.934 -5.351 73.605 1.00 3.97
ATOM 1502 CZ2 TRP 1 186	50.480 -3.032 73.217 1.00 3.97
ATOM 1503 CZ3 TRP 1 186	49.225 -4.887 72.341 1.00 3.97
ATOM 1504 CH2 TRP 1 186	49.983 -3.750 72.151 1.00 3.97
ATOM 1505 N GLN 1 187	46.325 -7.028 74.815 1.00 0.67
ATOM 1506 CA GLN 1 187	45.915 -7.248 73.464 1.00 0.67
ATOM 1507 C GLN 1 187	44.575 -6.618 73.279 1.00 0.67
ATOM 1508 O GLN 1 187	44.315 -6.017 72.237 1.00 0.67
ATOM 1509 CB GLN 1 187	45.782 -8.742 73.124 1.00 0.67
ATOM 1510 CG GLN 1 187	47.108 -9.501 73.209 1.00 0.67
ATOM 1511 CD GLN 1 187	46.844 -10.957 72.853 1.00 0.67
ATOM 1512 OE1 GLN 1 187	45.725 -11.334 72.508 1.00 0.67
ATOM 1513 NE2 GLN 1 187	47.905 -11.804 72.942 1.00 0.67
ATOM 1514 N ARG 1 188	43.674 -6.734 74.277 1.00 7.01
ATOM 1515 CA ARG 1 188	42.393 -6.152 74.025 1.00 7.01
ATOM 1516 C ARG 1 188	42.471 -4.662 73.982 1.00 7.01
ATOM 1517 O ARG 1 188	41.707 -4.025 73.259 1.00 7.01
ATOM 1518 CB ARG 1 188	41.205 -6.560 74.913 1.00 7.01

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ATOM	1519	CG	ARG	1	188	41.182	-6.124	76.366	1.00	7.01
ATOM	1520	CD	ARG	1	188	39.731	-6.059	76.851	1.00	7.01
ATOM	1521	NE	ARG	1	188	38.929	-7.004	76.016	1.00	7.01
ATOM	1522	CZ	ARG	1	188	38.255	-6.572	74.908	1.00	7.01
ATOM	1523	NH1	ARG	1	188	37.581	-7.464	74.124	1.00	7.01
ATOM	1524	NH2	ARG	1	188	38.254	-5.248	74.577	1.00	7.01
ATOM	1525	N	PHE	1	189	43.383	-4.052	74.760	1.00	0.98
ATOM	1526	CA	PHE	1	189	43.478	-2.623	74.707	1.00	0.98
ATOM	1527	C	PHE	1	189	43.840	-2.264	73.303	1.00	0.98
ATOM	1528	O	PHE	1	189	43.277	-1.338	72.727	1.00	0.98
ATOM	1529	CB	PHE	1	189	44.545	-2.041	75.652	1.00	0.98
ATOM	1530	CG	PHE	1	189	44.534	-0.555	75.493	1.00	0.98
ATOM	1531	CD1	PHE	1	189	43.528	0.202	76.051	1.00	0.98
ATOM	1532	CD2	PHE	1	189	45.574	0.092	74.866	1.00	0.98
ATOM	1533	CE1	PHE	1	189	43.539	1.574	75.949	1.00	0.98
ATOM	1534	CE2	PHE	1	189	45.595	1.465	74.769	1.00	0.98
ATOM	1535	CZ	PHE	1	189	44.573	2.210	75.305	1.00	0.98
ATOM	1536	N	TYR	1	190	44.766	-3.023	72.695	1.00	0.91
ATOM	1537	CA	TYR	1	190	45.206	-2.741	71.360	1.00	0.91
ATOM	1538	C	TYR	1	190	44.049	-2.805	70.410	1.00	0.91
ATOM	1539	O	TYR	1	190	43.888	-1.932	69.560	1.00	0.91
ATOM	1540	CB	TYR	1	190	46.262	-3.757	70.893	1.00	0.91
ATOM	1541	CG	TYR	1	190	46.582	-3.521	69.457	1.00	0.91
ATOM	1542	CD1	TYR	1	190	47.439	-2.514	69.079	1.00	0.91
ATOM	1543	CD2	TYR	1	190	46.117	-4.395	68.501	1.00	0.91
ATOM	1544	CE1	TYR	1	190	47.814	-2.374	67.764	1.00	0.91
ATOM	1545	CE2	TYR	1	190	46.490	-4.261	67.185	1.00	0.91
ATOM	1546	CZ	TYR	1	190	47.350	-3.257	66.818	1.00	0.91
ATOM	1547	OH	TYR	1	190	47.742	-3.121	65.469	1.00	0.91
ATOM	1548	N	GLN	1	191	43.200	-3.839	70.545	1.00	1.02
ATOM	1549	CA	GLN	1	191	42.095	-4.033	69.649	1.00	1.02
ATOM	1550	C	GLN	1	191	41.114	-2.906	69.735	1.00	1.02
ATOM	1551	O	GLN	1	191	40.672	-2.376	68.716	1.00	1.02
ATOM	1552	CB	GLN	1	191	41.316	-5.320	69.969	1.00	1.02
ATOM	1553	CG	GLN	1	191	42.146	-6.595	69.816	1.00	1.02
ATOM	1554	CD	GLN	1	191	41.267	-7.774	70.212	1.00	1.02
ATOM	1555	OE1	GLN	1	191	40.666	-7.783	71.285	1.00	1.02
ATOM	1556	NE2	GLN	1	191	41.183	-8.796	69.319	1.00	1.02
ATOM	1557	N	LEU	1	192	40.749	-2.506	70.966	1.00	1.00
ATOM	1558	CA	LEU	1	192	39.760	-1.485	71.157	1.00	1.00
ATOM	1559	C	LEU	1	192	40.237	-0.166	70.656	1.00	1.00
ATOM	1560	O	LEU	1	192	39.487	0.592	70.042	1.00	1.00
ATOM	1561	CB	LEU	1	192	39.385	-1.308	72.632	1.00	1.00
ATOM	1562	CG	LEU	1	192	38.748	-2.573	73.226	1.00	1.00
ATOM	1563	CD1	LEU	1	192	38.380	-2.363	74.698	1.00	1.00
ATOM	1564	CD2	LEU	1	192	37.567	-3.057	72.370	1.00	1.00
ATOM	1565	N	THR	1	193	41.512	0.142	70.927	1.00	4.43
ATOM	1566	CA	THR	1	193	42.060	1.403	70.562	1.00	4.43
ATOM	1567	C	THR	1	193	42.166	1.477	69.075	1.00	4.43

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ATOM 1568 O THR 1 193	41.979	2.540	68.488	1.00	4.43
ATOM 1569 CB THR 1 193	43.414	1.596	71.131	1.00	4.43
ATOM 1570 OG1 THR 1 193	43.458	1.208	72.490	1.00	4.43
ATOM 1571 CG2 THR 1 193	43.568	3.091	71.151	1.00	4.43
ATOM 1572 N LYS 1 194	42.494	0.339	68.433	1.00	6.16
ATOM 1573 CA LYS 1 194	42.623	0.290	67.005	1.00	6.16
ATOM 1574 C LYS 1 194	41.296	0.583	66.383	1.00	6.16
ATOM 1575 O LYS 1 194	41.212	1.253	65.356	1.00	6.16
ATOM 1576 CB LYS 1 194	43.111	-1.073	66.484	1.00	6.16
ATOM 1577 CG LYS 1 194	43.248	-1.117	64.961	1.00	6.16
ATOM 1578 CD LYS 1 194	44.290	-0.151	64.396	1.00	6.16
ATOM 1579 CE LYS 1 194	45.715	-0.698	64.418	1.00	6.16
ATOM 1580 NZ LYS 1 194	46.183	-0.792	65.815	1.00	6.16
ATOM 1581 N LEU 1 195	40.215	0.085	67.006	1.00	5.39
ATOM 1582 CA LEU 1 195	38.888	0.303	66.507	1.00	5.39
ATOM 1583 C LEU 1 195	38.613	1.771	66.485	1.00	5.39
ATOM 1584 O LEU 1 195	38.054	2.295	65.522	1.00	5.39
ATOM 1585 CB LEU 1 195	37.836	-0.398	67.397	1.00	5.39
ATOM 1586 CG LEU 1 195	36.356	-0.035	67.146	1.00	5.39
ATOM 1587 CD1 LEU 1 195	35.993	1.320	67.763	1.00	5.39
ATOM 1588 CD2 LEU 1 195	35.993	-0.081	65.660	1.00	5.39
ATOM 1589 N LEU 1 196	39.026	2.480	67.547	1.00	3.85
ATOM 1590 CA LEU 1 196	38.718	3.870	67.649	1.00	3.85
ATOM 1591 C LEU 1 196	39.453	4.591	66.553	1.00	3.85
ATOM 1592 O LEU 1 196	38.899	5.472	65.896	1.00	3.85
ATOM 1593 CB LEU 1 196	39.124	4.424	69.026	1.00	3.85
ATOM 1594 CG LEU 1 196	38.270	5.615	69.496	1.00	3.85
ATOM 1595 CD1 LEU 1 196	38.931	6.355	70.668	1.00	3.85
ATOM 1596 CD2 LEU 1 196	37.816	6.507	68.337	1.00	3.85
ATOM 1597 N ASP 1 197	40.727	4.227	66.300	1.00	5.56
ATOM 1598 CA ASP 1 197	41.420	4.912	65.248	1.00	5.56
ATOM 1599 C ASP 1 197	40.841	4.627	63.891	1.00	5.56
ATOM 1600 O ASP 1 197	40.842	5.491	63.016	1.00	5.56
ATOM 1601 CB ASP 1 197	42.966	4.858	65.312	1.00	5.56
ATOM 1602 CG ASP 1 197	43.553	3.465	65.392	1.00	5.56
ATOM 1603 OD1 ASP 1 197	44.144	3.024	64.378	1.00	5.56
ATOM 1604 OD2 ASP 1 197	43.477	2.844	66.481	1.00	5.56
ATOM 1605 N SER 1 198	40.292	3.417	63.689	1.00	0.90
ATOM 1606 CA SER 1 198	39.691	3.047	62.437	1.00	0.90
ATOM 1607 C SER 1 198	38.489	3.904	62.168	1.00	0.90
ATOM 1608 O SER 1 198	38.138	4.154	61.015	1.00	0.90
ATOM 1609 CB SER 1 198	39.224	1.580	62.412	1.00	0.90
ATOM 1610 OG SER 1 198	40.339	0.709	62.538	1.00	0.90
ATOM 1611 N MET 1 199	37.815	4.380	63.231	1.00	6.77
ATOM 1612 CA MET 1 199	36.599	5.121	63.049	1.00	6.77
ATOM 1613 C MET 1 199	36.816	6.395	62.286	1.00	6.77
ATOM 1614 O MET 1 199	35.907	6.887	61.620	1.00	6.77
ATOM 1615 CB MET 1 199	35.834	5.396	64.355	1.00	6.77
ATOM 1616 CG MET 1 199	34.394	5.851	64.099	1.00	6.77

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ATOM 1617 SD MET 1 199	33.245	5.583	65.483	1.00	6.77
ATOM 1618 CE MET 1 199	32.998	3.818	65.128	1.00	6.77
ATOM 1619 N HIS 1 200	38.025	6.981	62.351	1.00	0.84
ATOM 1620 CA HIS 1 200	38.228	8.211	61.639	1.00	0.84
ATOM 1621 C HIS 1 200	37.937	8.046	60.180	1.00	0.84
ATOM 1622 O HIS 1 200	37.260	8.881	59.582	1.00	0.84
ATOM 1623 CB HIS 1 200	39.665	8.736	61.742	1.00	0.84
ATOM 1624 CG HIS 1 200	40.009	9.172	63.128	1.00	0.84
ATOM 1625 ND1 HIS 1 200	40.741	8.424	64.024	1.00	0.84
ATOM 1626 CD2 HIS 1 200	39.683	10.322	63.777	1.00	0.84
ATOM 1627 CE1 HIS 1 200	40.831	9.159	65.160	1.00	0.84
ATOM 1628 NE2 HIS 1 200	40.208	10.319	65.056	1.00	0.84
ATOM 1629 N GLU 1 201	38.438	6.964	59.560	1.00	5.71
ATOM 1630 CA GLU 1 201	38.209	6.768	58.158	1.00	5.71
ATOM 1631 C GLU 1 201	36.749	6.560	57.910	1.00	5.71
ATOM 1632 O GLU 1 201	36.190	7.104	56.959	1.00	5.71
ATOM 1633 CB GLU 1 201	38.951	5.541	57.601	1.00	5.71
ATOM 1634 CG GLU 1 201	38.746	5.331	56.099	1.00	5.71
ATOM 1635 CD GLU 1 201	39.521	6.414	55.364	1.00	5.71
ATOM 1636 OE1 GLU 1 201	39.482	6.417	54.105	1.00	5.71
ATOM 1637 OE2 GLU 1 201	40.162	7.254	56.051	1.00	5.71
ATOM 1638 N VAL 1 202	36.085	5.767	58.774	1.00	4.12
ATOM 1639 CA VAL 1 202	34.702	5.475	58.539	1.00	4.12
ATOM 1640 C VAL 1 202	33.860	6.711	58.636	1.00	4.12
ATOM 1641 O VAL 1 202	32.983	6.939	57.805	1.00	4.12
ATOM 1642 CB VAL 1 202	34.121	4.440	59.465	1.00	4.12
ATOM 1643 CG1 VAL 1 202	34.911	3.132	59.287	1.00	4.12
ATOM 1644 CG2 VAL 1 202	34.084	4.979	60.901	1.00	4.12
ATOM 1645 N VAL 1 203	34.128	7.562	59.642	1.00	3.85
ATOM 1646 CA VAL 1 203	33.336	8.742	59.853	1.00	3.85
ATOM 1647 C VAL 1 203	33.475	9.690	58.699	1.00	3.85
ATOM 1648 O VAL 1 203	32.552	10.441	58.384	1.00	3.85
ATOM 1649 CB VAL 1 203	33.684	9.470	61.121	1.00	3.85
ATOM 1650 CG1 VAL 1 203	35.042	10.170	60.960	1.00	3.85
ATOM 1651 CG2 VAL 1 203	32.527	10.419	61.461	1.00	3.85
ATOM 1652 N GLU 1 204	34.643	9.682	58.032	1.00	3.18
ATOM 1653 CA GLU 1 204	34.877	10.585	56.942	1.00	3.18
ATOM 1654 C GLU 1 204	33.848	10.364	55.878	1.00	3.18
ATOM 1655 O GLU 1 204	33.364	11.319	55.272	1.00	3.18
ATOM 1656 CB GLU 1 204	36.260	10.392	56.298	1.00	3.18
ATOM 1657 CG GLU 1 204	36.552	11.380	55.167	1.00	3.18
ATOM 1658 CD GLU 1 204	37.941	11.076	54.626	1.00	3.18
ATOM 1659 OE1 GLU 1 204	38.216	9.881	54.339	1.00	3.18
ATOM 1660 OE2 GLU 1 204	38.749	12.036	54.497	1.00	3.18
ATOM 1661 N ASN 1 205	33.491	9.094	55.610	1.00	0.60
ATOM 1662 CA ASN 1 205	32.509	8.814	54.601	1.00	0.60
ATOM 1663 C ASN 1 205	31.180	9.372	55.011	1.00	0.60
ATOM 1664 O ASN 1 205	30.443	9.899	54.180	1.00	0.60
ATOM 1665 CB ASN 1 205	32.342	7.311	54.324	1.00	0.60

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ATOM 1666 CG ASN 1 205	33.573	6.857	53.551	1.00	0.60
ATOM 1667 OD1 ASN 1 205	33.971	7.491	52.575	1.00	0.60
ATOM 1668 ND2 ASN 1 205	34.200	5.737	54.000	1.00	0.60
ATOM 1669 N LEU 1 206	30.833	9.263	56.308	1.00	3.88
ATOM 1670 CA LEU 1 206	29.590	9.801	56.792	1.00	3.88
ATOM 1671 C LEU 1 206	29.590	11.288	56.603	1.00	3.88
ATOM 1672 O LEU 1 206	28.594	11.876	56.185	1.00	3.88
ATOM 1673 CB LEU 1 206	29.374	9.562	58.302	1.00	3.88
ATOM 1674 CG LEU 1 206	28.910	8.147	58.708	1.00	3.88
ATOM 1675 CD1 LEU 1 206	27.419	7.956	58.399	1.00	3.88
ATOM 1676 CD2 LEU 1 206	29.780	7.041	58.090	1.00	3.88
ATOM 1677 N LEU 1 207	30.728	11.935	56.906	1.00	4.19
ATOM 1678 CA LEU 1 207	30.855	13.361	56.816	1.00	4.19
ATOM 1679 C LEU 1 207	30.630	13.821	55.409	1.00	4.19
ATOM 1680 O LEU 1 207	29.925	14.802	55.175	1.00	4.19
ATOM 1681 CB LEU 1 207	32.253	13.792	57.322	1.00	4.19
ATOM 1682 CG LEU 1 207	32.675	15.259	57.113	1.00	4.19
ATOM 1683 CD1 LEU 1 207	33.895	15.597	57.985	1.00	4.19
ATOM 1684 CD2 LEU 1 207	33.001	15.538	55.636	1.00	4.19
ATOM 1685 N ASN 1 208	31.222	13.114	54.431	1.00	1.53
ATOM 1686 CA ASN 1 208	31.089	13.501	53.056	1.00	1.53
ATOM 1687 C ASN 1 208	29.664	13.377	52.611	1.00	1.53
ATOM 1688 O ASN 1 208	29.136	14.262	51.940	1.00	1.53
ATOM 1689 CB ASN 1 208	31.935	12.625	52.115	1.00	1.53
ATOM 1690 CG ASN 1 208	33.402	12.887	52.423	1.00	1.53
ATOM 1691 OD1 ASN 1 208	34.144	11.976	52.787	1.00	1.53
ATOM 1692 ND2 ASN 1 208	33.835	14.168	52.275	1.00	1.53
ATOM 1693 N TYR 1 209	28.999	12.269	52.989	1.00	0.82
ATOM 1694 CA TYR 1 209	27.651	12.014	52.564	1.00	0.82
ATOM 1695 C TYR 1 209	26.759	13.093	53.100	1.00	0.82
ATOM 1696 O TYR 1 209	25.914	13.623	52.379	1.00	0.82
ATOM 1697 CB TYR 1 209	27.142	10.657	53.088	1.00	0.82
ATOM 1698 CG TYR 1 209	25.798	10.364	52.512	1.00	0.82
ATOM 1699 CD1 TYR 1 209	24.653	10.876	53.079	1.00	0.82
ATOM 1700 CD2 TYR 1 209	25.682	9.497	51.449	1.00	0.82
ATOM 1701 CE1 TYR 1 209	23.415	10.537	52.584	1.00	0.82
ATOM 1702 CE2 TYR 1 209	24.447	9.155	50.950	1.00	0.82
ATOM 1703 CZ TYR 1 209	23.310	9.673	51.520	1.00	0.82
ATOM 1704 OH TYR 1 209	22.042	9.316	51.016	1.00	0.82
ATOM 1705 N CYS 1 210	26.937	13.457	54.387	1.00	3.72
ATOM 1706 CA CYS 1 210	26.103	14.462	54.986	1.00	3.72
ATOM 1707 C CYS 1 210	26.255	15.798	54.337	1.00	3.72
ATOM 1708 O CYS 1 210	25.267	16.467	54.042	1.00	3.72
ATOM 1709 CB CYS 1 210	26.370	14.703	56.480	1.00	3.72
ATOM 1710 SG CYS 1 210	25.473	13.553	57.554	1.00	3.72
ATOM 1711 N PHE 1 211	27.504	16.221	54.089	1.00	3.96
ATOM 1712 CA PHE 1 211	27.729	17.524	53.538	1.00	3.96
ATOM 1713 C PHE 1 211	27.103	17.603	52.183	1.00	3.96
ATOM 1714 O PHE 1 211	26.519	18.623	51.821	1.00	3.96

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ATOM 1715 CB PHE 1 211	29.226	17.848	53.386	1.00	3.96
ATOM 1716 CG PHE 1 211	29.342	19.260	52.924	1.00	3.96
ATOM 1717 CD1 PHE 1 211	29.233	19.575	51.590	1.00	3.96
ATOM 1718 CD2 PHE 1 211	29.575	20.268	53.831	1.00	3.96
ATOM 1719 CE1 PHE 1 211	29.352	20.879	51.167	1.00	3.96
ATOM 1720 CE2 PHE 1 211	29.695	21.573	53.415	1.00	3.96
ATOM 1721 CZ PHE 1 211	29.584	21.880	52.080	1.00	3.96
ATOM 1722 N GLN 1 212	27.218	16.519	51.393	1.00	0.53
ATOM 1723 CA GLN 1 212	26.678	16.508	50.064	1.00	0.53
ATOM 1724 C GLN 1 212	25.187	16.643	50.107	1.00	0.53
ATOM 1725 O GLN 1 212	24.606	17.437	49.370	1.00	0.53
ATOM 1726 CB GLN 1 212	26.989	15.200	49.317	1.00	0.53
ATOM 1727 CG GLN 1 212	28.483	14.969	49.083	1.00	0.53
ATOM 1728 CD GLN 1 212	28.642	13.649	48.342	1.00	0.53
ATOM 1729 OE1 GLN 1 212	27.660	12.976	48.030	1.00	0.53
ATOM 1730 NE2 GLN 1 212	29.913	13.265	48.052	1.00	0.53
ATOM 1731 N THR 1 213	24.529	15.873	50.993	1.00	0.65
ATOM 1732 CA THR 1 213	23.097	15.882	51.086	1.00	0.65
ATOM 1733 C THR 1 213	22.633	17.223	51.556	1.00	0.65
ATOM 1734 O THR 1 213	21.580	17.711	51.145	1.00	0.65
ATOM 1735 CB THR 1 213	22.573	14.864	52.051	1.00	0.65
ATOM 1736 OG1 THR 1 213	22.993	13.564	51.664	1.00	0.65
ATOM 1737 CG2 THR 1 213	21.039	14.939	52.041	1.00	0.65
ATOM 1738 N PHE 1 214	23.418	17.846	52.452	1.00	0.68
ATOM 1739 CA PHE 1 214	23.086	19.118	53.022	1.00	0.68
ATOM 1740 C PHE 1 214	22.996	20.140	51.926	1.00	0.68
ATOM 1741 O PHE 1 214	22.048	20.921	51.873	1.00	0.68
ATOM 1742 CB PHE 1 214	24.168	19.561	54.028	1.00	0.68
ATOM 1743 CG PHE 1 214	23.759	20.819	54.713	1.00	0.68
ATOM 1744 CD1 PHE 1 214	22.913	20.778	55.798	1.00	0.68
ATOM 1745 CD2 PHE 1 214	24.320	22.023	54.351	1.00	0.68
ATOM 1746 CE1 PHE 1 214	22.605	21.926	56.490	1.00	0.68
ATOM 1747 CE2 PHE 1 214	24.016	23.173	55.039	1.00	0.68
ATOM 1748 CZ PHE 1 214	23.156	23.126	56.110	1.00	0.68
ATOM 1749 N LEU 1 215	23.986	20.159	51.013	1.00	6.34
ATOM 1750 CA LEU 1 215	23.981	21.102	49.927	1.00	6.34
ATOM 1751 C LEU 1 215	22.856	20.758	48.986	1.00	6.34
ATOM 1752 O LEU 1 215	22.184	21.629	48.435	1.00	6.34
ATOM 1753 CB LEU 1 215	25.301	21.078	49.135	1.00	6.34
ATOM 1754 CG LEU 1 215	25.355	22.077	47.965	1.00	6.34
ATOM 1755 CD1 LEU 1 215	25.292	23.529	48.468	1.00	6.34
ATOM 1756 CD2 LEU 1 215	26.579	21.817	47.073	1.00	6.34
ATOM 1757 N ASP 1 216	22.653	19.440	48.808	1.00	3.90
ATOM 1758 CA ASP 1 216	21.725	18.719	47.975	1.00	3.90
ATOM 1759 C ASP 1 216	20.330	18.794	48.524	1.00	3.90
ATOM 1760 O ASP 1 216	19.397	18.265	47.924	1.00	3.90
ATOM 1761 CB ASP 1 216	22.104	17.232	47.855	1.00	3.90
ATOM 1762 CG ASP 1 216	21.375	16.629	46.662	1.00	3.90
ATOM 1763 OD1 ASP 1 216	20.696	17.393	45.926	1.00	3.90

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ATOM 1764 OD2 ASP 1 216	21.495	15.389	46.468	1.00	3.90
ATOM 1765 N LYS 1 217	20.165	19.463	49.680	1.00	3.84
ATOM 1766 CA LYS 1 217	18.980	19.529	50.495	1.00	3.84
ATOM 1767 C LYS 1 217	17.745	19.722	49.660	1.00	3.84
ATOM 1768 O LYS 1 217	16.658	19.309	50.062	1.00	3.84
ATOM 1769 CB LYS 1 217	19.089	20.703	51.485	1.00	3.84
ATOM 1770 CG LYS 1 217	17.973	20.790	52.519	1.00	3.84
ATOM 1771 CD LYS 1 217	18.318	21.703	53.696	1.00	3.84
ATOM 1772 CE LYS 1 217	17.234	21.758	54.772	1.00	3.84
ATOM 1773 NZ LYS 1 217	17.690	22.596	55.904	1.00	3.84
ATOM 1774 N THR 1 218	17.873	20.315	48.459	1.00	5.26
ATOM 1775 CA THR 1 218	16.766	20.514	47.558	1.00	5.26
ATOM 1776 C THR 1 218	16.108	19.182	47.278	1.00	5.26
ATOM 1777 O THR 1 218	14.979	19.132	46.791	1.00	5.26
ATOM 1778 CB THR 1 218	17.160	21.119	46.242	1.00	5.26
ATOM 1779 OG1 THR 1 218	16.001	21.528	45.529	1.00	5.26
ATOM 1780 CG2 THR 1 218	17.941	20.077	45.425	1.00	5.26
ATOM 1781 N MET 1 219	16.808	18.067	47.597	1.00	6.69
ATOM 1782 CA MET 1 219	16.430	16.677	47.470	1.00	6.69
ATOM 1783 C MET 1 219	15.188	16.447	48.280	1.00	6.69
ATOM 1784 O MET 1 219	14.613	15.356	48.276	1.00	6.69
ATOM 1785 CB MET 1 219	17.524	15.707	47.938	1.00	6.69
ATOM 1786 CG MET 1 219	17.292	14.281	47.443	1.00	6.69
ATOM 1787 SD MET 1 219	17.338	14.138	45.631	1.00	6.69
ATOM 1788 CE MET 1 219	19.001	14.846	45.455	1.00	6.69
ATOM 1789 N SER 1 220	14.809	17.467	49.072	1.00	4.00
ATOM 1790 CA SER 1 220	13.621	17.455	49.863	1.00	4.00
ATOM 1791 C SER 1 220	13.977	16.815	51.147	1.00	4.00
ATOM 1792 O SER 1 220	13.140	16.226	51.829	1.00	4.00
ATOM 1793 CB SER 1 220	12.434	16.720	49.215	1.00	4.00
ATOM 1794 OG SER 1 220	11.988	17.433	48.070	1.00	4.00
ATOM 1795 N ILE 1 221	15.270	16.937	51.492	1.00	4.77
ATOM 1796 CA ILE 1 221	15.760	16.481	52.750	1.00	4.77
ATOM 1797 C ILE 1 221	15.799	17.683	53.634	1.00	4.77
ATOM 1798 O ILE 1 221	16.357	18.715	53.274	1.00	4.77
ATOM 1799 CB ILE 1 221	17.158	15.938	52.702	1.00	4.77
ATOM 1800 CG1 ILE 1 221	17.582	15.490	54.109	1.00	4.77
ATOM 1801 CG2 ILE 1 221	18.086	16.978	52.051	1.00	4.77
ATOM 1802 CD1 ILE 1 221	18.995	14.921	54.165	1.00	4.77
ATOM 1803 N GLU 1 222	15.194	17.590	54.828	1.00	2.49
ATOM 1804 CA GLU 1 222	15.181	18.727	55.697	1.00	2.49
ATOM 1805 C GLU 1 222	16.154	18.509	56.812	1.00	2.49
ATOM 1806 O GLU 1 222	16.209	17.431	57.400	1.00	2.49
ATOM 1807 CB GLU 1 222	13.785	18.987	56.299	1.00	2.49
ATOM 1808 CG GLU 1 222	13.710	20.127	57.317	1.00	2.49
ATOM 1809 CD GLU 1 222	13.663	19.508	58.708	1.00	2.49
ATOM 1810 OE1 GLU 1 222	14.638	18.802	59.081	1.00	2.49
ATOM 1811 OE2 GLU 1 222	12.643	19.728	59.417	1.00	2.49
ATOM 1812 N PHE 1 223	16.977	19.540	57.101	1.00	0.93

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ATOM 1813 CA PHE 1 223	17.919	19.483	58.185	1.00	0.93
ATOM 1814 C PHE 1 223	17.459	20.474	59.211	1.00	0.93
ATOM 1815 O PHE 1 223	17.096	21.603	58.886	1.00	0.93
ATOM 1816 CB PHE 1 223	19.359	19.891	57.805	1.00	0.93
ATOM 1817 CG PHE 1 223	20.012	18.809	57.010	1.00	0.93
ATOM 1818 CD1 PHE 1 223	19.727	18.645	55.674	1.00	0.93
ATOM 1819 CD2 PHE 1 223	21.011	18.046	57.574	1.00	0.93
ATOM 1820 CE1 PHE 1 223	20.394	17.701	54.928	1.00	0.93
ATOM 1821 CE2 PHE 1 223	21.686	17.104	56.833	1.00	0.93
ATOM 1822 CZ PHE 1 223	21.372	16.927	55.507	1.00	0.93
ATOM 1823 N PRO 1 224	17.471	20.069	60.453	1.00	5.86
ATOM 1824 CA PRO 1 224	17.050	20.922	61.534	1.00	5.86
ATOM 1825 C PRO 1 224	18.090	21.970	61.789	1.00	5.86
ATOM 1826 O PRO 1 224	19.202	21.841	61.282	1.00	5.86
ATOM 1827 CB PRO 1 224	16.789	19.996	62.727	1.00	5.86
ATOM 1828 CG PRO 1 224	17.402	18.643	62.320	1.00	5.86
ATOM 1829 CD PRO 1 224	17.344	18.662	60.787	1.00	5.86
ATOM 1830 N GLU 1 225	17.739	23.020	62.559	1.00	2.88
ATOM 1831 CA GLU 1 225	18.615	24.135	62.793	1.00	2.88
ATOM 1832 C GLU 1 225	19.892	23.801	63.507	1.00	2.88
ATOM 1833 O GLU 1 225	20.962	24.232	63.082	1.00	2.88
ATOM 1834 CB GLU 1 225	17.942	25.263	63.597	1.00	2.88
ATOM 1835 CG GLU 1 225	16.853	26.013	62.825	1.00	2.88
ATOM 1836 CD GLU 1 225	15.579	25.180	62.839	1.00	2.88
ATOM 1837 OE1 GLU 1 225	15.375	24.422	63.825	1.00	2.88
ATOM 1838 OE2 GLU 1 225	14.790	25.294	61.863	1.00	2.88
ATOM 1839 N MET 1 226	19.833	23.028	64.608	1.00	6.09
ATOM 1840 CA MET 1 226	21.035	22.758	65.350	1.00	6.09
ATOM 1841 C MET 1 226	22.000	21.956	64.535	1.00	6.09
ATOM 1842 O MET 1 226	23.203	22.213	64.549	1.00	6.09
ATOM 1843 CB MET 1 226	20.783	21.997	66.666	1.00	6.09
ATOM 1844 CG MET 1 226	20.163	20.610	66.483	1.00	6.09
ATOM 1845 SD MET 1 226	18.403	20.624	66.032	1.00	6.09
ATOM 1846 CE MET 1 226	17.830	20.977	67.719	1.00	6.09
ATOM 1847 N LEU 1 227	21.491	20.948	63.806	1.00	0.72
ATOM 1848 CA LEU 1 227	22.336	20.113	63.004	1.00	0.72
ATOM 1849 C LEU 1 227	22.918	20.921	61.894	1.00	0.72
ATOM 1850 O LEU 1 227	24.082	20.756	61.533	1.00	0.72
ATOM 1851 CB LEU 1 227	21.582	18.934	62.364	1.00	0.72
ATOM 1852 CG LEU 1 227	22.481	18.028	61.504	1.00	0.72
ATOM 1853 CD1 LEU 1 227	23.563	17.344	62.352	1.00	0.72
ATOM 1854 CD2 LEU 1 227	21.647	17.030	60.684	1.00	0.72
ATOM 1855 N ALA 1 228	22.109	21.828	61.320	1.00	0.66
ATOM 1856 CA ALA 1 228	22.574	22.629	60.228	1.00	0.66
ATOM 1857 C ALA 1 228	23.726	23.463	60.695	1.00	0.66
ATOM 1858 O ALA 1 228	24.706	23.638	59.972	1.00	0.66
ATOM 1859 CB ALA 1 228	21.497	23.587	59.693	1.00	0.66
ATOM 1860 N GLU 1 229	23.645	24.002	61.925	1.00	4.93
ATOM 1861 CA GLU 1 229	24.691	24.869	62.386	1.00	4.93

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ATOM 1862 C GLU 1 229	25.999	24.149	62.529	1.00	4.93
ATOM 1863 O GLU 1 229	27.039	24.667	62.125	1.00	4.93
ATOM 1864 CB GLU 1 229	24.358	25.573	63.719	1.00	4.93
ATOM 1865 CG GLU 1 229	24.354	24.672	64.954	1.00	4.93
ATOM 1866 CD GLU 1 229	25.721	24.784	65.612	1.00	4.93
ATOM 1867 OE1 GLU 1 229	26.063	23.879	66.419	1.00	4.93
ATOM 1868 OE2 GLU 1 229	26.440	25.778	65.321	1.00	4.93
ATOM 1869 N ILE 1 230	25.992	22.927	63.095	1.00	5.97
ATOM 1870 CA ILE 1 230	27.224	22.216	63.298	1.00	5.97
ATOM 1871 C ILE 1 230	27.828	21.845	61.978	1.00	5.97
ATOM 1872 O ILE 1 230	29.046	21.898	61.806	1.00	5.97
ATOM 1873 CB ILE 1 230	27.042	20.975	64.125	1.00	5.97
ATOM 1874 CG1 ILE 1 230	28.399	20.479	64.647	1.00	5.97
ATOM 1875 CG2 ILE 1 230	26.271	19.943	63.286	1.00	5.97
ATOM 1876 CD1 ILE 1 230	28.275	19.512	65.823	1.00	5.97
ATOM 1877 N ILE 1 231	26.982	21.458	61.005	1.00	3.96
ATOM 1878 CA ILE 1 231	27.466	21.066	59.710	1.00	3.96
ATOM 1879 C ILE 1 231	28.172	22.240	59.102	1.00	3.96
ATOM 1880 O ILE 1 231	29.322	22.149	58.675	1.00	3.96
ATOM 1881 CB ILE 1 231	26.339	20.766	58.749	1.00	3.96
ATOM 1882 CG1 ILE 1 231	25.418	19.622	59.220	1.00	3.96
ATOM 1883 CG2 ILE 1 231	26.972	20.489	57.375	1.00	3.96
ATOM 1884 CD1 ILE 1 231	26.017	18.227	59.087	1.00	3.96
ATOM 1885 N THR 1 232	27.496	23.400	59.089	1.00	0.77
ATOM 1886 CA THR 1 232	28.027	24.564	58.444	1.00	0.77
ATOM 1887 C THR 1 232	29.275	25.027	59.109	1.00	0.77
ATOM 1888 O THR 1 232	30.232	25.418	58.442	1.00	0.77
ATOM 1889 CB THR 1 232	27.062	25.713	58.456	1.00	0.77
ATOM 1890 OG1 THR 1 232	25.861	25.351	57.791	1.00	0.77
ATOM 1891 CG2 THR 1 232	27.716	26.913	57.749	1.00	0.77
ATOM 1892 N ASN 1 233	29.303	25.013	60.451	1.00	2.07
ATOM 1893 CA ASN 1 233	30.466	25.538	61.089	1.00	2.07
ATOM 1894 C ASN 1 233	31.704	24.742	60.810	1.00	2.07
ATOM 1895 O ASN 1 233	32.734	25.302	60.450	1.00	2.07
ATOM 1896 CB ASN 1 233	30.309	25.644	62.614	1.00	2.07
ATOM 1897 CG ASN 1 233	29.322	26.763	62.916	1.00	2.07
ATOM 1898 OD1 ASN 1 233	28.277	26.880	62.278	1.00	2.07
ATOM 1899 ND2 ASN 1 233	29.668	27.620	63.914	1.00	2.07
ATOM 1900 N GLN 1 234	31.676	23.431	61.097	1.00	2.81
ATOM 1901 CA GLN 1 234	32.824	22.592	60.914	1.00	2.81
ATOM 1902 C GLN 1 234	33.052	21.633	59.765	1.00	2.81
ATOM 1903 O GLN 1 234	34.201	21.356	59.425	1.00	2.81
ATOM 1904 CB GLN 1 234	33.166	21.915	62.226	1.00	2.81
ATOM 1905 CG GLN 1 234	33.523	22.907	63.332	1.00	2.81
ATOM 1906 CD GLN 1 234	34.798	23.627	62.926	1.00	2.81
ATOM 1907 OE1 GLN 1 234	35.186	24.630	63.522	1.00	2.81
ATOM 1908 NE2 GLN 1 234	35.473	23.099	61.873	1.00	2.81
ATOM 1909 N ILE 1 235	31.996	21.074	59.135	1.00	7.20
ATOM 1910 CA ILE 1 235	32.227	19.974	58.228	1.00	7.20

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ATOM 1911 C ILE 1 235	33.138	20.265	57.073	1.00	7.20
ATOM 1912 O ILE 1 235	33.936	19.389	56.735	1.00	7.20
ATOM 1913 CB ILE 1 235	30.964	19.231	57.793	1.00	7.20
ATOM 1914 CG1 ILE 1 235	31.296	17.943	57.019	1.00	7.20
ATOM 1915 CG2 ILE 1 235	30.038	20.138	56.975	1.00	7.20
ATOM 1916 CD1 ILE 1 235	31.720	18.184	55.569	1.00	7.20
ATOM 1917 N PRO 1 236	33.124	21.394	56.428	1.00	1.16
ATOM 1918 CA PRO 1 236	34.020	21.577	55.326	1.00	1.16
ATOM 1919 C PRO 1 236	35.435	21.530	55.806	1.00	1.16
ATOM 1920 O PRO 1 236	36.296	21.042	55.076	1.00	1.16
ATOM 1921 CB PRO 1 236	33.632	22.909	54.688	1.00	1.16
ATOM 1922 CG PRO 1 236	32.150	23.083	55.073	1.00	1.16
ATOM 1923 CD PRO 1 236	32.015	22.333	56.408	1.00	1.16
ATOM 1924 N LYS 1 237	35.698	22.041	57.025	1.00	4.23
ATOM 1925 CA LYS 1 237	37.028	22.057	57.557	1.00	4.23
ATOM 1926 C LYS 1 237	37.491	20.659	57.812	1.00	4.23
ATOM 1927 O LYS 1 237	38.618	20.303	57.473	1.00	4.23
ATOM 1928 CB LYS 1 237	37.154	22.792	58.903	1.00	4.23
ATOM 1929 CG LYS 1 237	36.913	24.300	58.836	1.00	4.23
ATOM 1930 CD LYS 1 237	36.890	24.960	60.217	1.00	4.23
ATOM 1931 CE LYS 1 237	36.604	26.462	60.190	1.00	4.23
ATOM 1932 NZ LYS 1 237	35.143	26.695	60.175	1.00	4.23
ATOM 1933 N TYR 1 238	36.620	19.820	58.410	1.00	1.32
ATOM 1934 CA TYR 1 238	37.004	18.473	58.743	1.00	1.32
ATOM 1935 C TYR 1 238	37.385	17.756	57.503	1.00	1.32
ATOM 1936 O TYR 1 238	38.418	17.094	57.438	1.00	1.32
ATOM 1937 CB TYR 1 238	35.862	17.534	59.149	1.00	1.32
ATOM 1938 CG TYR 1 238	35.233	18.013	60.377	1.00	1.32
ATOM 1939 CD1 TYR 1 238	35.842	17.772	61.578	1.00	1.32
ATOM 1940 CD2 TYR 1 238	34.006	18.620	60.309	1.00	1.32
ATOM 1941 CE1 TYR 1 238	35.279	18.269	62.716	1.00	1.32
ATOM 1942 CE2 TYR 1 238	33.436	19.101	61.451	1.00	1.32
ATOM 1943 CZ TYR 1 238	34.106	18.973	62.640	1.00	1.32
ATOM 1944 OH TYR 1 238	33.673	19.698	63.760	1.00	1.32
ATOM 1945 N SER 1 239	36.514	17.867	56.489	1.00	3.15
ATOM 1946 CA SER 1 239	36.681	17.123	55.279	1.00	3.15
ATOM 1947 C SER 1 239	37.975	17.507	54.646	1.00	3.15
ATOM 1948 O SER 1 239	38.677	16.668	54.084	1.00	3.15
ATOM 1949 CB SER 1 239	35.564	17.398	54.258	1.00	3.15
ATOM 1950 OG SER 1 239	35.780	16.633	53.081	1.00	3.15
ATOM 1951 N ASN 1 240	38.318	18.802	54.734	1.00	0.86
ATOM 1952 CA ASN 1 240	39.522	19.324	54.162	1.00	0.86
ATOM 1953 C ASN 1 240	40.702	18.696	54.842	1.00	0.86
ATOM 1954 O ASN 1 240	41.765	18.555	54.242	1.00	0.86
ATOM 1955 CB ASN 1 240	39.644	20.850	54.319	1.00	0.86
ATOM 1956 CG ASN 1 240	38.554	21.496	53.475	1.00	0.86
ATOM 1957 OD1 ASN 1 240	38.152	20.962	52.442	1.00	0.86
ATOM 1958 ND2 ASN 1 240	38.059	22.679	53.925	1.00	0.86
ATOM 1959 N GLY 1 241	40.561	18.294	56.119	1.00	0.83

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ATOM	1960	CA	GLY	1 241	41.697	17.718	56.787	1.00	0.83
ATOM	1961	C	GLY	1 241	42.399	18.795	57.555	1.00	0.83
ATOM	1962	O	GLY	1 241	43.590	18.708	57.850	1.00	0.83
ATOM	1963	N	ASN	1 242	41.635	19.849	57.875	1.00	2.92
ATOM	1964	CA	ASN	1 242	42.002	21.027	58.606	1.00	2.92
ATOM	1965	C	ASN	1 242	42.169	20.756	60.070	1.00	2.92
ATOM	1966	O	ASN	1 242	42.453	21.686	60.813	1.00	2.92
ATOM	1967	CB	ASN	1 242	40.955	22.145	58.488	1.00	2.92
ATOM	1968	CG	ASN	1 242	40.942	22.624	57.046	1.00	2.92
ATOM	1969	OD1	ASN	1 242	40.035	23.340	56.624	1.00	2.92
ATOM	1970	ND2	ASN	1 242	41.975	22.212	56.264	1.00	2.92
ATOM	1971	N	ILE	1 243	41.868	19.533	60.551	1.00	9.49
ATOM	1972	CA	ILE	1 243	41.910	19.235	61.960	1.00	9.49
ATOM	1973	C	ILE	1 243	42.936	18.170	62.206	1.00	9.49
ATOM	1974	O	ILE	1 243	43.381	17.497	61.278	1.00	9.49
ATOM	1975	CB	ILE	1 243	40.570	18.707	62.420	1.00	9.49
ATOM	1976	CG1	ILE	1 243	39.491	19.762	62.159	1.00	9.49
ATOM	1977	CG2	ILE	1 243	40.625	18.309	63.901	1.00	9.49
ATOM	1978	CD1	ILE	1 243	39.734	21.041	62.954	1.00	9.49
ATOM	1979	N	LYS	1 244	43.387	18.011	63.470	1.00	6.69
ATOM	1980	CA	LYS	1 244	44.315	16.949	63.696	1.00	6.69
ATOM	1981	C	LYS	1 244	43.670	15.828	64.449	1.00	6.69
ATOM	1982	O	LYS	1 244	43.232	15.951	65.587	1.00	6.69
ATOM	1983	CB	LYS	1 244	45.660	17.380	64.330	1.00	6.69
ATOM	1984	CG	LYS	1 244	45.628	18.055	65.702	1.00	6.69
ATOM	1985	CD	LYS	1 244	45.487	17.102	66.888	1.00	6.69
ATOM	1986	CE	LYS	1 244	44.224	17.349	67.705	1.00	6.69
ATOM	1987	NZ	LYS	1 244	44.078	16.337	68.763	1.00	6.69
ATOM	1988	N	LYS	1 245	43.565	14.675	63.771	1.00	7.88
ATOM	1989	CA	LYS	1 245	42.994	13.498	64.343	1.00	7.88
ATOM	1990	C	LYS	1 245	43.983	12.850	65.261	1.00	7.88
ATOM	1991	O	LYS	1 245	45.162	12.739	64.936	1.00	7.88
ATOM	1992	CB	LYS	1 245	42.480	12.569	63.221	1.00	7.88
ATOM	1993	CG	LYS	1 245	42.550	11.058	63.427	1.00	7.88
ATOM	1994	CD	LYS	1 245	43.799	10.426	62.802	1.00	7.88
ATOM	1995	CE	LYS	1 245	45.020	10.292	63.705	1.00	7.88
ATOM	1996	NZ	LYS	1 245	46.153	9.761	62.911	1.00	7.88
ATOM	1997	N	LEU	1 246	43.525	12.433	66.461	1.00	1.24
ATOM	1998	CA	LEU	1 246	44.406	11.806	67.410	1.00	1.24
ATOM	1999	C	LEU	1 246	44.362	10.349	67.118	1.00	1.24
ATOM	2000	O	LEU	1 246	43.285	9.777	66.956	1.00	1.24
ATOM	2001	CB	LEU	1 246	43.975	11.978	68.876	1.00	1.24
ATOM	2002	CG	LEU	1 246	44.138	13.418	69.380	1.00	1.24
ATOM	2003	CD1	LEU	1 246	43.705	13.561	70.848	1.00	1.24
ATOM	2004	CD2	LEU	1 246	45.582	13.893	69.147	1.00	1.24
ATOM	2005	N	LEU	1 247	45.546	9.712	67.038	1.00	6.31
ATOM	2006	CA	LEU	1 247	45.532	8.332	66.672	1.00	6.31
ATOM	2007	C	LEU	1 247	46.366	7.621	67.690	1.00	6.31
ATOM	2008	O	LEU	1 247	47.468	8.058	68.016	1.00	6.31

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ATOM	2009	CB	LEU	1	247	46.199	8.117	65.308	1.00	6.31
ATOM	2010	CG	LEU	1	247	45.682	6.894	64.552	1.00	6.31
ATOM	2011	CD1	LEU	1	247	45.821	5.604	65.373	1.00	6.31
ATOM	2012	CD2	LEU	1	247	44.263	7.166	64.025	1.00	6.31
ATOM	2013	N	PHE	1	248	45.836	6.519	68.249	1.00	1.30
ATOM	2014	CA	PHE	1	248	46.539	5.746	69.229	1.00	1.30
ATOM	2015	C	PHE	1	248	47.648	4.947	68.648	1.00	1.30
ATOM	2016	O	PHE	1	248	48.649	4.687	69.313	1.00	1.30
ATOM	2017	CB	PHE	1	248	45.620	4.819	69.985	1.00	1.30
ATOM	2018	CG	PHE	1	248	44.791	5.716	70.834	1.00	1.30
ATOM	2019	CD1	PHE	1	248	45.240	6.092	72.080	1.00	1.30
ATOM	2020	CD2	PHE	1	248	43.504	6.020	70.458	1.00	1.30
ATOM	2021	CE1	PHE	1	248	44.419	6.778	72.942	1.00	1.30
ATOM	2022	CE2	PHE	1	248	42.682	6.713	71.314	1.00	1.30
ATOM	2023	CZ	PHE	1	248	43.133	7.075	72.562	1.00	1.30
ATOM	2024	N	HIS	1	249	47.487	4.497	67.396	1.00	3.57
ATOM	2025	CA	HIS	1	249	48.517	3.689	66.830	1.00	3.57
ATOM	2026	C	HIS	1	249	49.182	4.514	65.786	1.00	3.57
ATOM	2027	O	HIS	1	249	48.535	5.300	65.096	1.00	3.57
ATOM	2028	CB	HIS	1	249	47.959	2.401	66.206	1.00	3.57
ATOM	2029	CG	HIS	1	249	47.126	1.638	67.200	1.00	3.57
ATOM	2030	ND1	HIS	1	249	45.750	1.671	67.235	1.00	3.57
ATOM	2031	CD2	HIS	1	249	47.501	0.877	68.264	1.00	3.57
ATOM	2032	CE1	HIS	1	249	45.364	0.929	68.304	1.00	3.57
ATOM	2033	NE2	HIS	1	249	46.393	0.428	68.961	1.00	3.57
ATOM	2034	N	GLN	1	250	50.513	4.352	65.668	1.00	3.06
ATOM	2035	CA	GLN	1	250	51.307	5.130	64.766	1.00	3.06
ATOM	2036	C	GLN	1	250	50.873	4.894	63.360	1.00	3.06
ATOM	2037	O	GLN	1	250	49.793	4.366	63.101	1.00	3.06
ATOM	2038	CB	GLN	1	250	52.808	4.803	64.849	1.00	3.06
ATOM	2039	CG	GLN	1	250	53.426	5.104	66.217	1.00	3.06
ATOM	2040	CD	GLN	1	250	54.901	4.737	66.158	1.00	3.06
ATOM	2041	OE1	GLN	1	250	54.148	5.443	65.498	1.00	3.06
ATOM	2042	NE2	GLN	1	250	54.829	3.928	67.254	1.00	3.06
ATOM	2043	N	LYS	1	251	51.730	5.314	62.409	1.00	8.59
ATOM	2044	CA	LYS	1	251	51.464	5.195	61.006	1.00	8.59
ATOM	2045	C	LYS	1	251	50.081	5.753	60.685	1.00	8.59
ATOM	2046	O	LYS	1	251	49.467	6.412	61.567	1.00	8.59
ATOM	2047	CB	LYS	1	251	51.578	3.750	60.471	1.00	8.59
ATOM	2048	CG	LYS	1	251	50.546	2.755	61.013	1.00	8.59
ATOM	2049	CD	LYS	1	251	49.124	2.976	60.490	1.00	8.59
ATOM	2050	CE	LYS	1	251	49.003	2.835	58.971	1.00	8.59
ATOM	2051	NZ	LYS	1	251	47.603	3.062	58.549	1.00	8.59
ATOM	2052	OXT	LYS	1	251	49.624	5.533	59.532	1.00	8.59

END

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FIG 14

Sequence alignment of ER and GR used for the conformation of the C-terminal -helix (helix 12) in a PR-based GR-model for the study of binding of antagonists.

gr_er	522	PATLPQLTPT	LVSLLLEVIEP	EVLYAGYDSS	VPDSTWRIMT	TLNMLGGRQV
lerr	307	ALSLTADQ	MVSALLDAEP	PILYSEYDPT	RPFSEASMMG	LLTNLADREL
		. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gr_er	572	IAAVKWAKAI	PGFRNLHLDD	QMTLLQYSWM	FLMAFALGWR	SYRQSSANLL
lerr	355	VHMINWAKRV	PGFVDLTLHD	QVHLLECAWL	EILMIGLVWR	SMEHFG--KL
		. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gr_er	622	CFAPDLTINE	QRMTLP-OMY	DQCKHMLYVS	SELHRLQVSY	EEYLCMKTLL
lerr	403	LFAPNLLDDR	NQGKCVGEMV	EIFDMLLATS	SRFRMMNLQG	EEFVCLKSII
		. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gr_er	671	LLSSVPKDGL	KSQELFDEIR	MTYIKELGKA	IVKREG--NS	S-QNWQRFYQ
lerr	453	LLNSGVY---	---EEKDHIH	RVLDKITDTL	IHLMAKAGLT	LQQQHQRLAQ
		. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gr_er	718	LTKLLDSMHE	VVENLLNYCF	QTFLDKTMSI	EFPEMLAEII	TNQ
lerr	507	LLLILSHIRH	MSNKGMEHLY	SM-----P	L-YDLLLEML	DAH
		. . . . .	. . . . .	. . . . .	. . . . .	. . . . .

\* = identical amino acid residue

. = conservative amino acid substitution

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FIG. 15.

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HEADER    PROTEIN
COMPND    GR_ER_RAL
AUTHOR    GENERATED BY SYBYL, A PRODUCT OF TRIPOS, INC.
SEQRES    1 1 240 PRO ALA THR LEU PRO GLN LEU THR PRO THR LEU VAL SER
SEQRES    2 1 240 LEU LEU GLU VAL ILE GLU PRO GLU VAL LEU TYR ALA GLY
SEQRES    3 1 240 TYR ASP SER SER VAL PRO ASP SER THR TRP ARG ILE MET
SEQRES    4 1 240 THR THR LEU ASN MET LEU GLY GLY ARG GLN VAL ILE ALA
SEQRES    5 1 240 ALA VAL LYS TRP ALA LYS ALA ILE PRO GLY PHE ARG ASN
SEQRES    6 1 240 LEU HIS LEU ASP ASP GLN MET THR LEU LEU GLN TYR SER
SEQRES    7 1 240 TRP MET PHE LEU MET ALA PHE ALA LEU GLY TRP ARG SER
SEQRES    8 1 240 TYR ARG GLN SER SER ALA ASN LEU LEU CYS PHE ALA PRO
SEQRES    9 1 240 ASP LEU ILE ILE ASN GLU GLN ARG MET THR LEU PRO CYS
SEQRES    10 1 240 MET TYR ASP GLN CYS LYS HIS MET LEU TYR VAL SER SER
SEQRES    11 1 240 GLU LEU HIS ARG LEU GLN VAL SER TYR GLU GLU TYR LEU
SEQRES    12 1 240 CYS MET LYS THR LEU LEU LEU LEU SER SER VAL PRO LYS
SEQRES    13 1 240 ASP GLY LEU LYS SER GLN GLU LEU PHE ASP GLU ILE ARG
SEQRES    14 1 240 MET THR TYR ILE LYS GLU LEU GLY LYS ALA ILE VAL LYS
SEQRES    15 1 240 ARG GLU GLY ASN SER SER GLN ASN TRP GLN ARG PHE TYR
SEQRES    16 1 240 GLN LEU THR LYS LEU LEU ASP SER MET HIS GLU VAL VAL
SEQRES    17 1 240 GLU ASN LEU LEU ASN TYR CYS PHE GLN THR PHE LEU ASP
SEQRES    18 1 240 LYS THR MET SER ILE GLU PHE PRO GLU MET LEU ALA GLU
SEQRES    19 1 240 ILE ILE THR ASN GLN ILE
ATOM       1 N PRO 1 522 -16.028 23.289 -6.590 1.00 0.53
ATOM       2 CA PRO 1 522 -14.607 22.883 -6.755 1.00 0.53
ATOM       3 C PRO 1 522 -13.778 23.929 -6.090 1.00 0.53
ATOM       4 O PRO 1 522 -13.771 25.067 -6.553 1.00 0.53
ATOM       5 CB PRO 1 522 -14.354 22.795 -8.259 1.00 0.53
ATOM       6 CG PRO 1 522 -15.411 23.713 -8.885 1.00 0.53
ATOM       7 CD PRO 1 522 -16.614 23.612 -7.935 1.00 0.53
ATOM       8 N ALA 1 523 -13.092 23.572 -4.988 1.00 0.45
ATOM       9 CA ALA 1 523 -12.249 24.517 -4.317 1.00 0.45
ATOM      10 C ALA 1 523 -11.040 23.762 -3.879 1.00 0.45
ATOM      11 O ALA 1 523 -10.754 23.666 -2.687 1.00 0.45
ATOM      12 CB ALA 1 523 -12.896 25.104 -3.051 1.00 0.45
ATOM      13 N THR 1 524 -10.294 23.202 -4.846 1.00 0.32
ATOM      14 CA THR 1 524 -9.142 22.418 -4.509 1.00 0.32
ATOM      15 C THR 1 524 -8.086 23.314 -3.949 1.00 0.32
ATOM      16 O THR 1 524 -7.626 23.140 -2.823 1.00 0.32
ATOM      17 CB THR 1 524 -8.553 21.728 -5.703 1.00 0.32
ATOM      18 OG1 THR 1 524 -9.511 20.859 -6.289 1.00 0.32
ATOM      19 CG2 THR 1 524 -7.316 20.931 -5.257 1.00 0.32
ATOM      20 N LEU 1 525 -7.686 24.309 -4.755 1.00 0.35
ATOM      21 CA LEU 1 525 -6.691 25.285 -4.414 1.00 0.35
ATOM      22 C LEU 1 525 -7.181 26.176 -3.307 1.00 0.35
ATOM      23 O LEU 1 525 -6.374 26.650 -2.509 1.00 0.35
ATOM      24 CB LEU 1 525 -6.316 26.182 -5.605 1.00 0.35
ATOM      25 CG LEU 1 525 -5.676 25.395 -6.764 1.00 0.35
ATOM      26 CD1 LEU 1 525 -5.297 26.322 -7.929 1.00 0.35
ATOM      27 CD2 LEU 1 525 -4.502 24.534 -6.267 1.00 0.35
ATOM      28 N PRO 1 526 -8.450 26.471 -3.226 1.00 0.52
ATOM      29 CA PRO 1 526 -8.883 27.338 -2.161 1.00 0.52
ATOM      30 C PRO 1 526 -8.844 26.769 -0.776 1.00 0.52
ATOM      31 O PRO 1 526 -9.013 27.542 0.166 1.00 0.52
ATOM      32 CB PRO 1 526 -10.267 27.842 -2.564 1.00 0.52
ATOM      33 CG PRO 1 526 -10.218 27.841 -4.098 1.00 0.52
ATOM      34 CD PRO 1 526 -9.224 26.723 -4.438 1.00 0.52
ATOM      35 N GLN 1 527 -8.645 25.450 -0.600 1.00 0.57
ATOM      36 CA GLN 1 527 -8.683 24.919 0.734 1.00 0.57
ATOM      37 C GLN 1 527 -7.482 25.412 1.476 1.00 0.57
ATOM      38 O GLN 1 527 -6.393 25.495 0.914 1.00 0.57
ATOM      39 CB GLN 1 527 -8.653 23.380 0.770 1.00 0.57

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ATOM	40	CG	GLN 1 527	-9.756	22.711	-0.059	1.00	0.57
ATOM	41	CD	GLN 1 527	-11.110	22.880	0.620	1.00	0.57
ATOM	42	OE1	GLN 1 527	-12.023	22.093	0.375	1.00	0.57
ATOM	43	NE2	GLN 1 527	-11.257	23.918	1.487	1.00	0.57
ATOM	44	N	LEU 1 528	-7.636	25.784	2.763	1.00	0.58
ATOM	45	CA	LEU 1 528	-6.462	26.195	3.479	1.00	0.58
ATOM	46	C	LEU 1 528	-5.801	24.950	3.965	1.00	0.58
ATOM	47	O	LEU 1 528	-6.331	23.854	3.792	1.00	0.58
ATOM	48	CB	LEU 1 528	-6.675	27.159	4.667	1.00	0.58
ATOM	49	CG	LEU 1 528	-7.694	26.722	5.733	1.00	0.58
ATOM	50	CD1	LEU 1 528	-7.801	27.774	6.850	1.00	0.58
ATOM	51	CD2	LEU 1 528	-9.065	26.444	5.109	1.00	0.58
ATOM	52	N	THR 1 529	-4.612	25.079	4.583	1.00	0.58
ATOM	53	CA	THR 1 529	-3.936	23.879	4.963	1.00	0.58
ATOM	54	C	THR 1 529	-4.770	23.095	5.934	1.00	0.58
ATOM	55	O	THR 1 529	-4.788	21.870	5.819	1.00	0.58
ATOM	56	CB	THR 1 529	-2.501	24.061	5.426	1.00	0.58
ATOM	57	OG1	THR 1 529	-1.946	22.797	5.757	1.00	0.58
ATOM	58	CG2	THR 1 529	-2.363	25.038	6.602	1.00	0.58
ATOM	59	N	PRO 1 530	-5.490	23.667	6.870	1.00	0.40
ATOM	60	CA	PRO 1 530	-6.256	22.847	7.763	1.00	0.40
ATOM	61	C	PRO 1 530	-7.366	22.137	7.055	1.00	0.40
ATOM	62	O	PRO 1 530	-7.691	21.014	7.434	1.00	0.40
ATOM	63	CB	PRO 1 530	-6.764	23.777	8.864	1.00	0.40
ATOM	64	CG	PRO 1 530	-5.753	24.936	8.868	1.00	0.40
ATOM	65	CD	PRO 1 530	-5.255	24.995	7.414	1.00	0.40
ATOM	66	N	THR 1 531	-7.983	22.770	6.042	1.00	0.29
ATOM	67	CA	THR 1 531	-9.075	22.121	5.380	1.00	0.29
ATOM	68	C	THR 1 531	-8.576	20.949	4.613	1.00	0.29
ATOM	69	O	THR 1 531	-9.227	19.906	4.578	1.00	0.29
ATOM	70	CB	THR 1 531	-9.836	22.998	4.432	1.00	0.29
ATOM	71	OG1	THR 1 531	-10.469	24.049	5.145	1.00	0.29
ATOM	72	CG2	THR 1 531	-10.891	22.143	3.711	1.00	0.29
ATOM	73	N	LEU 1 532	-7.401	21.081	3.976	1.00	0.43
ATOM	74	CA	LEU 1 532	-6.959	19.997	3.159	1.00	0.43
ATOM	75	C	LEU 1 532	-6.677	18.816	4.031	1.00	0.43
ATOM	76	O	LEU 1 532	-7.015	17.685	3.683	1.00	0.43
ATOM	77	CB	LEU 1 532	-5.747	20.340	2.265	1.00	0.43
ATOM	78	CG	LEU 1 532	-4.353	20.319	2.913	1.00	0.43
ATOM	79	CD1	LEU 1 532	-3.873	18.879	3.165	1.00	0.43
ATOM	80	CD2	LEU 1 532	-3.361	21.138	2.069	1.00	0.43
ATOM	81	N	VAL 1 533	-6.067	19.049	5.209	1.00	0.49
ATOM	82	CA	VAL 1 533	-5.715	17.947	6.056	1.00	0.49
ATOM	83	C	VAL 1 533	-6.944	17.239	6.527	1.00	0.49
ATOM	84	O	VAL 1 533	-6.973	16.010	6.589	1.00	0.49
ATOM	85	CB	VAL 1 533	-4.900	18.342	7.257	1.00	0.49
ATOM	86	CG1	VAL 1 533	-5.708	19.275	8.167	1.00	0.49
ATOM	87	CG2	VAL 1 533	-4.467	17.053	7.963	1.00	0.49
ATOM	88	N	SER 1 534	-7.991	18.003	6.879	1.00	0.55
ATOM	89	CA	SER 1 534	-9.207	17.441	7.387	1.00	0.55
ATOM	90	C	SER 1 534	-9.854	16.647	6.309	1.00	0.55
ATOM	91	O	SER 1 534	-10.263	15.505	6.523	1.00	0.55
ATOM	92	CB	SER 1 534	-10.207	18.537	7.772	1.00	0.55
ATOM	93	OG	SER 1 534	-9.571	19.462	8.638	1.00	0.55
ATOM	94	N	LEU 1 535	-9.927	17.235	5.100	1.00	0.57
ATOM	95	CA	LEU 1 535	-10.614	16.574	4.038	1.00	0.57
ATOM	96	C	LEU 1 535	-9.930	15.269	3.823	1.00	0.57
ATOM	97	O	LEU 1 535	-10.590	14.235	3.815	1.00	0.57
ATOM	98	CB	LEU 1 535	-10.646	17.394	2.728	1.00	0.57
ATOM	99	CG	LEU 1 535	-9.329	17.490	1.931	1.00	0.57
ATOM	100	CD1	LEU 1 535	-9.023	16.194	1.160	1.00	0.57

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ATOM	101	CD2 LEU 1 535	-9.326	18.725	1.017	1.00	0.57
ATOM	102	N LEU 1 536	-8.585	15.266	3.780	1.00	0.36
ATOM	103	CA LEU 1 536	-7.854	14.065	3.497	1.00	0.36
ATOM	104	C LEU 1 536	-8.202	13.040	4.523	1.00	0.36
ATOM	105	O LEU 1 536	-8.454	11.880	4.202	1.00	0.36
ATOM	106	CB LEU 1 536	-6.330	14.267	3.528	1.00	0.36
ATOM	107	CG LEU 1 536	-5.795	15.178	2.406	1.00	0.36
ATOM	108	CD1 LEU 1 536	-4.268	15.327	2.499	1.00	0.36
ATOM	109	CD2 LEU 1 536	-6.252	14.697	1.019	1.00	0.36
ATOM	110	N GLU 1 537	-8.286	13.471	5.789	1.00	0.30
ATOM	111	CA GLU 1 537	-8.523	12.577	6.880	1.00	0.30
ATOM	112	C GLU 1 537	-9.791	11.829	6.603	1.00	0.30
ATOM	113	O GLU 1 537	-9.855	10.616	6.795	1.00	0.30
ATOM	114	CB GLU 1 537	-8.758	13.357	8.187	1.00	0.30
ATOM	115	CG GLU 1 537	-7.578	14.236	8.617	1.00	0.30
ATOM	116	CD GLU 1 537	-6.858	13.565	9.776	1.00	0.30
ATOM	117	OE1 GLU 1 537	-7.484	12.693	10.434	1.00	0.30
ATOM	118	OE2 GLU 1 537	-5.676	13.924	10.026	1.00	0.30
ATOM	119	N VAL 1 538	-10.840	12.536	6.138	1.00	0.42
ATOM	120	CA VAL 1 538	-12.105	11.892	5.920	1.00	0.42
ATOM	121	C VAL 1 538	-12.006	10.913	4.790	1.00	0.42
ATOM	122	O VAL 1 538	-12.638	9.860	4.833	1.00	0.42
ATOM	123	CB VAL 1 538	-13.248	12.823	5.614	1.00	0.42
ATOM	124	CG1 VAL 1 538	-13.139	13.335	4.172	1.00	0.42
ATOM	125	CG2 VAL 1 538	-14.561	12.066	5.876	1.00	0.42
ATOM	126	N ILE 1 539	-11.197	11.220	3.755	1.00	0.45
ATOM	127	CA ILE 1 539	-11.156	10.375	2.592	1.00	0.45
ATOM	128	C ILE 1 539	-10.713	9.001	2.955	1.00	0.45
ATOM	129	O ILE 1 539	-11.189	8.053	2.331	1.00	0.45
ATOM	130	CB ILE 1 539	-10.184	10.755	1.482	1.00	0.45
ATOM	131	CG1 ILE 1 539	-10.455	12.113	0.848	1.00	0.45
ATOM	132	CG2 ILE 1 539	-10.253	9.685	0.381	1.00	0.45
ATOM	133	CD1 ILE 1 539	-9.752	13.325	1.403	1.00	0.45
ATOM	134	N GLU 1 540	-9.802	8.870	3.950	1.00	0.40
ATOM	135	CA GLU 1 540	-9.162	7.620	4.284	1.00	0.40
ATOM	136	C GLU 1 540	-10.111	6.470	4.207	1.00	0.40
ATOM	137	O GLU 1 540	-11.258	6.517	4.643	1.00	0.40
ATOM	138	CB GLU 1 540	-8.435	7.601	5.638	1.00	0.40
ATOM	139	CG GLU 1 540	-7.105	8.365	5.615	1.00	0.40
ATOM	140	CD GLU 1 540	-6.012	7.490	5.001	1.00	0.40
ATOM	141	OE1 GLU 1 540	-5.911	7.472	3.745	1.00	0.40
ATOM	142	OE2 GLU 1 540	-5.264	6.835	5.776	1.00	0.40
ATOM	143	N PRO 1 541	-9.627	5.476	3.519	1.00	0.41
ATOM	144	CA PRO 1 541	-10.361	4.273	3.259	1.00	0.41
ATOM	145	C PRO 1 541	-10.454	3.492	4.522	1.00	0.41
ATOM	146	O PRO 1 541	-9.655	3.728	5.426	1.00	0.41
ATOM	147	CB PRO 1 541	-9.593	3.541	2.157	1.00	0.41
ATOM	148	CG PRO 1 541	-8.192	4.181	2.174	1.00	0.41
ATOM	149	CD PRO 1 541	-8.451	5.609	2.679	1.00	0.41
ATOM	150	N GLU 1 542	-11.438	2.578	4.608	1.00	0.55
ATOM	151	CA GLU 1 542	-11.611	1.777	5.784	1.00	0.55
ATOM	152	C GLU 1 542	-10.650	0.635	5.706	1.00	0.55
ATOM	153	O GLU 1 542	-10.161	0.290	4.632	1.00	0.55
ATOM	154	CB GLU 1 542	-13.021	1.175	5.913	1.00	0.55
ATOM	155	CG GLU 1 542	-13.381	0.217	4.774	1.00	0.55
ATOM	156	CD GLU 1 542	-13.569	1.035	3.503	1.00	0.55
ATOM	157	OE1 GLU 1 542	-13.850	2.258	3.621	1.00	0.55
ATOM	158	OE2 GLU 1 542	-13.435	0.446	2.398	1.00	0.55
ATOM	159	N VAL 1 543	-10.345	0.019	6.866	1.00	0.62
ATOM	160	CA VAL 1 543	-9.445	-1.094	6.867	1.00	0.62
ATOM	161	C VAL 1 543	-10.277	-2.304	6.592	1.00	0.62

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ATOM	162	O	VAL 1 543	-11.280	-2.557	7.257	1.00	0.62
ATOM	163	CB	VAL 1 543	-8.728	-1.292	8.174	1.00	0.62
ATOM	164	CG1	VAL 1 543	-7.825	-0.070	8.417	1.00	0.62
ATOM	165	CG2	VAL 1 543	-9.761	-1.519	9.291	1.00	0.62
ATOM	166	N	LEU 1 544	-9.879	-3.078	5.568	1.00	0.55
ATOM	167	CA	LEU 1 544	-10.688	-4.183	5.156	1.00	0.55
ATOM	168	C	LEU 1 544	-10.086	-5.420	5.775	1.00	0.55
ATOM	169	O	LEU 1 544	-8.950	-5.384	6.242	1.00	0.55
ATOM	170	CB	LEU 1 544	-10.673	-4.279	3.619	1.00	0.55
ATOM	171	CG	LEU 1 544	-11.936	-4.888	2.996	1.00	0.55
ATOM	172	CD1	LEU 1 544	-12.128	-6.370	3.323	1.00	0.55
ATOM	173	CD2	LEU 1 544	-13.153	-4.023	3.367	1.00	0.55
ATOM	174	N	TYR 1 545	-10.839	-6.543	5.819	1.00	0.30
ATOM	175	CA	TYR 1 545	-10.348	-7.774	6.387	1.00	0.30
ATOM	176	C	TYR 1 545	-10.140	-8.792	5.312	1.00	0.30
ATOM	177	O	TYR 1 545	-10.716	-8.721	4.228	1.00	0.30
ATOM	178	CB	TYR 1 545	-11.290	-8.448	7.403	1.00	0.30
ATOM	179	CG	TYR 1 545	-11.220	-7.730	8.701	1.00	0.30
ATOM	180	CD1	TYR 1 545	-11.929	-6.571	8.912	1.00	0.30
ATOM	181	CD2	TYR 1 545	-10.443	-8.236	9.719	1.00	0.30
ATOM	182	CE1	TYR 1 545	-11.858	-5.921	10.122	1.00	0.30
ATOM	183	CE2	TYR 1 545	-10.367	-7.590	10.930	1.00	0.30
ATOM	184	CZ	TYR 1 545	-11.075	-6.429	11.131	1.00	0.30
ATOM	185	OH	TYR 1 545	-11.002	-5.762	12.372	1.00	0.30
ATOM	186	N	ALA 1 546	-9.278	-9.785	5.615	1.00	0.14
ATOM	187	CA	ALA 1 546	-8.982	-10.841	4.694	1.00	0.14
ATOM	188	C	ALA 1 546	-10.145	-11.770	4.684	1.00	0.14
ATOM	189	O	ALA 1 546	-10.982	-11.740	5.587	1.00	0.14
ATOM	190	CB	ALA 1 546	-7.738	-11.662	5.083	1.00	0.14
ATOM	191	N	GLY 1 547	-10.216	-12.613	3.630	1.00	0.34
ATOM	192	CA	GLY 1 547	-11.275	-13.568	3.511	1.00	0.34
ATOM	193	C	GLY 1 547	-11.244	-14.321	4.785	1.00	0.34
ATOM	194	O	GLY 1 547	-10.171	-14.684	5.265	1.00	0.34
ATOM	195	N	TYR 1 548	-12.449	-14.541	5.345	1.00	0.58
ATOM	196	CA	TYR 1 548	-12.684	-15.135	6.626	1.00	0.58
ATOM	197	C	TYR 1 548	-11.775	-16.315	6.726	1.00	0.58
ATOM	198	O	TYR 1 548	-11.435	-16.897	5.699	1.00	0.58
ATOM	199	CB	TYR 1 548	-14.140	-15.607	6.753	1.00	0.58
ATOM	200	CG	TYR 1 548	-14.519	-15.633	8.188	1.00	0.58
ATOM	201	CD1	TYR 1 548	-14.196	-16.688	9.009	1.00	0.58
ATOM	202	CD2	TYR 1 548	-15.222	-14.569	8.705	1.00	0.58
ATOM	203	CE1	TYR 1 548	-14.573	-16.672	10.332	1.00	0.58
ATOM	204	CE2	TYR 1 548	-15.600	-14.550	10.024	1.00	0.58
ATOM	205	CZ	TYR 1 548	-15.276	-15.605	10.840	1.00	0.58
ATOM	206	OH	TYR 1 548	-15.663	-15.589	12.197	1.00	0.58
ATOM	207	N	ASP 1 549	-11.358	-16.651	7.969	1.00	0.54
ATOM	208	CA	ASP 1 549	-10.379	-17.663	8.288	1.00	0.54
ATOM	209	C	ASP 1 549	-10.510	-18.822	7.361	1.00	0.54
ATOM	210	O	ASP 1 549	-11.474	-19.585	7.410	1.00	0.54
ATOM	211	CB	ASP 1 549	-10.504	-18.197	9.724	1.00	0.54
ATOM	212	CG	ASP 1 549	-9.269	-19.029	10.034	1.00	0.54
ATOM	213	OD1	ASP 1 549	-8.168	-18.659	9.548	1.00	0.54
ATOM	214	OD2	ASP 1 549	-9.412	-20.054	10.752	1.00	0.54
ATOM	215	N	SER 1 550	-9.516	-18.955	6.468	1.00	0.52
ATOM	216	CA	SER 1 550	-9.517	-19.997	5.491	1.00	0.52
ATOM	217	C	SER 1 550	-8.795	-21.150	6.105	1.00	0.52
ATOM	218	O	SER 1 550	-9.384	-21.939	6.843	1.00	0.52
ATOM	219	CB	SER 1 550	-8.791	-19.574	4.201	1.00	0.52
ATOM	220	OG	SER 1 550	-9.124	-20.448	3.134	1.00	0.52
ATOM	221	N	SER 1 551	-7.485	-21.273	5.821	1.00	0.82
ATOM	222	CA	SER 1 551	-6.734	-22.361	6.369	1.00	0.82

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ATOM	223	C	SER 1 551	-5.454	-21.817	6.918	1.00	0.82
ATOM	224	O	SER 1 551	-4.927	-20.803	6.454	1.00	0.82
ATOM	225	CB	SER 1 551	-6.370	-23.444	5.341	1.00	0.82
ATOM	226	OG	SER 1 551	-5.631	-24.481	5.968	1.00	0.82
ATOM	227	N	VAL 1 552	-4.895	-22.551	7.898	1.00	1.25
ATOM	228	CA	VAL 1 552	-3.740	-22.163	8.639	1.00	1.25
ATOM	229	C	VAL 1 552	-2.505	-22.265	7.824	1.00	1.25
ATOM	230	O	VAL 1 552	-2.276	-21.246	7.175	1.00	1.25
ATOM	231	CB	VAL 1 552	-3.665	-22.788	10.017	1.00	1.25
ATOM	232	CG1	VAL 1 552	-4.317	-24.185	10.023	1.00	1.25
ATOM	233	CG2	VAL 1 552	-2.212	-22.736	10.521	1.00	1.25
ATOM	234	N	PRO 1 553	-1.656	-23.294	7.852	1.00	1.24
ATOM	235	CA	PRO 1 553	-0.494	-23.299	7.002	1.00	1.24
ATOM	236	C	PRO 1 553	-1.006	-23.041	5.633	1.00	1.24
ATOM	237	O	PRO 1 553	-1.720	-23.877	5.077	1.00	1.24
ATOM	238	CB	PRO 1 553	0.109	-24.700	7.080	1.00	1.24
ATOM	239	CG	PRO 1 553	-0.775	-25.455	8.087	1.00	1.24
ATOM	240	CD	PRO 1 553	-2.092	-24.663	8.072	1.00	1.24
ATOM	241	N	ASP 1 554	-0.651	-21.875	5.086	1.00	0.74
ATOM	242	CA	ASP 1 554	-1.205	-21.454	3.852	1.00	0.74
ATOM	243	C	ASP 1 554	-0.299	-22.024	2.812	1.00	0.74
ATOM	244	O	ASP 1 554	0.819	-22.433	3.122	1.00	0.74
ATOM	245	CB	ASP 1 554	-1.198	-19.915	3.772	1.00	0.74
ATOM	246	CG	ASP 1 554	-2.288	-19.460	2.829	1.00	0.74
ATOM	247	OD1	ASP 1 554	-2.369	-20.056	1.729	1.00	0.74
ATOM	248	OD2	ASP 1 554	-3.047	-18.523	3.186	1.00	0.74
ATOM	249	N	SER 1 555	-0.788	-22.127	1.566	1.00	0.52
ATOM	250	CA	SER 1 555	0.017	-22.585	0.482	1.00	0.52
ATOM	251	C	SER 1 555	0.411	-21.346	-0.245	1.00	0.52
ATOM	252	O	SER 1 555	-0.037	-20.255	0.102	1.00	0.52
ATOM	253	CB	SER 1 555	-0.745	-23.477	-0.511	1.00	0.52
ATOM	254	OG	SER 1 555	0.119	-23.884	-1.560	1.00	0.52
ATOM	255	N	THR 1 556	1.283	-21.469	-1.261	1.00	0.67
ATOM	256	CA	THR 1 556	1.635	-20.279	-1.968	1.00	0.67
ATOM	257	C	THR 1 556	0.398	-19.746	-2.613	1.00	0.67
ATOM	258	O	THR 1 556	0.010	-18.605	-2.377	1.00	0.67
ATOM	259	CB	THR 1 556	2.656	-20.525	-3.041	1.00	0.67
ATOM	260	OG1	THR 1 556	2.149	-21.432	-4.009	1.00	0.67
ATOM	261	CG2	THR 1 556	3.923	-21.104	-2.388	1.00	0.67
ATOM	262	N	TRP 1 557	-0.301	-20.612	-3.368	1.00	0.70
ATOM	263	CA	TRP 1 557	-1.440	-20.245	-4.162	1.00	0.70
ATOM	264	C	TRP 1 557	-2.526	-19.719	-3.283	1.00	0.70
ATOM	265	O	TRP 1 557	-3.155	-18.706	-3.583	1.00	0.70
ATOM	266	CB	TRP 1 557	-1.997	-21.469	-4.910	1.00	0.70
ATOM	267	CG	TRP 1 557	-3.196	-21.218	-5.788	1.00	0.70
ATOM	268	CD1	TRP 1 557	-4.524	-21.206	-5.474	1.00	0.70
ATOM	269	CD2	TRP 1 557	-3.109	-20.981	-7.202	1.00	0.70
ATOM	270	NE1	TRP 1 557	-5.270	-20.973	-6.604	1.00	0.70
ATOM	271	CE2	TRP 1 557	-4.412	-20.834	-7.676	1.00	0.70
ATOM	272	CE3	TRP 1 557	-2.032	-20.898	-8.037	1.00	0.70
ATOM	273	CZ2	TRP 1 557	-4.659	-20.602	-8.999	1.00	0.70
ATOM	274	CZ3	TRP 1 557	-2.284	-20.658	-9.369	1.00	0.70
ATOM	275	CH2	TRP 1 557	-3.572	-20.513	-9.841	1.00	0.70
ATOM	276	N	ARG 1 558	-2.761	-20.403	-2.156	1.00	0.62
ATOM	277	CA	ARG 1 558	-3.840	-20.090	-1.271	1.00	0.62
ATOM	278	C	ARG 1 558	-3.595	-18.732	-0.674	1.00	0.62
ATOM	279	O	ARG 1 558	-4.516	-17.927	-0.531	1.00	0.62
ATOM	280	CB	ARG 1 558	-3.922	-21.191	-0.201	1.00	0.62
ATOM	281	CG	ARG 1 558	-5.283	-21.459	0.429	1.00	0.62
ATOM	282	CD	ARG 1 558	-5.232	-22.749	1.249	1.00	0.62
ATOM	283	NE	ARG 1 558	-6.617	-23.150	1.607	1.00	0.62

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ATOM	284	CZ	ARG	1 558	-7.220	-22.547	2.666	1.00	0.62
ATOM	285	NH1	ARG	1 558	-6.619	-21.461	3.233	1.00	0.62
ATOM	286	NH2	ARG	1 558	-8.394	-23.043	3.159	1.00	0.62
ATOM	287	N	ILE	1 559	-2.328	-18.441	-0.319	1.00	0.68
ATOM	288	CA	ILE	1 559	-1.993	-17.195	0.305	1.00	0.68
ATOM	289	C	ILE	1 559	-2.140	-16.110	-0.727	1.00	0.68
ATOM	290	O	ILE	1 559	-2.665	-15.035	-0.434	1.00	0.68
ATOM	291	CB	ILE	1 559	-0.591	-17.232	0.870	1.00	0.68
ATOM	292	CG1	ILE	1 559	-0.472	-16.357	2.130	1.00	0.68
ATOM	293	CG2	ILE	1 559	0.421	-16.889	-0.235	1.00	0.68
ATOM	294	CD1	ILE	1 559	-0.907	-14.910	1.959	1.00	0.68
ATOM	295	N	MET	1 560	-1.714	-16.347	-1.989	1.00	0.55
ATOM	296	CA	MET	1 560	-1.890	-15.270	-2.919	1.00	0.55
ATOM	297	C	MET	1 560	-3.342	-15.050	-3.136	1.00	0.55
ATOM	298	O	MET	1 560	-3.758	-13.942	-3.463	1.00	0.55
ATOM	299	CB	MET	1 560	-1.182	-15.317	-4.293	1.00	0.55
ATOM	300	CG	MET	1 560	-1.169	-16.608	-5.100	1.00	0.55
ATOM	301	SD	MET	1 560	0.410	-17.486	-4.965	1.00	0.55
ATOM	302	CE	MET	1 560	1.404	-15.974	-5.136	1.00	0.55
ATOM	303	N	THR	1 561	-4.159	-16.104	-2.982	1.00	0.35
ATOM	304	CA	THR	1 561	-5.567	-15.934	-3.165	1.00	0.35
ATOM	305	C	THR	1 561	-6.036	-14.922	-2.169	1.00	0.35
ATOM	306	O	THR	1 561	-6.763	-13.993	-2.519	1.00	0.35
ATOM	307	CB	THR	1 561	-6.332	-17.202	-2.922	1.00	0.35
ATOM	308	OG1	THR	1 561	-5.891	-18.216	-3.812	1.00	0.35
ATOM	309	CG2	THR	1 561	-7.829	-16.923	-3.138	1.00	0.35
ATOM	310	N	THR	1 562	-5.616	-15.058	-0.897	1.00	0.42
ATOM	311	CA	THR	1 562	-6.088	-14.116	0.072	1.00	0.42
ATOM	312	C	THR	1 562	-5.571	-12.755	-0.281	1.00	0.42
ATOM	313	O	THR	1 562	-6.331	-11.790	-0.291	1.00	0.42
ATOM	314	CB	THR	1 562	-5.697	-14.444	1.491	1.00	0.42
ATOM	315	OG1	THR	1 562	-6.420	-13.617	2.390	1.00	0.42
ATOM	316	CG2	THR	1 562	-4.189	-14.233	1.693	1.00	0.42
ATOM	317	N	LEU	1 563	-4.274	-12.628	-0.630	1.00	0.48
ATOM	318	CA	LEU	1 563	-3.812	-11.295	-0.893	1.00	0.48
ATOM	319	C	LEU	1 563	-4.507	-10.730	-2.086	1.00	0.48
ATOM	320	O	LEU	1 563	-4.833	-9.546	-2.102	1.00	0.48
ATOM	321	CB	LEU	1 563	-2.312	-11.103	-1.184	1.00	0.48
ATOM	322	CG	LEU	1 563	-1.359	-11.510	-0.054	1.00	0.48
ATOM	323	CD1	LEU	1 563	-0.892	-12.955	-0.232	1.00	0.48
ATOM	324	CD2	LEU	1 563	-0.222	-10.500	0.130	1.00	0.48
ATOM	325	N	ASN	1 564	-4.738	-11.543	-3.133	1.00	0.45
ATOM	326	CA	ASN	1 564	-5.334	-10.982	-4.308	1.00	0.45
ATOM	327	C	ASN	1 564	-6.723	-10.530	-3.997	1.00	0.45
ATOM	328	O	ASN	1 564	-7.157	-9.479	-4.468	1.00	0.45
ATOM	329	CB	ASN	1 564	-5.342	-11.908	-5.547	1.00	0.45
ATOM	330	CG	ASN	1 564	-6.153	-13.175	-5.323	1.00	0.45
ATOM	331	OD1	ASN	1 564	-7.341	-13.161	-5.012	1.00	0.45
ATOM	332	ND2	ASN	1 564	-5.478	-14.336	-5.537	1.00	0.45
ATOM	333	N	MET	1 565	-7.457	-11.302	-3.178	1.00	0.57
ATOM	334	CA	MET	1 565	-8.801	-10.924	-2.869	1.00	0.57
ATOM	335	C	MET	1 565	-8.751	-9.606	-2.162	1.00	0.57
ATOM	336	O	MET	1 565	-9.518	-8.697	-2.478	1.00	0.57
ATOM	337	CB	MET	1 565	-9.497	-11.922	-1.926	1.00	0.57
ATOM	338	CG	MET	1 565	-9.752	-13.294	-2.552	1.00	0.57
ATOM	339	SD	MET	1 565	-11.044	-13.308	-3.832	1.00	0.57
ATOM	340	CE	MET	1 565	-12.418	-13.115	-2.659	1.00	0.57
ATOM	341	N	LEU	1 566	-7.810	-9.457	-1.207	1.00	0.62
ATOM	342	CA	LEU	1 566	-7.746	-8.253	-0.424	1.00	0.62
ATOM	343	C	LEU	1 566	-7.560	-7.082	-1.330	1.00	0.62
ATOM	344	O	LEU	1 566	-8.369	-6.156	-1.346	1.00	0.62

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ATOM	345	CB	LEU	1 566	-6.494	-8.156	0.468	1.00	0.62
ATOM	346	CG	LEU	1 566	-6.327	-9.185	1.593	1.00	0.62
ATOM	347	CD1	LEU	1 566	-5.025	-8.912	2.356	1.00	0.62
ATOM	348	CD2	LEU	1 566	-7.526	-9.206	2.544	1.00	0.62
ATOM	349	N	GLY	1 567	-6.508	-7.138	-2.163	1.00	0.32
ATOM	350	CA	GLY	1 567	-6.125	-6.004	-2.951	1.00	0.32
ATOM	351	C	GLY	1 567	-7.264	-5.586	-3.817	1.00	0.32
ATOM	352	O	GLY	1 567	-7.508	-4.391	-3.993	1.00	0.32
ATOM	353	N	GLY	1 568	-7.985	-6.561	-4.396	1.00	0.15
ATOM	354	CA	GLY	1 568	-9.067	-6.225	-5.273	1.00	0.15
ATOM	355	C	GLY	1 568	-10.115	-5.496	-4.497	1.00	0.15
ATOM	356	O	GLY	1 568	-10.693	-4.518	-4.966	1.00	0.15
ATOM	357	N	ARG	1 569	-10.416	-5.965	-3.279	1.00	0.29
ATOM	358	CA	ARG	1 569	-11.425	-5.314	-2.501	1.00	0.29
ATOM	359	C	ARG	1 569	-10.953	-3.935	-2.166	1.00	0.29
ATOM	360	O	ARG	1 569	-11.705	-2.966	-2.267	1.00	0.29
ATOM	361	CB	ARG	1 569	-11.706	-6.079	-1.199	1.00	0.29
ATOM	362	CG	ARG	1 569	-12.507	-7.367	-1.421	1.00	0.29
ATOM	363	CD	ARG	1 569	-12.352	-8.380	-0.287	1.00	0.29
ATOM	364	NE	ARG	1 569	-11.653	-7.671	0.816	1.00	0.29
ATOM	365	CZ	ARG	1 569	-10.466	-8.155	1.286	1.00	0.29
ATOM	366	NH1	ARG	1 569	-10.029	-9.385	0.889	1.00	0.29
ATOM	367	NH2	ARG	1 569	-9.718	-7.402	2.145	1.00	0.29
ATOM	368	N	GLN	1 570	-9.673	-3.797	-1.780	1.00	0.39
ATOM	369	CA	GLN	1 570	-9.166	-2.514	-1.394	1.00	0.39
ATOM	370	C	GLN	1 570	-9.169	-1.588	-2.572	1.00	0.39
ATOM	371	O	GLN	1 570	-9.385	-0.387	-2.413	1.00	0.39
ATOM	372	CB	GLN	1 570	-7.741	-2.554	-0.795	1.00	0.39
ATOM	373	CG	GLN	1 570	-7.646	-3.202	0.597	1.00	0.39
ATOM	374	CD	GLN	1 570	-6.226	-3.075	1.130	1.00	0.39
ATOM	375	OE1	GLN	1 570	-5.984	-2.404	2.132	1.00	0.39
ATOM	376	NE2	GLN	1 570	-5.255	-3.728	0.438	1.00	0.39
ATOM	377	N	VAL	1 571	-8.955	-2.114	-3.796	1.00	0.43
ATOM	378	CA	VAL	1 571	-8.860	-1.235	-4.928	1.00	0.43
ATOM	379	C	VAL	1 571	-10.133	-0.455	-5.052	1.00	0.43
ATOM	380	O	VAL	1 571	-10.111	0.714	-5.429	1.00	0.43
ATOM	381	CB	VAL	1 571	-8.624	-1.921	-6.244	1.00	0.43
ATOM	382	CG1	VAL	1 571	-9.932	-2.569	-6.721	1.00	0.43
ATOM	383	CG2	VAL	1 571	-8.070	-0.884	-7.233	1.00	0.43
ATOM	384	N	ILE	1 572	-11.286	-1.072	-4.735	1.00	0.36
ATOM	385	CA	ILE	1 572	-12.526	-0.363	-4.890	1.00	0.36
ATOM	386	C	ILE	1 572	-12.559	0.843	-3.992	1.00	0.36
ATOM	387	O	ILE	1 572	-12.992	1.917	-4.407	1.00	0.36
ATOM	388	CB	ILE	1 572	-13.750	-1.197	-4.607	1.00	0.36
ATOM	389	CG1	ILE	1 572	-15.002	-0.501	-5.160	1.00	0.36
ATOM	390	CG2	ILE	1 572	-13.842	-1.473	-3.099	1.00	0.36
ATOM	391	CD1	ILE	1 572	-16.238	-1.400	-5.177	1.00	0.36
ATOM	392	N	ALA	1 573	-12.095	0.712	-2.737	1.00	0.18
ATOM	393	CA	ALA	1 573	-12.146	1.810	-1.808	1.00	0.18
ATOM	394	C	ALA	1 573	-11.235	2.896	-2.281	1.00	0.18
ATOM	395	O	ALA	1 573	-11.529	4.080	-2.128	1.00	0.18
ATOM	396	CB	ALA	1 573	-11.693	1.413	-0.393	1.00	0.18
ATOM	397	N	ALA	1 574	-10.102	2.505	-2.886	1.00	0.10
ATOM	398	CA	ALA	1 574	-9.103	3.437	-3.319	1.00	0.10
ATOM	399	C	ALA	1 574	-9.701	4.372	-4.319	1.00	0.10
ATOM	400	O	ALA	1 574	-9.374	5.557	-4.339	1.00	0.10
ATOM	401	CB	ALA	1 574	-7.897	2.757	-3.989	1.00	0.10
ATOM	402	N	VAL	1 575	-10.594	3.861	-5.186	1.00	0.13
ATOM	403	CA	VAL	1 575	-11.188	4.703	-6.181	1.00	0.13
ATOM	404	C	VAL	1 575	-11.953	5.790	-5.492	1.00	0.13
ATOM	405	O	VAL	1 575	-11.871	6.956	-5.876	1.00	0.13

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ATOM	406	CB VAL 1 575	-12.150	3.966	-7.066	1.00	0.13
ATOM	407	CG1 VAL 1 575	-12.748	4.963	-8.073	1.00	0.13
ATOM	408	CG2 VAL 1 575	-11.410	2.787	-7.721	1.00	0.13
ATOM	409	N LYS 1 576	-12.708	5.434	-4.434	1.00	0.27
ATOM	410	CA LYS 1 576	-13.506	6.397	-3.726	1.00	0.27
ATOM	411	C LYS 1 576	-12.598	7.442	-3.153	1.00	0.27
ATOM	412	O LYS 1 576	-12.867	8.637	-3.244	1.00	0.27
ATOM	413	CB LYS 1 576	-14.254	5.786	-2.530	1.00	0.27
ATOM	414	CG LYS 1 576	-15.304	4.736	-2.900	1.00	0.27
ATOM	415	CD LYS 1 576	-15.768	3.912	-1.697	1.00	0.27
ATOM	416	CE LYS 1 576	-16.829	2.861	-2.034	1.00	0.27
ATOM	417	NZ LYS 1 576	-18.125	3.522	-2.303	1.00	0.27
ATOM	418	N TRP 1 577	-11.490	6.999	-2.532	1.00	0.34
ATOM	419	CA TRP 1 577	-10.507	7.863	-1.941	1.00	0.34
ATOM	420	C TRP 1 577	-9.883	8.746	-2.973	1.00	0.34
ATOM	421	O TRP 1 577	-9.815	9.963	-2.800	1.00	0.34
ATOM	422	CB TRP 1 577	-9.498	7.010	-1.129	1.00	0.34
ATOM	423	CG TRP 1 577	-8.000	7.274	-1.103	1.00	0.34
ATOM	424	CD1 TRP 1 577	-7.050	6.298	-1.185	1.00	0.34
ATOM	425	CD2 TRP 1 577	-7.281	8.520	-1.094	1.00	0.34
ATOM	426	NE1 TRP 1 577	-5.795	6.847	-1.172	1.00	0.34
ATOM	427	CE2 TRP 1 577	-5.919	8.214	-1.134	1.00	0.34
ATOM	428	CE3 TRP 1 577	-7.705	9.813	-1.069	1.00	0.34
ATOM	429	CZ2 TRP 1 577	-4.970	9.194	-1.145	1.00	0.34
ATOM	430	CZ3 TRP 1 577	-6.746	10.801	-1.073	1.00	0.34
ATOM	431	CH2 TRP 1 577	-5.403	10.498	-1.108	1.00	0.34
ATOM	432	N ALA 1 578	-9.500	8.184	-4.123	1.00	0.38
ATOM	433	CA ALA 1 578	-8.844	8.981	-5.119	1.00	0.38
ATOM	434	C ALA 1 578	-9.740	10.111	-5.529	1.00	0.38
ATOM	435	O ALA 1 578	-9.284	11.234	-5.737	1.00	0.38
ATOM	436	CB ALA 1 578	-8.500	8.174	-6.382	1.00	0.38
ATOM	437	N LYS 1 579	-11.054	9.855	-5.618	1.00	0.46
ATOM	438	CA LYS 1 579	-11.975	10.855	-6.081	1.00	0.46
ATOM	439	C LYS 1 579	-11.960	12.028	-5.153	1.00	0.46
ATOM	440	O LYS 1 579	-12.185	13.160	-5.567	1.00	0.46
ATOM	441	CB LYS 1 579	-13.420	10.341	-6.175	1.00	0.46
ATOM	442	CG LYS 1 579	-13.604	9.242	-7.225	1.00	0.46
ATOM	443	CD LYS 1 579	-13.276	9.676	-8.658	1.00	0.46
ATOM	444	CE LYS 1 579	-14.392	10.474	-9.336	1.00	0.46
ATOM	445	NZ LYS 1 579	-14.077	10.676	-10.769	1.00	0.46
ATOM	446	N ALA 1 580	-11.758	11.774	-3.855	1.00	0.43
ATOM	447	CA ALA 1 580	-11.760	12.785	-2.845	1.00	0.43
ATOM	448	C ALA 1 580	-10.472	13.579	-2.782	1.00	0.43
ATOM	449	O ALA 1 580	-10.416	14.609	-2.111	1.00	0.43
ATOM	450	CB ALA 1 580	-12.158	12.208	-1.493	1.00	0.43
ATOM	451	N ILE 1 581	-9.379	13.106	-3.418	1.00	0.38
ATOM	452	CA ILE 1 581	-8.121	13.804	-3.321	1.00	0.38
ATOM	453	C ILE 1 581	-8.170	15.059	-4.148	1.00	0.38
ATOM	454	O ILE 1 581	-8.457	15.055	-5.344	1.00	0.38
ATOM	455	CB ILE 1 581	-6.970	12.914	-3.708	1.00	0.38
ATOM	456	CG1 ILE 1 581	-5.622	13.452	-3.247	1.00	0.38
ATOM	457	CG2 ILE 1 581	-7.005	12.663	-5.211	1.00	0.38
ATOM	458	CD1 ILE 1 581	-4.559	12.380	-3.445	1.00	0.38
ATOM	459	N PRO 1 582	-7.861	16.159	-3.513	1.00	0.28
ATOM	460	CA PRO 1 582	-8.000	17.439	-4.147	1.00	0.28
ATOM	461	C PRO 1 582	-7.240	17.551	-5.426	1.00	0.28
ATOM	462	O PRO 1 582	-6.035	17.309	-5.439	1.00	0.28
ATOM	463	CB PRO 1 582	-7.651	18.469	-3.077	1.00	0.28
ATOM	464	CG PRO 1 582	-8.048	17.760	-1.764	1.00	0.28
ATOM	465	CD PRO 1 582	-7.884	16.257	-2.063	1.00	0.28
ATOM	466	N GLY 1 583	-7.948	17.938	-6.507	1.00	0.17

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ATOM	467	CA	GLY 1 583	-7.365	18.131	-7.802	1.00	0.17
ATOM	468	C	GLY 1 583	-7.628	16.926	-8.654	1.00	0.17
ATOM	469	O	GLY 1 583	-7.624	17.002	-9.880	1.00	0.17
ATOM	470	N	PHE 1 584	-7.905	15.780	-8.015	1.00	0.34
ATOM	471	CA	PHE 1 584	-8.062	14.534	-8.710	1.00	0.34
ATOM	472	C	PHE 1 584	-9.230	14.603	-9.654	1.00	0.34
ATOM	473	O	PHE 1 584	-9.114	14.236	-10.823	1.00	0.34
ATOM	474	CB	PHE 1 584	-8.349	13.418	-7.697	1.00	0.34
ATOM	475	CG	PHE 1 584	-7.943	12.078	-8.200	1.00	0.34
ATOM	476	CD1	PHE 1 584	-6.610	11.776	-8.364	1.00	0.34
ATOM	477	CD2	PHE 1 584	-8.882	11.106	-8.446	1.00	0.34
ATOM	478	CE1	PHE 1 584	-6.221	10.535	-8.807	1.00	0.34
ATOM	479	CE2	PHE 1 584	-8.498	9.865	-8.885	1.00	0.34
ATOM	480	CZ	PHE 1 584	-7.168	9.577	-9.072	1.00	0.34
ATOM	481	N	ARG 1 585	-10.384	15.099	-9.174	1.00	0.46
ATOM	482	CA	ARG 1 585	-11.600	15.107	-9.947	1.00	0.46
ATOM	483	C	ARG 1 585	-11.539	16.089	-11.077	1.00	0.46
ATOM	484	O	ARG 1 585	-12.288	15.959	-12.041	1.00	0.46
ATOM	485	CB	ARG 1 585	-12.877	15.408	-9.147	1.00	0.46
ATOM	486	CG	ARG 1 585	-12.958	16.807	-8.540	1.00	0.46
ATOM	487	CD	ARG 1 585	-14.368	17.134	-8.044	1.00	0.46
ATOM	488	NE	ARG 1 585	-15.276	17.029	-9.224	1.00	0.46
ATOM	489	CZ	ARG 1 585	-16.560	16.590	-9.074	1.00	0.46
ATOM	490	NH1	ARG 1 585	-17.032	16.261	-7.836	1.00	0.46
ATOM	491	NH2	ARG 1 585	-17.373	16.476	-10.166	1.00	0.46
ATOM	492	N	ASN 1 586	-10.706	17.139	-10.973	1.00	0.45
ATOM	493	CA	ASN 1 586	-10.634	18.120	-12.021	1.00	0.45
ATOM	494	C	ASN 1 586	-10.111	17.463	-13.259	1.00	0.45
ATOM	495	O	ASN 1 586	-10.475	17.821	-14.380	1.00	0.45
ATOM	496	CB	ASN 1 586	-9.703	19.293	-11.678	1.00	0.45
ATOM	497	CG	ASN 1 586	-10.385	20.101	-10.584	1.00	0.45
ATOM	498	OD1	ASN 1 586	-11.610	20.195	-10.547	1.00	0.45
ATOM	499	ND2	ASN 1 586	-9.575	20.697	-9.668	1.00	0.45
ATOM	500	N	LEU 1 587	-9.231	16.473	-13.068	1.00	0.55
ATOM	501	CA	LEU 1 587	-8.562	15.751	-14.107	1.00	0.55
ATOM	502	C	LEU 1 587	-9.618	15.063	-14.928	1.00	0.55
ATOM	503	O	LEU 1 587	-10.739	14.850	-14.466	1.00	0.55
ATOM	504	CB	LEU 1 587	-7.668	14.679	-13.445	1.00	0.55
ATOM	505	CG	LEU 1 587	-6.461	14.146	-14.232	1.00	0.55
ATOM	506	CD1	LEU 1 587	-5.335	15.186	-14.287	1.00	0.55
ATOM	507	CD2	LEU 1 587	-5.960	12.826	-13.636	1.00	0.55
ATOM	508	N	HIS 1 588	-9.286	14.733	-16.194	1.00	0.46
ATOM	509	CA	HIS 1 588	-10.187	14.045	-17.076	1.00	0.46
ATOM	510	C	HIS 1 588	-10.210	12.614	-16.641	1.00	0.46
ATOM	511	O	HIS 1 588	-9.337	12.160	-15.904	1.00	0.46
ATOM	512	CB	HIS 1 588	-9.735	14.093	-18.548	1.00	0.46
ATOM	513	CG	HIS 1 588	-10.650	13.385	-19.503	1.00	0.46
ATOM	514	ND1	HIS 1 588	-10.514	12.066	-19.867	1.00	0.46
ATOM	515	CD2	HIS 1 588	-11.733	13.848	-20.188	1.00	0.46
ATOM	516	CE1	HIS 1 588	-11.511	11.795	-20.748	1.00	0.46
ATOM	517	NE2	HIS 1 588	-12.276	12.848	-20.974	1.00	0.46
ATOM	518	N	LEU 1 589	-11.222	11.856	-17.102	1.00	0.27
ATOM	519	CA	LEU 1 589	-11.395	10.496	-16.683	1.00	0.27
ATOM	520	C	LEU 1 589	-10.182	9.706	-17.062	1.00	0.27
ATOM	521	O	LEU 1 589	-9.646	8.945	-16.259	1.00	0.27
ATOM	522	CB	LEU 1 589	-12.588	9.823	-17.381	1.00	0.27
ATOM	523	CG	LEU 1 589	-12.792	8.365	-16.941	1.00	0.27
ATOM	524	CD1	LEU 1 589	-13.192	8.310	-15.463	1.00	0.27
ATOM	525	CD2	LEU 1 589	-13.781	7.624	-17.853	1.00	0.27
ATOM	526	N	ASP 1 590	-9.705	9.894	-18.303	1.00	0.25
ATOM	527	CA	ASP 1 590	-8.603	9.138	-18.816	1.00	0.25

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ATOM	528	C	ASP	1	590	-7.387	9.404	-17.984	1.00	0.25
ATOM	529	O	ASP	1	590	-6.620	8.491	-17.685	1.00	0.25
ATOM	530	CB	ASP	1	590	-8.266	9.512	-20.271	1.00	0.25
ATOM	531	CG	ASP	1	590	-7.255	8.515	-20.817	1.00	0.25
ATOM	532	OD1	ASP	1	590	-6.868	7.583	-20.062	1.00	0.25
ATOM	533	OD2	ASP	1	590	-6.854	8.676	-22.000	1.00	0.25
ATOM	534	N	ASP	1	591	-7.173	10.673	-17.597	1.00	0.27
ATOM	535	CA	ASP	1	591	-6.010	11.033	-16.832	1.00	0.27
ATOM	536	C	ASP	1	591	-6.104	10.438	-15.472	1.00	0.27
ATOM	537	O	ASP	1	591	-5.102	10.074	-14.858	1.00	0.27
ATOM	538	CB	ASP	1	591	-5.840	12.551	-16.683	1.00	0.27
ATOM	539	CG	ASP	1	591	-5.433	13.097	-18.043	1.00	0.27
ATOM	540	OD1	ASP	1	591	-5.096	12.274	-18.335	1.00	0.27
ATOM	541	OD2	ASP	1	591	-5.449	14.346	-18.205	1.00	0.27
ATOM	542	N	GLN	1	592	-7.329	10.349	-14.945	1.00	0.31
ATOM	543	CA	GLN	1	592	-7.504	9.815	-13.638	1.00	0.31
ATOM	544	C	GLN	1	592	-7.058	8.389	-13.686	1.00	0.31
ATOM	545	O	GLN	1	592	-6.317	7.920	-12.824	1.00	0.31
ATOM	546	CB	GLN	1	592	-8.975	9.908	-13.238	1.00	0.31
ATOM	547	CG	GLN	1	592	-9.192	9.833	-11.742	1.00	0.31
ATOM	548	CD	GLN	1	592	-10.516	10.522	-11.463	1.00	0.31
ATOM	549	OE1	GLN	1	592	-11.571	9.893	-11.437	1.00	0.31
ATOM	550	NE2	GLN	1	592	-10.464	11.865	-11.264	1.00	0.31
ATOM	551	N	MET	1	593	-7.452	7.680	-14.758	1.00	0.38
ATOM	552	CA	MET	1	593	-7.117	6.295	-14.927	1.00	0.38
ATOM	553	C	MET	1	593	-5.622	6.167	-14.920	1.00	0.38
ATOM	554	O	MET	1	593	-5.081	5.268	-14.279	1.00	0.38
ATOM	555	CB	MET	1	593	-7.537	5.763	-16.303	1.00	0.38
ATOM	556	CG	MET	1	593	-9.038	5.737	-16.573	1.00	0.38
ATOM	557	SD	MET	1	593	-9.425	5.580	-18.341	1.00	0.38
ATOM	558	CE	MET	1	593	-8.466	4.055	-18.571	1.00	0.38
ATOM	559	N	THR	1	594	-4.908	7.070	-15.631	1.00	0.56
ATOM	560	CA	THR	1	594	-3.485	6.913	-15.743	1.00	0.56
ATOM	561	C	THR	1	594	-2.854	7.055	-14.395	1.00	0.56
ATOM	562	O	THR	1	594	-1.938	6.317	-14.040	1.00	0.56
ATOM	563	CB	THR	1	594	-2.822	7.881	-16.689	1.00	0.56
ATOM	564	OG1	THR	1	594	-1.494	7.455	-16.954	1.00	0.56
ATOM	565	CG2	THR	1	594	-2.784	9.284	-16.069	1.00	0.56
ATOM	566	N	LEU	1	595	-3.351	8.014	-13.606	1.00	0.67
ATOM	567	CA	LEU	1	595	-2.873	8.315	-12.298	1.00	0.67
ATOM	568	C	LEU	1	595	-3.015	7.054	-11.476	1.00	0.67
ATOM	569	O	LEU	1	595	-2.042	6.553	-10.914	1.00	0.67
ATOM	570	CB	LEU	1	595	-3.808	9.433	-11.781	1.00	0.67
ATOM	571	CG	LEU	1	595	-3.358	10.276	-10.593	1.00	0.67
ATOM	572	CD1	LEU	1	595	-3.379	9.462	-9.298	1.00	0.67
ATOM	573	CD2	LEU	1	595	-2.040	10.998	-10.916	1.00	0.67
ATOM	574	N	LEU	1	596	-4.221	6.451	-11.441	1.00	0.48
ATOM	575	CA	LEU	1	596	-4.421	5.274	-10.631	1.00	0.48
ATOM	576	C	LEU	1	596	-3.625	4.118	-11.126	1.00	0.48
ATOM	577	O	LEU	1	596	-3.050	3.384	-10.328	1.00	0.48
ATOM	578	CB	LEU	1	596	-5.871	4.749	-10.534	1.00	0.48
ATOM	579	CG	LEU	1	596	-6.844	5.622	-9.720	1.00	0.48
ATOM	580	CD1	LEU	1	596	-7.309	6.853	-10.504	1.00	0.48
ATOM	581	CD2	LEU	1	596	-8.006	4.788	-9.167	1.00	0.48
ATOM	582	N	GLN	1	597	-3.549	3.933	-12.453	1.00	0.43
ATOM	583	CA	GLN	1	597	-2.931	2.746	-12.967	1.00	0.43
ATOM	584	C	GLN	1	597	-1.514	2.677	-12.471	1.00	0.43
ATOM	585	O	GLN	1	597	-1.040	1.603	-12.105	1.00	0.43
ATOM	586	CB	GLN	1	597	-2.919	2.701	-14.499	1.00	0.43
ATOM	587	CG	GLN	1	597	-2.335	1.403	-15.054	1.00	0.43
ATOM	588	CD	GLN	1	597	-2.383	1.487	-16.570	1.00	0.43

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ATOM	589	OE1 GLN 1 597	-2.999	2.391	-17.132	1.00	0.43
ATOM	590	NE2 GLN 1 597	-1.718	0.519	-17.255	1.00	0.43
ATOM	591	N TYR 1 598	-0.805	3.822	-12.449	1.00	0.63
ATOM	592	CA TYR 1 598	0.575	3.879	-12.039	1.00	0.63
ATOM	593	C TYR 1 598	0.754	3.705	-10.541	1.00	0.63
ATOM	594	O TYR 1 598	1.622	2.956	-10.095	1.00	0.63
ATOM	595	CB TYR 1 598	1.202	5.233	-12.413	1.00	0.63
ATOM	596	CG TYR 1 598	2.682	5.140	-12.280	1.00	0.63
ATOM	597	CD1 TYR 1 598	3.287	5.130	-11.044	1.00	0.63
ATOM	598	CD2 TYR 1 598	3.471	5.079	-13.406	1.00	0.63
ATOM	599	CE1 TYR 1 598	4.655	5.052	-10.936	1.00	0.63
ATOM	600	CE2 TYR 1 598	4.838	5.000	-13.304	1.00	0.63
ATOM	601	CZ TYR 1 598	5.433	4.983	-12.066	1.00	0.63
ATOM	602	OH TYR 1 598	6.837	4.903	-11.956	1.00	0.63
ATOM	603	N SER 1 599	-0.058	4.423	-9.734	1.00	0.57
ATOM	604	CA SER 1 599	0.007	4.569	-8.295	1.00	0.57
ATOM	605	C SER 1 599	-0.481	3.412	-7.472	1.00	0.57
ATOM	606	O SER 1 599	-0.041	3.263	-6.333	1.00	0.57
ATOM	607	CB SER 1 599	-0.841	5.750	-7.781	1.00	0.57
ATOM	608	OG SER 1 599	-0.367	6.985	-8.291	1.00	0.57
ATOM	609	N TRP 1 600	-1.382	2.566	-8.001	1.00	0.39
ATOM	610	CA TRP 1 600	-2.151	1.642	-7.200	1.00	0.39
ATOM	611	C TRP 1 600	-1.310	0.848	-6.233	1.00	0.39
ATOM	612	O TRP 1 600	-1.618	0.807	-5.043	1.00	0.39
ATOM	613	CB TRP 1 600	-2.900	0.632	-8.088	1.00	0.39
ATOM	614	CG TRP 1 600	-1.988	-0.338	-8.803	1.00	0.39
ATOM	615	CD1 TRP 1 600	-1.190	-0.146	-9.895	1.00	0.39
ATOM	616	CD2 TRP 1 600	-1.834	-1.714	-8.423	1.00	0.39
ATOM	617	NE1 TRP 1 600	-0.553	-1.321	-10.220	1.00	0.39
ATOM	618	CE2 TRP 1 600	-0.938	-2.293	-9.321	1.00	0.39
ATOM	619	CE3 TRP 1 600	-2.392	-2.436	-7.406	1.00	0.39
ATOM	620	CZ2 TRP 1 600	-0.589	-3.611	-9.217	1.00	0.39
ATOM	621	CZ3 TRP 1 600	-2.036	-3.763	-7.303	1.00	0.39
ATOM	622	CH2 TRP 1 600	-1.152	-4.338	-8.192	1.00	0.39
ATOM	623	N MET 1 601	-0.216	0.219	-6.690	1.00	0.53
ATOM	624	CA MET 1 601	0.564	-0.617	-5.819	1.00	0.53
ATOM	625	C MET 1 601	1.217	0.228	-4.766	1.00	0.53
ATOM	626	O MET 1 601	1.278	-0.154	-3.600	1.00	0.53
ATOM	627	CB MET 1 601	1.661	-1.370	-6.587	1.00	0.53
ATOM	628	CG MET 1 601	2.274	-2.606	-5.910	1.00	0.53
ATOM	629	SD MET 1 601	3.005	-2.371	-4.261	1.00	0.53
ATOM	630	CE MET 1 601	1.511	-2.869	-3.358	1.00	0.53
ATOM	631	N PHE 1 602	1.716	1.419	-5.147	1.00	0.69
ATOM	632	CA PHE 1 602	2.386	2.277	-4.208	1.00	0.69
ATOM	633	C PHE 1 602	1.406	2.538	-3.102	1.00	0.69
ATOM	634	O PHE 1 602	1.709	2.405	-1.917	1.00	0.69
ATOM	635	CB PHE 1 602	2.653	3.682	-4.783	1.00	0.69
ATOM	636	CG PHE 1 602	3.515	3.647	-5.996	1.00	0.69
ATOM	637	CD1 PHE 1 602	2.987	3.225	-7.192	1.00	0.69
ATOM	638	CD2 PHE 1 602	4.825	4.072	-5.957	1.00	0.69
ATOM	639	CE1 PHE 1 602	3.754	3.200	-8.331	1.00	0.69
ATOM	640	CE2 PHE 1 602	5.597	4.050	-7.096	1.00	0.69
ATOM	641	CZ PHE 1 602	5.062	3.615	-8.285	1.00	0.69
ATOM	642	N LEU 1 603	0.168	2.892	-3.473	1.00	0.63
ATOM	643	CA LEU 1 603	-0.807	3.239	-2.483	1.00	0.63
ATOM	644	C LEU 1 603	-1.101	2.078	-1.589	1.00	0.63
ATOM	645	O LEU 1 603	-1.198	2.243	-0.376	1.00	0.63
ATOM	646	CB LEU 1 603	-2.148	3.718	-3.063	1.00	0.63
ATOM	647	CG LEU 1 603	-2.117	5.146	-3.640	1.00	0.63
ATOM	648	CD1 LEU 1 603	-1.172	5.264	-4.843	1.00	0.63
ATOM	649	CD2 LEU 1 603	-3.536	5.648	-3.942	1.00	0.63

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ATOM	650	N	MET	1	604	-1.252	0.867	-2.148	1.00	0.49
ATOM	651	CA	MET	1	604	-1.562	-0.244	-1.299	1.00	0.49
ATOM	652	C	MET	1	604	-0.425	-0.409	-0.343	1.00	0.49
ATOM	653	O	MET	1	604	-0.629	-0.699	0.835	1.00	0.49
ATOM	654	CB	MET	1	604	-1.713	-1.566	-2.070	1.00	0.49
ATOM	655	CG	MET	1	604	-2.928	-1.602	-2.999	1.00	0.49
ATOM	656	SD	MET	1	604	-3.371	-3.261	-3.593	1.00	0.49
ATOM	657	CE	MET	1	604	-4.703	-2.693	-4.687	1.00	0.49
ATOM	658	N	ALA	1	605	0.813	-0.234	-0.842	1.00	0.46
ATOM	659	CA	ALA	1	605	1.973	-0.428	-0.025	1.00	0.46
ATOM	660	C	ALA	1	605	2.080	0.598	1.060	1.00	0.46
ATOM	661	O	ALA	1	605	2.354	0.234	2.202	1.00	0.46
ATOM	662	CB	ALA	1	605	3.284	-0.438	-0.820	1.00	0.46
ATOM	663	N	PHE	1	606	1.856	1.899	0.761	1.00	0.53
ATOM	664	CA	PHE	1	606	1.972	2.853	1.833	1.00	0.53
ATOM	665	C	PHE	1	606	0.986	2.488	2.897	1.00	0.53
ATOM	666	O	PHE	1	606	1.304	2.529	4.080	1.00	0.53
ATOM	667	CB	PHE	1	606	1.665	4.323	1.489	1.00	0.53
ATOM	668	CG	PHE	1	606	2.879	4.986	0.949	1.00	0.53
ATOM	669	CD1	PHE	1	606	4.053	4.947	1.664	1.00	0.53
ATOM	670	CD2	PHE	1	606	2.835	5.709	-0.220	1.00	0.53
ATOM	671	CE1	PHE	1	606	5.185	5.570	1.198	1.00	0.53
ATOM	672	CE2	PHE	1	606	3.965	6.340	-0.684	1.00	0.53
ATOM	673	CZ	PHE	1	606	5.143	6.262	0.015	1.00	0.53
ATOM	674	N	ALA	1	607	-0.235	2.084	2.531	1.00	0.30
ATOM	675	CA	ALA	1	607	-1.186	1.776	3.560	1.00	0.30
ATOM	676	C	ALA	1	607	-0.664	0.648	4.398	1.00	0.30
ATOM	677	O	ALA	1	607	-0.782	0.671	5.624	1.00	0.30
ATOM	678	CB	ALA	1	607	-2.548	1.336	2.997	1.00	0.30
ATOM	679	N	LEU	1	608	-0.062	-0.373	3.759	1.00	0.08
ATOM	680	CA	LEU	1	608	0.419	-1.510	4.492	1.00	0.08
ATOM	681	C	LEU	1	608	1.488	-1.092	5.451	1.00	0.08
ATOM	682	O	LEU	1	608	1.457	-1.456	6.626	1.00	0.08
ATOM	683	CB	LEU	1	608	1.031	-2.598	3.589	1.00	0.08
ATOM	684	CG	LEU	1	608	1.572	-3.821	4.364	1.00	0.08
ATOM	685	CD1	LEU	1	608	0.457	-4.567	5.110	1.00	0.08
ATOM	686	CD2	LEU	1	608	2.388	-4.743	3.445	1.00	0.08
ATOM	687	N	GLY	1	609	2.461	-0.290	4.986	1.00	0.10
ATOM	688	CA	GLY	1	609	3.544	0.074	5.850	1.00	0.10
ATOM	689	C	GLY	1	609	3.006	0.831	7.024	1.00	0.10
ATOM	690	O	GLY	1	609	3.383	0.583	8.169	1.00	0.10
ATOM	691	N	TRP	1	610	2.087	1.776	6.766	1.00	0.19
ATOM	692	CA	TRP	1	610	1.563	2.603	7.814	1.00	0.19
ATOM	693	C	TRP	1	610	0.869	1.794	8.865	1.00	0.19
ATOM	694	O	TRP	1	610	1.122	1.963	10.058	1.00	0.19
ATOM	695	CB	TRP	1	610	0.576	3.658	7.279	1.00	0.19
ATOM	696	CG	TRP	1	610	-0.277	4.343	8.322	1.00	0.19
ATOM	697	CD1	TRP	1	610	-1.553	4.017	8.665	1.00	0.19
ATOM	698	CD2	TRP	1	610	0.088	5.465	9.148	1.00	0.19
ATOM	699	NE1	TRP	1	610	-2.010	4.864	9.645	1.00	0.19
ATOM	700	CE2	TRP	1	610	-1.011	5.758	9.955	1.00	0.19
ATOM	701	CE3	TRP	1	610	1.237	6.195	9.234	1.00	0.19
ATOM	702	CZ2	TRP	1	610	-0.976	6.783	10.855	1.00	0.19
ATOM	703	CZ3	TRP	1	610	1.272	7.227	10.145	1.00	0.19
ATOM	704	CH2	TRP	1	610	0.185	7.517	10.942	1.00	0.19
ATOM	705	N	ARG	1	611	-0.018	0.874	8.461	1.00	0.36
ATOM	706	CA	ARG	1	611	-0.765	0.113	9.420	1.00	0.36
ATOM	707	C	ARG	1	611	0.129	-0.825	10.166	1.00	0.36
ATOM	708	O	ARG	1	611	-0.172	-1.222	11.290	1.00	0.36
ATOM	709	CB	ARG	1	611	-1.947	-0.656	8.795	1.00	0.36
ATOM	710	CG	ARG	1	611	-1.594	-1.605	7.649	1.00	0.36

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ATOM	711	CD	ARG	1	611	-2.843	-2.052	6.878	1.00	0.36
ATOM	712	NE	ARG	1	611	-2.414	-2.804	5.665	1.00	0.36
ATOM	713	CZ	ARG	1	611	-3.338	-3.131	4.715	1.00	0.36
ATOM	714	NH1	ARG	1	611	-4.631	-2.718	4.857	1.00	0.36
ATOM	715	NH2	ARG	1	611	-2.979	-3.868	3.623	1.00	0.36
ATOM	716	N	SER	1	612	1.225	-1.249	9.522	1.00	0.43
ATOM	717	CA	SER	1	612	2.174	-2.186	10.050	1.00	0.43
ATOM	718	C	SER	1	612	3.117	-1.602	11.065	1.00	0.43
ATOM	719	O	SER	1	612	3.787	-2.381	11.742	1.00	0.43
ATOM	720	CB	SER	1	612	2.991	-2.907	8.960	1.00	0.43
ATOM	721	OG	SER	1	612	3.707	-1.977	8.165	1.00	0.43
ATOM	722	N	TYR	1	613	3.223	-0.256	11.197	1.00	0.36
ATOM	723	CA	TYR	1	613	4.276	0.291	12.022	1.00	0.36
ATOM	724	C	TYR	1	613	4.237	-0.287	13.399	1.00	0.36
ATOM	725	O	TYR	1	613	5.247	-0.796	13.878	1.00	0.36
ATOM	726	CB	TYR	1	613	4.256	1.814	12.241	1.00	0.36
ATOM	727	CG	TYR	1	613	4.256	2.505	10.930	1.00	0.36
ATOM	728	CD1	TYR	1	613	5.079	2.095	9.908	1.00	0.36
ATOM	729	CD2	TYR	1	613	3.376	3.534	10.714	1.00	0.36
ATOM	730	CE1	TYR	1	613	5.053	2.732	8.690	1.00	0.36
ATOM	731	CE2	TYR	1	613	3.354	4.176	9.505	1.00	0.36
ATOM	732	CZ	TYR	1	613	4.189	3.781	8.489	1.00	0.36
ATOM	733	OH	TYR	1	613	4.146	4.451	7.248	1.00	0.36
ATOM	734	N	ARG	1	614	3.061	-0.308	14.042	1.00	0.35
ATOM	735	CA	ARG	1	614	3.003	-0.756	15.402	1.00	0.35
ATOM	736	C	ARG	1	614	3.435	-2.187	15.518	1.00	0.35
ATOM	737	O	ARG	1	614	4.107	-2.550	16.482	1.00	0.35
ATOM	738	CB	ARG	1	614	1.608	-0.581	16.027	1.00	0.35
ATOM	739	CG	ARG	1	614	1.273	0.899	16.238	1.00	0.35
ATOM	740	CD	ARG	1	614	0.000	1.165	17.044	1.00	0.35
ATOM	741	NE	ARG	1	614	-0.083	2.640	17.244	1.00	0.35
ATOM	742	CZ	ARG	1	614	-1.118	3.186	17.948	1.00	0.35
ATOM	743	NH1	ARG	1	614	-2.094	2.383	18.461	1.00	0.35
ATOM	744	NH2	ARG	1	614	-1.175	4.536	18.139	1.00	0.35
ATOM	745	N	GLN	1	615	3.075	-3.054	14.552	1.00	0.40
ATOM	746	CA	GLN	1	615	3.466	-4.428	14.697	1.00	0.40
ATOM	747	C	GLN	1	615	4.811	-4.597	14.072	1.00	0.40
ATOM	748	O	GLN	1	615	4.927	-4.855	12.876	1.00	0.40
ATOM	749	CB	GLN	1	615	2.505	-5.418	14.012	1.00	0.40
ATOM	750	CG	GLN	1	615	1.105	-5.450	14.637	1.00	0.40
ATOM	751	CD	GLN	1	615	0.327	-4.230	14.160	1.00	0.40
ATOM	752	OE1	GLN	1	615	-0.699	-3.875	14.736	1.00	0.40
ATOM	753	NE2	GLN	1	615	0.820	-3.575	13.076	1.00	0.40
ATOM	754	N	SER	1	616	5.871	-4.490	14.893	1.00	0.38
ATOM	755	CA	SER	1	616	7.205	-4.567	14.381	1.00	0.38
ATOM	756	C	SER	1	616	7.603	-5.993	14.244	1.00	0.38
ATOM	757	O	SER	1	616	7.004	-6.872	14.861	1.00	0.38
ATOM	758	CB	SER	1	616	8.246	-3.885	15.283	1.00	0.38
ATOM	759	OG	SER	1	616	8.331	-4.563	16.528	1.00	0.38
ATOM	760	N	SER	1	617	8.618	-6.216	13.380	1.00	0.34
ATOM	761	CA	SER	1	617	9.277	-7.462	13.112	1.00	0.34
ATOM	762	C	SER	1	617	9.101	-7.783	11.679	1.00	0.34
ATOM	763	O	SER	1	617	8.136	-7.370	11.044	1.00	0.34
ATOM	764	CB	SER	1	617	8.794	-8.691	13.909	1.00	0.34
ATOM	765	OG	SER	1	617	9.025	-8.493	15.296	1.00	0.34
ATOM	766	N	ALA	1	618	10.038	-8.574	11.133	1.00	0.31
ATOM	767	CA	ALA	1	618	9.912	-8.986	9.772	1.00	0.31
ATOM	768	C	ALA	1	618	8.631	-9.736	9.743	1.00	0.31
ATOM	769	O	ALA	1	618	7.901	-9.753	8.753	1.00	0.31
ATOM	770	CB	ALA	1	618	11.029	-9.947	9.330	1.00	0.31
ATOM	771	N	ASN	1	619	8.349	-10.365	10.891	1.00	0.35

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ATOM	772	CA	ASN 1 619	7.190	-11.142	11.140	1.00	0.35
ATOM	773	C	ASN 1 619	5.960	-10.277	11.190	1.00	0.35
ATOM	774	O	ASN 1 619	4.845	-10.793	11.173	1.00	0.35
ATOM	775	CB	ASN 1 619	7.280	-11.924	12.461	1.00	0.35
ATOM	776	CG	ASN 1 619	8.427	-12.924	12.335	1.00	0.35
ATOM	777	OD1	ASN 1 619	9.382	-12.881	13.109	1.00	0.35
ATOM	778	ND2	ASN 1 619	8.339	-13.845	11.338	1.00	0.35
ATOM	779	N	LEU 1 620	6.076	-8.940	11.292	1.00	0.39
ATOM	780	CA	LEU 1 620	4.804	-8.298	11.401	1.00	0.39
ATOM	781	C	LEU 1 620	4.526	-7.328	10.294	1.00	0.39
ATOM	782	O	LEU 1 620	5.102	-6.243	10.228	1.00	0.39
ATOM	783	CB	LEU 1 620	4.612	-7.574	12.743	1.00	0.39
ATOM	784	CG	LEU 1 620	4.585	-8.531	13.951	1.00	0.39
ATOM	785	CD1	LEU 1 620	3.372	-9.470	13.893	1.00	0.39
ATOM	786	CD2	LEU 1 620	5.911	-9.294	14.094	1.00	0.39
ATOM	787	N	LEU 1 621	3.606	-7.728	9.391	1.00	0.36
ATOM	788	CA	LEU 1 621	3.051	-6.876	8.378	1.00	0.36
ATOM	789	C	LEU 1 621	1.576	-7.096	8.477	1.00	0.36
ATOM	790	O	LEU 1 621	1.109	-8.233	8.431	1.00	0.36
ATOM	791	CB	LEU 1 621	3.454	-7.225	6.936	1.00	0.36
ATOM	792	CG	LEU 1 621	4.927	-6.933	6.605	1.00	0.36
ATOM	793	CD1	LEU 1 621	5.248	-7.307	5.150	1.00	0.36
ATOM	794	CD2	LEU 1 621	5.296	-5.479	6.940	1.00	0.36
ATOM	795	N	CYS 1 622	0.790	-6.014	8.626	1.00	0.33
ATOM	796	CA	CYS 1 622	-0.619	-6.208	8.778	1.00	0.33
ATOM	797	C	CYS 1 622	-1.297	-6.000	7.469	1.00	0.33
ATOM	798	O	CYS 1 622	-1.742	-4.897	7.161	1.00	0.33
ATOM	799	CB	CYS 1 622	-1.277	-5.221	9.753	1.00	0.33
ATOM	800	SG	CYS 1 622	-0.819	-5.533	11.478	1.00	0.33
ATOM	801	N	PHE 1 623	-1.427	-7.066	6.663	1.00	0.23
ATOM	802	CA	PHE 1 623	-2.157	-6.892	5.446	1.00	0.23
ATOM	803	C	PHE 1 623	-3.554	-6.558	5.847	1.00	0.23
ATOM	804	O	PHE 1 623	-4.206	-5.711	5.237	1.00	0.23
ATOM	805	CB	PHE 1 623	-2.223	-8.146	4.554	1.00	0.23
ATOM	806	CG	PHE 1 623	-0.889	-8.312	3.914	1.00	0.23
ATOM	807	CD1	PHE 1 623	-0.599	-7.645	2.748	1.00	0.23
ATOM	808	CD2	PHE 1 623	0.077	-9.109	4.477	1.00	0.23
ATOM	809	CE1	PHE 1 623	0.627	-7.783	2.141	1.00	0.23
ATOM	810	CE2	PHE 1 623	1.304	-9.251	3.874	1.00	0.23
ATOM	811	CZ	PHE 1 623	1.586	-8.588	2.704	1.00	0.23
ATOM	812	N	ALA 1 624	-4.046	-7.248	6.892	1.00	0.28
ATOM	813	CA	ALA 1 624	-5.351	-7.021	7.439	1.00	0.28
ATOM	814	C	ALA 1 624	-5.229	-7.359	8.890	1.00	0.28
ATOM	815	O	ALA 1 624	-4.285	-8.041	9.285	1.00	0.28
ATOM	816	CB	ALA 1 624	-6.438	-7.938	6.848	1.00	0.28
ATOM	817	N	PRO 1 625	-6.130	-6.898	9.714	1.00	0.58
ATOM	818	CA	PRO 1 625	-6.054	-7.227	11.107	1.00	0.58
ATOM	819	C	PRO 1 625	-6.288	-8.688	11.219	1.00	0.58
ATOM	820	O	PRO 1 625	-5.817	-9.328	12.159	1.00	0.58
ATOM	821	CB	PRO 1 625	-7.083	-6.329	11.806	1.00	0.58
ATOM	822	CG	PRO 1 625	-7.869	-5.658	10.659	1.00	0.58
ATOM	823	CD	PRO 1 625	-6.896	-5.691	9.471	1.00	0.58
ATOM	824	N	ASP 1 626	-7.035	-9.206	10.241	1.00	0.59
ATOM	825	CA	ASP 1 626	-7.416	-10.568	10.093	1.00	0.59
ATOM	826	C	ASP 1 626	-6.220	-11.387	9.713	1.00	0.59
ATOM	827	O	ASP 1 626	-6.154	-12.571	10.037	1.00	0.59
ATOM	828	CB	ASP 1 626	-8.458	-10.697	8.972	1.00	0.59
ATOM	829	CG	ASP 1 626	-9.119	-12.035	9.151	1.00	0.59
ATOM	830	OD1	ASP 1 626	-8.700	-12.723	10.116	1.00	0.59
ATOM	831	OD2	ASP 1 626	-10.033	-12.389	8.359	1.00	0.59
ATOM	832	N	LEU 1 627	-5.262	-10.799	8.959	1.00	0.40

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ATOM	833	CA	LEU 1 627	-4.156	-11.601	8.517	1.00	0.40
ATOM	834	C	LEU 1 627	-2.873	-10.863	8.760	1.00	0.40
ATOM	835	O	LEU 1 627	-2.474	-10.015	7.967	1.00	0.40
ATOM	836	CB	LEU 1 627	-4.237	-11.897	7.006	1.00	0.40
ATOM	837	CG	LEU 1 627	-3.086	-12.752	6.449	1.00	0.40
ATOM	838	CD1	LEU 1 627	-3.121	-14.176	7.031	1.00	0.40
ATOM	839	CD2	LEU 1 627	-3.074	-12.736	4.911	1.00	0.40
ATOM	840	N	ILE 1 628	-2.165	-11.203	9.856	1.00	0.54
ATOM	841	CA	ILE 1 628	-0.900	-10.585	10.128	1.00	0.54
ATOM	842	C	ILE 1 628	0.130	-11.549	9.617	1.00	0.54
ATOM	843	O	ILE 1 628	0.138	-12.727	9.968	1.00	0.54
ATOM	844	CB	ILE 1 628	-0.685	-10.303	11.591	1.00	0.54
ATOM	845	CG1	ILE 1 628	0.537	-9.397	11.795	1.00	0.54
ATOM	846	CG2	ILE 1 628	-0.632	-11.634	12.360	1.00	0.54
ATOM	847	CD1	ILE 1 628	0.594	-8.779	13.191	1.00	0.54
ATOM	848	N	ILE 1 629	1.027	-11.047	8.752	1.00	0.64
ATOM	849	CA	ILE 1 629	1.979	-11.834	8.023	1.00	0.64
ATOM	850	C	ILE 1 629	3.342	-11.573	8.573	1.00	0.64
ATOM	851	O	ILE 1 629	3.671	-10.449	8.948	1.00	0.64
ATOM	852	CB	ILE 1 629	1.927	-11.403	6.579	1.00	0.64
ATOM	853	CG1	ILE 1 629	2.792	-12.233	5.626	1.00	0.64
ATOM	854	CG2	ILE 1 629	2.287	-9.911	6.572	1.00	0.64
ATOM	855	CD1	ILE 1 629	4.281	-11.955	5.781	1.00	0.64
ATOM	856	N	ASN 1 630	4.169	-12.635	8.633	1.00	0.41
ATOM	857	CA	ASN 1 630	5.482	-12.552	9.194	1.00	0.41
ATOM	858	C	ASN 1 630	6.475	-12.894	8.133	1.00	0.41
ATOM	859	O	ASN 1 630	6.129	-13.466	7.103	1.00	0.41
ATOM	860	CB	ASN 1 630	5.654	-13.509	10.396	1.00	0.41
ATOM	861	CG	ASN 1 630	5.480	-14.950	9.969	1.00	0.41
ATOM	862	OD1	ASN 1 630	5.193	-15.240	8.812	1.00	0.41
ATOM	863	ND2	ASN 1 630	5.644	-15.888	10.938	1.00	0.41
ATOM	864	N	GLU 1 631	7.758	-12.570	8.376	1.00	0.35
ATOM	865	CA	GLU 1 631	8.759	-12.772	7.371	1.00	0.35
ATOM	866	C	GLU 1 631	8.763	-14.218	6.985	1.00	0.35
ATOM	867	O	GLU 1 631	8.946	-14.556	5.819	1.00	0.35
ATOM	868	CB	GLU 1 631	10.186	-12.437	7.834	1.00	0.35
ATOM	869	CG	GLU 1 631	10.707	-13.352	8.945	1.00	0.35
ATOM	870	CD	GLU 1 631	12.203	-13.111	9.077	1.00	0.35
ATOM	871	OE1	GLU 1 631	12.733	-12.257	8.317	1.00	0.35
ATOM	872	OE2	GLU 1 631	12.839	-13.780	9.934	1.00	0.35
ATOM	873	N	GLN 1 632	8.557	-15.133	7.941	1.00	0.52
ATOM	874	CA	GLN 1 632	8.618	-16.517	7.571	1.00	0.52
ATOM	875	C	GLN 1 632	7.574	-16.821	6.535	1.00	0.52
ATOM	876	O	GLN 1 632	7.866	-17.470	5.531	1.00	0.52
ATOM	877	CB	GLN 1 632	8.368	-17.464	8.756	1.00	0.52
ATOM	878	CG	GLN 1 632	9.510	-17.490	9.774	1.00	0.52
ATOM	879	CD	GLN 1 632	10.662	-18.261	9.145	1.00	0.52
ATOM	880	OE1	GLN 1 632	11.721	-18.428	9.747	1.00	0.52
ATOM	881	NE2	GLN 1 632	10.448	-18.754	7.895	1.00	0.52
ATOM	882	N	ARG 1 633	6.333	-16.344	6.737	1.00	0.65
ATOM	883	CA	ARG 1 633	5.256	-16.668	5.845	1.00	0.65
ATOM	884	C	ARG 1 633	5.429	-16.003	4.512	1.00	0.65
ATOM	885	O	ARG 1 633	4.965	-16.513	3.496	1.00	0.65
ATOM	886	CB	ARG 1 633	3.849	-16.355	6.388	1.00	0.65
ATOM	887	CG	ARG 1 633	3.556	-14.883	6.649	1.00	0.65
ATOM	888	CD	ARG 1 633	2.143	-14.652	7.187	1.00	0.65
ATOM	889	NE	ARG 1 633	2.200	-14.773	8.672	1.00	0.65
ATOM	890	CZ	ARG 1 633	2.009	-15.985	9.271	1.00	0.65
ATOM	891	NH1	ARG 1 633	1.776	-17.093	8.509	1.00	0.65
ATOM	892	NH2	ARG 1 633	2.050	-16.087	10.631	1.00	0.65
ATOM	893	N	MET 1 634	6.112	-14.849	4.465	1.00	0.68

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ATOM	894	CA	MET	1 634	6.269	-14.113	3.239	1.00	0.68
ATOM	895	C	MET	1 634	6.987	-14.978	2.246	1.00	0.68
ATOM	896	O	MET	1 634	6.900	-14.757	1.039	1.00	0.68
ATOM	897	CB	MET	1 634	7.101	-12.828	3.408	1.00	0.68
ATOM	898	CG	MET	1 634	8.600	-13.100	3.547	1.00	0.68
ATOM	899	SD	MET	1 634	9.560	-11.763	4.321	1.00	0.68
ATOM	900	CE	MET	1 634	10.886	-12.819	4.967	1.00	0.68
ATOM	901	N	THR	1 635	7.711	-15.993	2.745	1.00	0.73
ATOM	902	CA	THR	1 635	8.559	-16.864	1.977	1.00	0.73
ATOM	903	C	THR	1 635	7.806	-17.553	0.873	1.00	0.73
ATOM	904	O	THR	1 635	8.424	-17.994	-0.094	1.00	0.73
ATOM	905	CB	THR	1 635	9.194	-17.939	2.807	1.00	0.73
ATOM	906	OG1	THR	1 635	10.204	-18.603	2.060	1.00	0.73
ATOM	907	CG2	THR	1 635	8.106	-18.942	3.230	1.00	0.73
ATOM	908	N	LEU	1 636	6.469	-17.684	0.969	1.00	0.86
ATOM	909	CA	LEU	1 636	5.751	-18.430	-0.032	1.00	0.86
ATOM	910	C	LEU	1 636	6.039	-17.924	-1.433	1.00	0.86
ATOM	911	O	LEU	1 636	6.092	-18.772	-2.322	1.00	0.86
ATOM	912	CB	LEU	1 636	4.229	-18.455	0.191	1.00	0.86
ATOM	913	CG	LEU	1 636	3.802	-19.425	1.312	1.00	0.86
ATOM	914	CD1	LEU	1 636	4.438	-19.066	2.661	1.00	0.86
ATOM	915	CD2	LEU	1 636	2.275	-19.537	1.396	1.00	0.86
ATOM	916	N	PRO	1 637	6.111	-16.634	-1.719	1.00	0.89
ATOM	917	CA	PRO	1 637	6.582	-16.193	-3.029	1.00	0.89
ATOM	918	C	PRO	1 637	7.954	-15.629	-2.840	1.00	0.89
ATOM	919	O	PRO	1 637	8.410	-15.566	-1.705	1.00	0.89
ATOM	920	CB	PRO	1 637	5.629	-15.087	-3.481	1.00	0.89
ATOM	921	CG	PRO	1 637	4.391	-15.244	-2.588	1.00	0.89
ATOM	922	CD	PRO	1 637	4.954	-15.859	-1.299	1.00	0.89
ATOM	923	N	CYS	1 638	8.632	-15.137	-3.899	1.00	0.83
ATOM	924	CA	CYS	1 638	9.892	-14.475	-3.665	1.00	0.83
ATOM	925	C	CYS	1 638	9.581	-13.084	-3.175	1.00	0.83
ATOM	926	O	CYS	1 638	10.144	-12.095	-3.645	1.00	0.83
ATOM	927	CB	CYS	1 638	10.749	-14.344	-4.937	1.00	0.83
ATOM	928	SG	CYS	1 638	9.943	-13.342	-6.223	1.00	0.83
ATOM	929	N	MET	1 639	8.647	-13.005	-2.208	1.00	0.83
ATOM	930	CA	MET	1 639	8.116	-11.864	-1.524	1.00	0.83
ATOM	931	C	MET	1 639	9.159	-11.384	-0.570	1.00	0.83
ATOM	932	O	MET	1 639	9.200	-10.210	-0.221	1.00	0.83
ATOM	933	CB	MET	1 639	6.911	-12.243	-0.642	1.00	0.83
ATOM	934	CG	MET	1 639	5.951	-11.093	-0.332	1.00	0.83
ATOM	935	SD	MET	1 639	4.622	-10.856	-1.556	1.00	0.83
ATOM	936	CE	MET	1 639	5.572	-11.366	-3.016	1.00	0.83
ATOM	937	N	TYR	1 640	10.041	-12.301	-0.142	1.00	0.81
ATOM	938	CA	TYR	1 640	10.993	-12.101	0.914	1.00	0.81
ATOM	939	C	TYR	1 640	11.701	-10.796	0.742	1.00	0.81
ATOM	940	O	TYR	1 640	11.752	-9.991	1.673	1.00	0.81
ATOM	941	CB	TYR	1 640	12.046	-13.227	0.874	1.00	0.81
ATOM	942	CG	TYR	1 640	13.176	-12.967	1.810	1.00	0.81
ATOM	943	CD1	TYR	1 640	13.113	-13.365	3.122	1.00	0.81
ATOM	944	CD2	TYR	1 640	14.316	-12.340	1.361	1.00	0.81
ATOM	945	CE1	TYR	1 640	14.160	-13.132	3.982	1.00	0.81
ATOM	946	CE2	TYR	1 640	15.367	-12.103	2.213	1.00	0.81
ATOM	947	CZ	TYR	1 640	15.290	-12.500	3.526	1.00	0.81
ATOM	948	OH	TYR	1 640	16.369	-12.260	4.403	1.00	0.81
ATOM	949	N	ASP	1 641	12.237	-10.525	-0.455	1.00	0.63
ATOM	950	CA	ASP	1 641	12.986	-9.314	-0.604	1.00	0.63
ATOM	951	C	ASP	1 641	12.114	-8.124	-0.342	1.00	0.63
ATOM	952	O	ASP	1 641	12.479	-7.252	0.444	1.00	0.63
ATOM	953	CB	ASP	1 641	13.614	-9.163	-2.002	1.00	0.63
ATOM	954	CG	ASP	1 641	12.512	-9.127	-3.054	1.00	0.63

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ATOM	955	OD1 ASP 1 641	11.468	-9.804	-2.855	1.00	0.63
ATOM	956	OD2 ASP 1 641	12.702	-8.415	-4.077	1.00	0.63
ATOM	957	N GLN 1 642	10.927	-8.061	-0.971	1.00	0.38
ATOM	958	CA GLN 1 642	10.081	-6.911	-0.818	1.00	0.38
ATOM	959	C GLN 1 642	9.535	-6.842	0.573	1.00	0.38
ATOM	960	O GLN 1 642	9.455	-5.769	1.166	1.00	0.38
ATOM	961	CB GLN 1 642	8.901	-6.886	-1.805	1.00	0.38
ATOM	962	CG GLN 1 642	7.900	-8.030	-1.641	1.00	0.38
ATOM	963	CD GLN 1 642	6.823	-7.829	-2.700	1.00	0.38
ATOM	964	OE1 GLN 1 642	5.800	-8.511	-2.711	1.00	0.38
ATOM	965	NE2 GLN 1 642	7.061	-6.858	-3.622	1.00	0.38
ATOM	966	N CYS 1 643	9.164	-7.995	1.145	1.00	0.24
ATOM	967	CA CYS 1 643	8.557	-7.993	2.439	1.00	0.24
ATOM	968	C CYS 1 643	9.519	-7.380	3.393	1.00	0.24
ATOM	969	O CYS 1 643	9.125	-6.579	4.239	1.00	0.24
ATOM	970	CB CYS 1 643	8.202	-9.401	2.928	1.00	0.24
ATOM	971	SG CYS 1 643	7.433	-9.392	4.575	1.00	0.24
ATOM	972	N LYS 1 644	10.814	-7.727	3.277	1.00	0.26
ATOM	973	CA LYS 1 644	11.765	-7.146	4.177	1.00	0.26
ATOM	974	C LYS 1 644	11.804	-5.669	3.942	1.00	0.26
ATOM	975	O LYS 1 644	11.795	-4.888	4.892	1.00	0.26
ATOM	976	CB LYS 1 644	13.197	-7.679	4.004	1.00	0.26
ATOM	977	CG LYS 1 644	13.377	-9.124	4.470	1.00	0.26
ATOM	978	CD LYS 1 644	14.778	-9.673	4.194	1.00	0.26
ATOM	979	CE LYS 1 644	15.843	-9.093	5.128	1.00	0.26
ATOM	980	NZ LYS 1 644	17.170	-9.665	4.809	1.00	0.26
ATOM	981	N HIS 1 645	11.820	-5.237	2.665	1.00	0.33
ATOM	982	CA HIS 1 645	11.905	-3.827	2.417	1.00	0.33
ATOM	983	C HIS 1 645	10.707	-3.166	3.024	1.00	0.33
ATOM	984	O HIS 1 645	10.823	-2.137	3.686	1.00	0.33
ATOM	985	CB HIS 1 645	11.985	-3.468	0.924	1.00	0.33
ATOM	986	CG HIS 1 645	13.330	-3.796	0.341	1.00	0.33
ATOM	987	ND1 HIS 1 645	13.639	-4.977	-0.296	1.00	0.33
ATOM	988	CD2 HIS 1 645	14.477	-3.062	0.333	1.00	0.33
ATOM	989	CE1 HIS 1 645	14.945	-4.899	-0.655	1.00	0.33
ATOM	990	NE2 HIS 1 645	15.497	-3.754	-0.293	1.00	0.33
ATOM	991	N MET 1 646	9.522	-3.770	2.850	1.00	0.28
ATOM	992	CA MET 1 646	8.324	-3.212	3.401	1.00	0.28
ATOM	993	C MET 1 646	8.498	-3.168	4.887	1.00	0.28
ATOM	994	O MET 1 646	8.093	-2.216	5.553	1.00	0.28
ATOM	995	CB MET 1 646	7.085	-4.072	3.102	1.00	0.28
ATOM	996	CG MET 1 646	6.769	-4.179	1.609	1.00	0.28
ATOM	997	SD MET 1 646	5.313	-5.191	1.211	1.00	0.28
ATOM	998	CE MET 1 646	5.515	-5.055	-0.588	1.00	0.28
ATOM	999	N LEU 1 647	9.135	-4.203	5.453	1.00	0.37
ATOM	1000	CA LEU 1 647	9.302	-4.259	6.877	1.00	0.37
ATOM	1001	C LEU 1 647	10.067	-3.044	7.293	1.00	0.37
ATOM	1002	O LEU 1 647	9.695	-2.348	8.239	1.00	0.37
ATOM	1003	CB LEU 1 647	10.155	-5.470	7.283	1.00	0.37
ATOM	1004	CG LEU 1 647	9.510	-6.823	6.937	1.00	0.37
ATOM	1005	CD1 LEU 1 647	10.517	-7.972	7.083	1.00	0.37
ATOM	1006	CD2 LEU 1 647	8.221	-7.048	7.744	1.00	0.37
ATOM	1007	N TYR 1 648	11.150	-2.750	6.552	1.00	0.59
ATOM	1008	CA TYR 1 648	12.029	-1.671	6.883	1.00	0.59
ATOM	1009	C TYR 1 648	11.295	-0.372	6.764	1.00	0.59
ATOM	1010	O TYR 1 648	11.471	0.520	7.593	1.00	0.59
ATOM	1011	CB TYR 1 648	13.257	-1.613	5.958	1.00	0.59
ATOM	1012	CG TYR 1 648	14.105	-0.469	6.394	1.00	0.59
ATOM	1013	CD1 TYR 1 648	13.869	0.806	5.932	1.00	0.59
ATOM	1014	CD2 TYR 1 648	15.140	-0.677	7.274	1.00	0.59
ATOM	1015	CE1 TYR 1 648	14.656	1.855	6.342	1.00	0.59

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ATOM	1016	CE2 TYR 1 648	15.932	0.368	7.689	1.00	0.59
ATOM	1017	CZ TYR 1 648	15.689	1.636	7.222	1.00	0.59
ATOM	1018	OH TYR 1 648	16.499	2.713	7.644	1.00	0.59
ATOM	1019	N VAL 1 649	10.440	-0.215	5.737	1.00	0.47
ATOM	1020	CA VAL 1 649	9.815	1.070	5.594	1.00	0.47
ATOM	1021	C VAL 1 649	8.989	1.394	6.805	1.00	0.47
ATOM	1022	O VAL 1 649	9.124	2.473	7.373	1.00	0.47
ATOM	1023	CB VAL 1 649	8.949	1.194	4.368	1.00	0.47
ATOM	1024	CG1 VAL 1 649	7.719	0.283	4.498	1.00	0.47
ATOM	1025	CG2 VAL 1 649	8.591	2.680	4.187	1.00	0.47
ATOM	1026	N SER 1 650	8.143	0.468	7.285	1.00	0.27
ATOM	1027	CA SER 1 650	7.306	0.811	8.402	1.00	0.27
ATOM	1028	C SER 1 650	8.180	1.111	9.573	1.00	0.27
ATOM	1029	O SER 1 650	7.870	1.984	10.385	1.00	0.27
ATOM	1030	CB SER 1 650	6.341	-0.324	8.797	1.00	0.27
ATOM	1031	OG SER 1 650	7.061	-1.448	9.279	1.00	0.27
ATOM	1032	N SER 1 651	9.308	0.391	9.701	1.00	0.27
ATOM	1033	CA SER 1 651	10.133	0.627	10.846	1.00	0.27
ATOM	1034	C SER 1 651	10.635	2.032	10.785	1.00	0.27
ATOM	1035	O SER 1 651	10.673	2.728	11.799	1.00	0.27
ATOM	1036	CB SER 1 651	11.336	-0.332	10.964	1.00	0.27
ATOM	1037	OG SER 1 651	12.300	-0.081	9.954	1.00	0.27
ATOM	1038	N GLU 1 652	11.015	2.499	9.582	1.00	0.28
ATOM	1039	CA GLU 1 652	11.531	3.830	9.462	1.00	0.28
ATOM	1040	C GLU 1 652	10.443	4.785	9.825	1.00	0.28
ATOM	1041	O GLU 1 652	10.691	5.801	10.469	1.00	0.28
ATOM	1042	CB GLU 1 652	12.038	4.159	8.047	1.00	0.28
ATOM	1043	CG GLU 1 652	12.859	5.451	7.989	1.00	0.28
ATOM	1044	CD GLU 1 652	13.572	5.497	6.646	1.00	0.28
ATOM	1045	OE1 GLU 1 652	13.370	4.553	5.836	1.00	0.28
ATOM	1046	OE2 GLU 1 652	14.332	6.475	6.413	1.00	0.28
ATOM	1047	N LEU 1 653	9.192	4.485	9.431	1.00	0.34
ATOM	1048	CA LEU 1 653	8.137	5.394	9.768	1.00	0.34
ATOM	1049	C LEU 1 653	7.999	5.464	11.253	1.00	0.34
ATOM	1050	O LEU 1 653	7.721	6.536	11.790	1.00	0.34
ATOM	1051	CB LEU 1 653	6.785	5.063	9.134	1.00	0.34
ATOM	1052	CG LEU 1 653	6.705	5.465	7.648	1.00	0.34
ATOM	1053	CD1 LEU 1 653	6.707	6.993	7.496	1.00	0.34
ATOM	1054	CD2 LEU 1 653	7.799	4.799	6.804	1.00	0.34
ATOM	1055	N HIS 1 654	8.171	4.335	11.973	1.00	0.45
ATOM	1056	CA HIS 1 654	8.119	4.466	13.401	1.00	0.45
ATOM	1057	C HIS 1 654	9.228	5.343	13.852	1.00	0.45
ATOM	1058	O HIS 1 654	9.014	6.248	14.656	1.00	0.45
ATOM	1059	CB HIS 1 654	8.345	3.192	14.220	1.00	0.45
ATOM	1060	CG HIS 1 654	7.108	2.675	14.865	1.00	0.45
ATOM	1061	ND1 HIS 1 654	6.329	3.395	15.744	1.00	0.45
ATOM	1062	CD2 HIS 1 654	6.539	1.451	14.785	1.00	0.45
ATOM	1063	CE1 HIS 1 654	5.330	2.571	16.148	1.00	0.45
ATOM	1064	NE2 HIS 1 654	5.416	1.377	15.590	1.00	0.45
ATOM	1065	N ARG 1 655	10.440	5.109	13.317	1.00	0.58
ATOM	1066	CA ARG 1 655	11.582	5.841	13.780	1.00	0.58
ATOM	1067	C ARG 1 655	11.304	7.297	13.588	1.00	0.58
ATOM	1068	O ARG 1 655	11.511	8.106	14.489	1.00	0.58
ATOM	1069	CB ARG 1 655	12.862	5.497	13.001	1.00	0.58
ATOM	1070	CG ARG 1 655	13.315	4.046	13.187	1.00	0.58
ATOM	1071	CD ARG 1 655	14.588	3.696	12.415	1.00	0.58
ATOM	1072	NE ARG 1 655	15.730	4.359	13.105	1.00	0.58
ATOM	1073	CZ ARG 1 655	16.357	3.731	14.141	1.00	0.58
ATOM	1074	NH1 ARG 1 655	15.945	2.493	14.540	1.00	0.58
ATOM	1075	NH2 ARG 1 655	17.400	4.340	14.778	1.00	0.58
ATOM	1076	N LEU 1 656	10.783	7.659	12.406	1.00	0.65

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ATOM	1077	CA	LEU	1	656	10.457	9.023	12.107	1.00	0.65
ATOM	1078	C	LEU	1	656	9.298	9.465	12.943	1.00	0.65
ATOM	1079	O	LEU	1	656	9.103	10.663	13.143	1.00	0.65
ATOM	1080	CB	LEU	1	656	10.115	9.278	10.627	1.00	0.65
ATOM	1081	CG	LEU	1	656	11.347	9.325	9.698	1.00	0.65
ATOM	1082	CD1	LEU	1	656	12.123	8.001	9.689	1.00	0.65
ATOM	1083	CD2	LEU	1	656	10.954	9.789	8.287	1.00	0.65
ATOM	1084	N	GLN	1	657	8.485	8.516	13.445	1.00	0.65
ATOM	1085	CA	GLN	1	657	7.319	8.910	14.179	1.00	0.65
ATOM	1086	C	GLN	1	657	6.418	9.589	13.207	1.00	0.65
ATOM	1087	O	GLN	1	657	5.896	10.673	13.462	1.00	0.65
ATOM	1088	CB	GLN	1	657	7.620	9.893	15.324	1.00	0.65
ATOM	1089	CG	GLN	1	657	8.497	9.301	16.429	1.00	0.65
ATOM	1090	CD	GLN	1	657	8.712	10.375	17.486	1.00	0.65
ATOM	1091	OE1	GLN	1	657	9.386	10.151	18.490	1.00	0.65
ATOM	1092	NE2	GLN	1	657	8.124	11.582	17.257	1.00	0.65
ATOM	1093	N	VAL	1	659	6.212	8.936	12.049	1.00	0.48
ATOM	1094	CA	VAL	1	658	5.390	9.515	11.028	1.00	0.48
ATOM	1095	C	VAL	1	658	4.052	9.814	11.615	1.00	0.48
ATOM	1096	O	VAL	1	658	3.559	9.094	12.481	1.00	0.48
ATOM	1097	CB	VAL	1	658	5.186	8.627	9.835	1.00	0.48
ATOM	1098	CG1	VAL	1	658	4.409	7.379	10.285	1.00	0.48
ATOM	1099	CG2	VAL	1	658	4.476	9.439	8.740	1.00	0.48
ATOM	1100	N	SER	1	659	3.433	10.913	11.145	1.00	0.33
ATOM	1101	CA	SER	1	659	2.174	11.328	11.685	1.00	0.33
ATOM	1102	C	SER	1	659	1.103	11.079	10.671	1.00	0.33
ATOM	1103	O	SER	1	659	1.317	11.168	9.463	1.00	0.33
ATOM	1104	CB	SER	1	659	2.133	12.823	12.043	1.00	0.33
ATOM	1105	OG	SER	1	659	3.071	13.105	13.069	1.00	0.33
ATOM	1106	N	TYR	1	660	-0.109	10.799	11.175	1.00	0.39
ATOM	1107	CA	TYR	1	660	-1.245	10.449	10.377	1.00	0.39
ATOM	1108	C	TYR	1	660	-1.494	11.533	9.376	1.00	0.39
ATOM	1109	O	TYR	1	660	-1.664	11.257	8.191	1.00	0.39
ATOM	1110	CB	TYR	1	660	-2.492	10.287	11.262	1.00	0.39
ATOM	1111	CG	TYR	1	660	-3.708	10.080	10.430	1.00	0.39
ATOM	1112	CD1	TYR	1	660	-4.415	11.165	9.970	1.00	0.39
ATOM	1113	CD2	TYR	1	660	-4.142	8.814	10.116	1.00	0.39
ATOM	1114	CE1	TYR	1	660	-5.545	10.989	9.211	1.00	0.39
ATOM	1115	CE2	TYR	1	660	-5.274	8.632	9.356	1.00	0.39
ATOM	1116	CZ	TYR	1	660	-5.975	9.723	8.904	1.00	0.39
ATOM	1117	OH	TYR	1	660	-7.137	9.553	8.127	1.00	0.39
ATOM	1118	N	GLU	1	661	-1.466	12.804	9.817	1.00	0.36
ATOM	1119	CA	GLU	1	661	-1.754	13.901	8.938	1.00	0.36
ATOM	1120	C	GLU	1	661	-0.746	13.930	7.832	1.00	0.36
ATOM	1121	O	GLU	1	661	-1.076	14.301	6.706	1.00	0.36
ATOM	1122	CB	GLU	1	661	-1.719	15.268	9.645	1.00	0.36
ATOM	1123	CG	GLU	1	661	-2.864	15.467	10.642	1.00	0.36
ATOM	1124	CD	GLU	1	661	-2.565	14.634	11.881	1.00	0.36
ATOM	1125	OE1	GLU	1	661	-1.391	14.207	12.038	1.00	0.36
ATOM	1126	OE2	GLU	1	661	-3.508	14.418	12.688	1.00	0.36
ATOM	1127	N	GLU	1	662	0.524	13.591	8.133	1.00	0.23
ATOM	1128	CA	GLU	1	662	1.551	13.575	7.125	1.00	0.23
ATOM	1129	C	GLU	1	662	1.317	12.434	6.184	1.00	0.23
ATOM	1130	O	GLU	1	662	1.569	12.533	4.984	1.00	0.23
ATOM	1131	CB	GLU	1	662	2.968	13.378	7.687	1.00	0.23
ATOM	1132	CG	GLU	1	662	3.493	14.567	8.489	1.00	0.23
ATOM	1133	CD	GLU	1	662	4.891	14.209	8.965	1.00	0.23
ATOM	1134	OE1	GLU	1	662	5.669	13.651	8.145	1.00	0.23
ATOM	1135	OE2	GLU	1	662	5.204	14.494	10.151	1.00	0.23
ATOM	1136	N	TYR	1	663	0.819	11.313	6.731	1.00	0.31
ATOM	1137	CA	TYR	1	663	0.667	10.083	6.013	1.00	0.31

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ATOM 1138 C TYR 1 663	-0.231	10.312	4.845	1.00	0.31
ATOM 1139 O TYR 1 663	0.076	9.940	3.710	1.00	0.31
ATOM 1140 CB TYR 1 663	-0.070	9.047	6.866	1.00	0.31
ATOM 1141 CG TYR 1 663	0.473	7.805	6.318	1.00	0.31
ATOM 1142 CD1 TYR 1 663	1.757	7.581	6.691	1.00	0.31
ATOM 1143 CD2 TYR 1 663	-0.175	6.941	5.463	1.00	0.31
ATOM 1144 CE1 TYR 1 663	2.411	6.485	6.248	1.00	0.31
ATOM 1145 CE2 TYR 1 663	0.491	5.822	5.012	1.00	0.31
ATOM 1146 CZ TYR 1 663	1.789	5.609	5.421	1.00	0.31
ATOM 1147 OH TYR 1 663	2.569	4.512	5.023	1.00	0.31
ATOM 1148 N LEU 1 664	-1.376	10.951	5.113	1.00	0.36
ATOM 1149 CA LEU 1 664	-2.358	11.202	4.104	1.00	0.36
ATOM 1150 C LEU 1 664	-1.794	12.138	3.088	1.00	0.36
ATOM 1151 O LEU 1 664	-2.156	12.078	1.914	1.00	0.36
ATOM 1152 CB LEU 1 664	-3.654	11.824	4.650	1.00	0.36
ATOM 1153 CG LEU 1 664	-4.516	10.837	5.459	1.00	0.36
ATOM 1154 CD1 LEU 1 664	-3.780	10.338	6.710	1.00	0.36
ATOM 1155 CD2 LEU 1 664	-5.896	11.435	5.776	1.00	0.36
ATOM 1156 N CYS 1 665	-0.926	13.065	3.522	1.00	0.37
ATOM 1157 CA CYS 1 665	-0.336	13.982	2.594	1.00	0.37
ATOM 1158 C CYS 1 665	0.482	13.184	1.632	1.00	0.37
ATOM 1159 O CYS 1 665	0.372	13.358	0.421	1.00	0.37
ATOM 1160 CB CYS 1 665	0.625	14.981	3.259	1.00	0.37
ATOM 1161 SG CYS 1 665	-0.212	16.121	4.393	1.00	0.37
ATOM 1162 N MET 1 666	1.293	12.246	2.154	1.00	0.45
ATOM 1163 CA MET 1 666	2.172	11.464	1.336	1.00	0.45
ATOM 1164 C MET 1 666	1.375	10.673	0.347	1.00	0.45
ATOM 1165 O MET 1 666	1.759	10.575	-0.814	1.00	0.45
ATOM 1166 CB MET 1 666	3.018	10.467	2.147	1.00	0.45
ATOM 1167 CG MET 1 666	3.956	9.633	1.274	1.00	0.45
ATOM 1168 SD MET 1 666	5.010	8.470	2.189	1.00	0.45
ATOM 1169 CE MET 1 666	6.373	9.637	2.459	1.00	0.45
ATOM 1170 N LYS 1 667	0.237	10.088	0.757	1.00	0.30
ATOM 1171 CA LYS 1 667	-0.507	9.286	-0.175	1.00	0.30
ATOM 1172 C LYS 1 667	-0.958	10.133	-1.326	1.00	0.30
ATOM 1173 O LYS 1 667	-0.840	9.744	-2.487	1.00	0.30
ATOM 1174 CB LYS 1 667	-1.785	8.696	0.426	1.00	0.30
ATOM 1175 CG LYS 1 667	-1.550	7.656	1.515	1.00	0.30
ATOM 1176 CD LYS 1 667	-2.849	7.288	2.226	1.00	0.30
ATOM 1177 CE LYS 1 667	-2.758	6.022	3.068	1.00	0.30
ATOM 1178 NZ LYS 1 667	-4.121	5.496	3.299	1.00	0.30
ATOM 1179 N THR 1 668	-1.476	11.336	-1.031	1.00	0.20
ATOM 1180 CA THR 1 668	-1.979	12.209	-2.052	1.00	0.20
ATOM 1181 C THR 1 668	-0.879	12.491	-3.017	1.00	0.20
ATOM 1182 O THR 1 668	-1.107	12.489	-4.228	1.00	0.20
ATOM 1183 CB THR 1 668	-2.402	13.536	-1.484	1.00	0.20
ATOM 1184 OG1 THR 1 668	-3.495	13.371	-0.595	1.00	0.20
ATOM 1185 CG2 THR 1 668	-2.732	14.526	-2.617	1.00	0.20
ATOM 1186 N LEU 1 669	0.343	12.742	-2.503	1.00	0.37
ATOM 1187 CA LEU 1 669	1.433	13.036	-3.388	1.00	0.37
ATOM 1188 C LEU 1 669	1.656	11.861	-4.283	1.00	0.37
ATOM 1189 O LEU 1 669	1.853	12.038	-5.484	1.00	0.37
ATOM 1190 CB LEU 1 669	2.822	13.276	-2.742	1.00	0.37
ATOM 1191 CG LEU 1 669	3.081	14.631	-2.046	1.00	0.37
ATOM 1192 CD1 LEU 1 669	2.497	14.704	-0.634	1.00	0.37
ATOM 1193 CD2 LEU 1 669	4.577	14.979	-2.072	1.00	0.37
ATOM 1194 N LEU 1 670	1.629	10.629	-3.732	1.00	0.59
ATOM 1195 CA LEU 1 670	1.882	9.492	-4.572	1.00	0.59
ATOM 1196 C LEU 1 670	0.874	9.452	-5.663	1.00	0.59
ATOM 1197 O LEU 1 670	1.230	9.194	-6.811	1.00	0.59
ATOM 1198 CB LEU 1 670	1.785	8.122	-3.883	1.00	0.59

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ATOM 1199	CG LEU 1 670	3.047	7.742	-3.111	1.00	0.59
ATOM 1200	CD1 LEU 1 670	4.214	7.424	-4.058	1.00	0.59
ATOM 1201	CD2 LEU 1 670	3.402	8.843	-2.123	1.00	0.59
ATOM 1202	N LEU 1 671	-0.409	9.705	-5.340	1.00	0.65
ATOM 1203	CA LEU 1 671	-1.397	9.629	-6.375	1.00	0.65
ATOM 1204	C LEU 1 671	-1.038	10.568	-7.470	1.00	0.65
ATOM 1205	O LEU 1 671	-0.835	10.166	-8.610	1.00	0.65
ATOM 1206	CB LEU 1 671	-2.799	10.126	-5.970	1.00	0.65
ATOM 1207	CG LEU 1 671	-3.703	9.172	-5.185	1.00	0.65
ATOM 1208	CD1 LEU 1 671	-5.038	9.852	-4.883	1.00	0.65
ATOM 1209	CD2 LEU 1 671	-3.954	7.872	-5.951	1.00	0.65
ATOM 1210	N LEU 1 672	-0.900	11.852	-7.135	1.00	0.38
ATOM 1211	CA LEU 1 672	-0.726	12.829	-8.161	1.00	0.38
ATOM 1212	C LEU 1 672	0.607	12.768	-8.850	1.00	0.38
ATOM 1213	O LEU 1 672	0.650	13.085	-10.033	1.00	0.38
ATOM 1214	CB LEU 1 672	-1.020	14.240	-7.643	1.00	0.38
ATOM 1215	CG LEU 1 672	-2.500	14.386	-7.248	1.00	0.38
ATOM 1216	CD1 LEU 1 672	-2.818	15.790	-6.727	1.00	0.38
ATOM 1217	CD2 LEU 1 672	-3.419	13.962	-8.403	1.00	0.38
ATOM 1218	N SER 1 673	1.705	12.430	-8.134	1.00	0.29
ATOM 1219	CA SER 1 673	3.082	12.426	-8.596	1.00	0.29
ATOM 1220	C SER 1 673	3.549	11.254	-9.428	1.00	0.29
ATOM 1221	O SER 1 673	4.437	11.413	-10.265	1.00	0.29
ATOM 1222	CB SER 1 673	4.077	12.541	-7.428	1.00	0.29
ATOM 1223	OG SER 1 673	5.410	12.535	-7.921	1.00	0.29
ATOM 1224	N SER 1 674	3.027	10.038	-9.221	1.00	0.48
ATOM 1225	CA SER 1 674	3.583	8.903	-9.911	1.00	0.48
ATOM 1226	C SER 1 674	3.374	8.971	-11.400	1.00	0.48
ATOM 1227	O SER 1 674	4.267	8.606	-12.161	1.00	0.48
ATOM 1228	CB SER 1 674	2.982	7.579	-9.435	1.00	0.48
ATOM 1229	OG SER 1 674	1.642	7.481	-9.888	1.00	0.48
ATOM 1230	N VAL 1 675	2.190	9.408	-11.869	1.00	0.57
ATOM 1231	CA VAL 1 675	1.945	9.412	-13.290	1.00	0.57
ATOM 1232	C VAL 1 675	1.945	10.799	-13.936	1.00	0.57
ATOM 1233	O VAL 1 675	1.416	10.900	-15.043	1.00	0.57
ATOM 1234	CB VAL 1 675	0.635	8.762	-13.627	1.00	0.57
ATOM 1235	CG1 VAL 1 675	-0.491	9.748	-13.281	1.00	0.57
ATOM 1236	CG2 VAL 1 675	0.655	8.272	-15.086	1.00	0.57
ATOM 1237	N PRO 1 676	2.488	11.888	-13.439	1.00	0.65
ATOM 1238	CA PRO 1 676	2.417	13.095	-14.211	1.00	0.65
ATOM 1239	C PRO 1 676	3.203	13.051	-15.468	1.00	0.65
ATOM 1240	O PRO 1 676	2.954	13.897	-16.323	1.00	0.65
ATOM 1241	CB PRO 1 676	2.950	14.214	-13.339	1.00	0.65
ATOM 1242	CG PRO 1 676	2.582	13.762	-11.938	1.00	0.65
ATOM 1243	CD PRO 1 676	2.432	12.239	-12.039	1.00	0.65
ATOM 1244	N LYS 1 677	4.169	12.127	-15.600	1.00	0.81
ATOM 1245	CA LYS 1 677	4.988	12.215	-16.772	1.00	0.81
ATOM 1246	C LYS 1 677	4.357	11.485	-17.906	1.00	0.81
ATOM 1247	O LYS 1 677	5.035	10.801	-18.672	1.00	0.81
ATOM 1248	CB LYS 1 677	6.414	11.670	-16.591	1.00	0.81
ATOM 1249	CG LYS 1 677	6.511	10.152	-16.450	1.00	0.81
ATOM 1250	CD LYS 1 677	7.937	9.637	-16.666	1.00	0.81
ATOM 1251	CE LYS 1 677	8.078	8.121	-16.535	1.00	0.81
ATOM 1252	NZ LYS 1 677	9.482	7.727	-16.788	1.00	0.81
ATOM 1253	N ASP 1 678	3.030	11.611	-18.057	1.00	0.80
ATOM 1254	CA ASP 1 678	2.404	11.004	-19.187	1.00	0.80
ATOM 1255	C ASP 1 678	1.320	11.940	-19.604	1.00	0.80
ATOM 1256	O ASP 1 678	0.978	12.874	-18.882	1.00	0.80
ATOM 1257	CB ASP 1 678	1.746	9.646	-18.885	1.00	0.80
ATOM 1258	CG ASP 1 678	2.859	8.628	-18.686	1.00	0.80
ATOM 1259	OD1 ASP 1 678	3.855	8.684	-19.456	1.00	0.80

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ATOM 1260	OD2 ASP 1 678	2.726	7.775	-17.767	1.00	0.80
ATOM 1261	N GLY 1 679	0.778	11.730	-20.816	1.00	0.77
ATOM 1262	CA GLY 1 679	-0.315	12.523	-21.302	1.00	0.77
ATOM 1263	C GLY 1 679	0.169	13.900	-21.640	1.00	0.77
ATOM 1264	O GLY 1 679	0.890	14.513	-20.858	1.00	0.77
ATOM 1265	N LEU 1 680	-0.158	14.402	-22.851	1.00	1.01
ATOM 1266	CA LEU 1 680	0.175	15.758	-23.203	1.00	1.01
ATOM 1267	C LEU 1 680	-0.728	16.705	-22.482	1.00	1.01
ATOM 1268	O LEU 1 680	-0.252	17.616	-21.805	1.00	1.01
ATOM 1269	CB LEU 1 680	0.021	16.043	-24.713	1.00	1.01
ATOM 1270	CG LEU 1 680	0.318	17.497	-25.160	1.00	1.01
ATOM 1271	CD1 LEU 1 680	-0.825	18.473	-24.825	1.00	1.01
ATOM 1272	CD2 LEU 1 680	1.670	17.981	-24.612	1.00	1.01
ATOM 1273	N LYS 1 681	-2.053	16.438	-22.600	1.00	1.15
ATOM 1274	CA LYS 1 681	-3.194	17.213	-22.173	1.00	1.15
ATOM 1275	C LYS 1 681	-2.806	18.505	-21.555	1.00	1.15
ATOM 1276	O LYS 1 681	-3.104	18.782	-20.396	1.00	1.15
ATOM 1277	CB LYS 1 681	-4.149	16.469	-21.217	1.00	1.15
ATOM 1278	CG LYS 1 681	-5.363	17.294	-20.764	1.00	1.15
ATOM 1279	CD LYS 1 681	-6.308	17.721	-21.892	1.00	1.15
ATOM 1280	CE LYS 1 681	-5.970	19.085	-22.502	1.00	1.15
ATOM 1281	NZ LYS 1 681	-6.934	19.413	-23.578	1.00	1.15
ATOM 1282	N SER 1 682	-2.145	19.337	-22.371	1.00	1.05
ATOM 1283	CA SER 1 682	-1.702	20.644	-22.022	1.00	1.05
ATOM 1284	C SER 1 682	-0.818	20.681	-20.819	1.00	1.05
ATOM 1285	O SER 1 682	-0.938	19.922	-19.859	1.00	1.05
ATOM 1286	CB SER 1 682	-2.842	21.658	-21.831	1.00	1.05
ATOM 1287	OG SER 1 682	-2.302	22.944	-21.572	1.00	1.05
ATOM 1288	N GLN 1 683	0.158	21.601	-20.869	1.00	0.99
ATOM 1289	CA GLN 1 683	0.986	21.803	-19.729	1.00	0.99
ATOM 1290	C GLN 1 683	0.069	22.382	-18.708	1.00	0.99
ATOM 1291	O GLN 1 683	0.325	22.312	-17.509	1.00	0.99
ATOM 1292	CB GLN 1 683	2.164	22.774	-19.941	1.00	0.99
ATOM 1293	CG GLN 1 683	1.767	24.207	-20.292	1.00	0.99
ATOM 1294	CD GLN 1 683	1.612	24.282	-21.802	1.00	0.99
ATOM 1295	OE1 GLN 1 683	1.650	23.263	-22.491	1.00	0.99
ATOM 1296	NE2 GLN 1 683	1.440	25.520	-22.335	1.00	0.99
ATOM 1297	N GLU 1 684	-1.033	22.982	-19.192	1.00	0.75
ATOM 1298	CA GLU 1 684	-2.011	23.633	-18.374	1.00	0.75
ATOM 1299	C GLU 1 684	-2.541	22.635	-17.391	1.00	0.75
ATOM 1300	O GLU 1 684	-2.633	22.918	-16.198	1.00	0.75
ATOM 1301	CB GLU 1 684	-3.209	24.109	-19.213	1.00	0.75
ATOM 1302	CG GLU 1 684	-3.940	25.323	-18.649	1.00	0.75
ATOM 1303	CD GLU 1 684	-3.232	26.542	-19.221	1.00	0.75
ATOM 1304	OE1 GLU 1 684	-2.717	26.434	-20.366	1.00	0.75
ATOM 1305	OE2 GLU 1 684	-3.192	27.592	-18.527	1.00	0.75
ATOM 1306	N LEU 1 685	-2.901	21.428	-17.867	1.00	0.40
ATOM 1307	CA LEU 1 685	-3.422	20.422	-16.986	1.00	0.40
ATOM 1308	C LEU 1 685	-2.344	20.017	-16.029	1.00	0.40
ATOM 1309	O LEU 1 685	-2.601	19.817	-14.844	1.00	0.40
ATOM 1310	CB LEU 1 685	-3.924	19.177	-17.735	1.00	0.40
ATOM 1311	CG LEU 1 685	-5.213	19.443	-18.538	1.00	0.40
ATOM 1312	CD1 LEU 1 685	-6.401	19.716	-17.603	1.00	0.40
ATOM 1313	CD2 LEU 1 685	-5.014	20.567	-19.569	1.00	0.40
ATOM 1314	N PHE 1 686	-1.094	19.908	-16.519	1.00	0.20
ATOM 1315	CA PHE 1 686	-0.004	19.513	-15.673	1.00	0.20
ATOM 1316	C PHE 1 686	0.119	20.522	-14.590	1.00	0.20
ATOM 1317	O PHE 1 686	0.333	20.181	-13.429	1.00	0.20
ATOM 1318	CB PHE 1 686	1.374	19.552	-16.353	1.00	0.20
ATOM 1319	CG PHE 1 686	1.516	18.437	-17.319	1.00	0.20
ATOM 1320	CD1 PHE 1 686	1.108	18.581	-18.622	1.00	0.20

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ATOM	1321	CD2 PHE 1 686	2.074	17.251	-16.908	1.00	0.20
ATOM	1322	CE1 PHE 1 686	1.252	17.545	-19.510	1.00	0.20
ATOM	1323	CE2 PHE 1 686	2.221	16.209	-17.786	1.00	0.20
ATOM	1324	CZ PHE 1 686	1.811	16.365	-19.085	1.00	0.20
ATOM	1325	N ASP 1 687	-0.023	21.803	-14.961	1.00	0.18
ATOM	1326	CA ASP 1 687	0.161	22.880	-14.041	1.00	0.18
ATOM	1327	C ASP 1 687	-0.821	22.719	-12.931	1.00	0.18
ATOM	1328	O ASP 1 687	-0.471	22.872	-11.761	1.00	0.18
ATOM	1329	CB ASP 1 687	-0.105	24.251	-14.688	1.00	0.18
ATOM	1330	CG ASP 1 687	0.351	25.336	-13.726	1.00	0.18
ATOM	1331	OD1 ASP 1 687	1.266	25.055	-12.907	1.00	0.18
ATOM	1332	OD2 ASP 1 687	-0.219	26.458	-13.789	1.00	0.18
ATOM	1333	N GLU 1 688	-2.072	22.360	-13.266	1.00	0.34
ATOM	1334	CA GLU 1 688	-3.077	22.276	-12.249	1.00	0.34
ATOM	1335	C GLU 1 688	-2.642	21.283	-11.225	1.00	0.34
ATOM	1336	O GLU 1 688	-2.756	21.530	-10.026	1.00	0.34
ATOM	1337	CB GLU 1 688	-4.446	21.820	-12.785	1.00	0.34
ATOM	1338	CG GLU 1 688	-5.126	22.848	-13.690	1.00	0.34
ATOM	1339	CD GLU 1 688	-6.457	22.266	-14.139	1.00	0.34
ATOM	1340	OE1 GLU 1 688	-6.749	21.099	-13.761	1.00	0.34
ATOM	1341	OE2 GLU 1 688	-7.202	22.977	-14.864	1.00	0.34
ATOM	1342	N ILE 1 689	-2.134	20.120	-11.661	1.00	0.52
ATOM	1343	CA ILE 1 689	-1.692	19.186	-10.674	1.00	0.52
ATOM	1344	C ILE 1 689	-0.476	19.711	-9.981	1.00	0.52
ATOM	1345	O ILE 1 689	-0.302	19.488	-8.787	1.00	0.52
ATOM	1346	CB ILE 1 689	-1.580	17.763	-11.167	1.00	0.52
ATOM	1347	CG1 ILE 1 689	-0.713	17.619	-12.424	1.00	0.52
ATOM	1348	CG2 ILE 1 689	-3.007	17.219	-11.322	1.00	0.52
ATOM	1349	CD1 ILE 1 689	-0.618	16.168	-12.902	1.00	0.52
ATOM	1350	N ARG 1 690	0.375	20.475	-10.685	1.00	0.58
ATOM	1351	CA ARG 1 690	1.570	21.000	-10.086	1.00	0.58
ATOM	1352	C ARG 1 690	1.205	21.876	-8.919	1.00	0.58
ATOM	1353	O ARG 1 690	1.872	21.838	-7.887	1.00	0.58
ATOM	1354	CB ARG 1 690	2.395	21.846	-11.073	1.00	0.58
ATOM	1355	CG ARG 1 690	2.876	21.049	-12.289	1.00	0.58
ATOM	1356	CD ARG 1 690	3.698	21.869	-13.287	1.00	0.58
ATOM	1357	NE ARG 1 690	5.061	22.037	-12.708	1.00	0.58
ATOM	1358	CZ ARG 1 690	6.127	22.282	-13.526	1.00	0.58
ATOM	1359	NH1 ARG 1 690	5.949	22.370	-14.877	1.00	0.58
ATOM	1360	NH2 ARG 1 690	7.373	22.439	-12.991	1.00	0.58
ATOM	1361	N MET 1 691	0.148	22.704	-9.052	1.00	0.57
ATOM	1362	CA MET 1 691	-0.257	23.562	-7.971	1.00	0.57
ATOM	1363	C MET 1 691	-0.751	22.736	-6.830	1.00	0.57
ATOM	1364	O MET 1 691	-0.517	23.066	-5.668	1.00	0.57
ATOM	1365	CB MET 1 691	-1.405	24.534	-8.307	1.00	0.57
ATOM	1366	CG MET 1 691	-1.007	25.800	-9.067	1.00	0.57
ATOM	1367	SD MET 1 691	-0.638	25.574	-10.827	1.00	0.57
ATOM	1368	CE MET 1 691	-0.327	27.335	-11.148	1.00	0.57
ATOM	1369	N THR 1 692	-1.487	21.649	-7.108	1.00	0.47
ATOM	1370	CA THR 1 692	-1.976	20.900	-5.993	1.00	0.47
ATOM	1371	C THR 1 692	-0.798	20.310	-5.283	1.00	0.47
ATOM	1372	O THR 1 692	-0.778	20.269	-4.052	1.00	0.47
ATOM	1373	CB THR 1 692	-2.930	19.795	-6.349	1.00	0.47
ATOM	1374	OG1 THR 1 692	-3.587	19.327	-5.181	1.00	0.47
ATOM	1375	CG2 THR 1 692	-2.147	18.640	-6.976	1.00	0.47
ATOM	1376	N TYR 1 693	0.229	19.855	-6.039	1.00	0.41
ATOM	1377	CA TYR 1 693	1.366	19.242	-5.406	1.00	0.41
ATOM	1378	C TYR 1 693	1.979	20.255	-4.506	1.00	0.41
ATOM	1379	O TYR 1 693	2.279	19.971	-3.347	1.00	0.41
ATOM	1380	CB TYR 1 693	2.564	18.873	-6.316	1.00	0.41
ATOM	1381	CG TYR 1 693	2.140	18.002	-7.437	1.00	0.41

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ATOM	1382	CD1 TYR 1 693	1.664	16.735	-7.211	1.00	0.41
ATOM	1383	CD2 TYR 1 693	2.219	18.473	-8.724	1.00	0.41
ATOM	1384	CE1 TYR 1 693	1.261	15.968	-8.273	1.00	0.41
ATOM	1385	CE2 TYR 1 693	1.814	17.709	-9.788	1.00	0.41
ATOM	1386	CZ TYR 1 693	1.330	16.449	-9.554	1.00	0.41
ATOM	1387	OH TYR 1 693	0.901	15.648	-10.626	1.00	0.41
ATOM	1388	N ILE 1 694	2.176	21.482	-5.022	1.00	0.49
ATOM	1389	CA ILE 1 694	2.828	22.476	-4.228	1.00	0.49
ATOM	1390	C ILE 1 694	1.964	22.742	-3.047	1.00	0.49
ATOM	1391	O ILE 1 694	2.454	22.994	-1.949	1.00	0.49
ATOM	1392	CB ILE 1 694	3.091	23.776	-4.943	1.00	0.49
ATOM	1393	CG1 ILE 1 694	4.098	24.616	-4.141	1.00	0.49
ATOM	1394	CG2 ILE 1 694	1.758	24.501	-5.174	1.00	0.49
ATOM	1395	CD1 ILE 1 694	5.495	24.000	-4.085	1.00	0.49
ATOM	1396	N LYS 1 695	0.636	22.677	-3.244	1.00	0.48
ATOM	1397	CA LYS 1 695	-0.261	22.939	-2.163	1.00	0.48
ATOM	1398	C LYS 1 695	-0.026	21.937	-1.074	1.00	0.48
ATOM	1399	O LYS 1 695	0.007	22.294	0.103	1.00	0.48
ATOM	1400	CB LYS 1 695	-1.731	22.841	-2.580	1.00	0.48
ATOM	1401	CG LYS 1 695	-2.652	23.125	-1.404	1.00	0.48
ATOM	1402	CD LYS 1 695	-4.097	23.419	-1.775	1.00	0.48
ATOM	1403	CE LYS 1 695	-4.909	23.685	-0.516	1.00	0.48
ATOM	1404	NZ LYS 1 695	-4.012	24.318	0.480	1.00	0.48
ATOM	1405	N GLU 1 696	0.150	20.653	-1.435	1.00	0.53
ATOM	1406	CA GLU 1 696	0.333	19.620	-0.456	1.00	0.53
ATOM	1407	C GLU 1 696	1.620	19.825	0.281	1.00	0.53
ATOM	1408	O GLU 1 696	1.708	19.539	1.474	1.00	0.53
ATOM	1409	CB GLU 1 696	0.324	18.217	-1.073	1.00	0.53
ATOM	1410	CG GLU 1 696	0.482	17.109	-0.039	1.00	0.53
ATOM	1411	CD GLU 1 696	-0.216	15.890	-0.609	1.00	0.53
ATOM	1412	OE1 GLU 1 696	0.118	15.476	-1.754	1.00	0.53
ATOM	1413	OE2 GLU 1 696	-1.124	15.376	0.094	1.00	0.53
ATOM	1414	N LEU 1 697	2.664	20.309	-0.413	1.00	0.53
ATOM	1415	CA LEU 1 697	3.923	20.528	0.235	1.00	0.53
ATOM	1416	C LEU 1 697	3.675	21.553	1.294	1.00	0.53
ATOM	1417	O LEU 1 697	4.124	21.409	2.431	1.00	0.53
ATOM	1418	CB LEU 1 697	4.979	21.072	-0.754	1.00	0.53
ATOM	1419	CG LEU 1 697	6.432	21.204	-0.237	1.00	0.53
ATOM	1420	CD1 LEU 1 697	7.343	21.760	-1.342	1.00	0.53
ATOM	1421	CD2 LEU 1 697	6.556	22.030	1.052	1.00	0.53
ATOM	1422	N GLY 1 698	2.918	22.610	0.947	1.00	0.46
ATOM	1423	CA GLY 1 698	2.678	23.669	1.882	1.00	0.46
ATOM	1424	C GLY 1 698	2.004	23.090	3.082	1.00	0.46
ATOM	1425	O GLY 1 698	2.368	23.403	4.215	1.00	0.46
ATOM	1426	N LYS 1 699	1.007	22.213	2.863	1.00	0.51
ATOM	1427	CA LYS 1 699	0.292	21.641	3.965	1.00	0.51
ATOM	1428	C LYS 1 699	1.257	20.845	4.780	1.00	0.51
ATOM	1429	O LYS 1 699	1.223	20.891	6.008	1.00	0.51
ATOM	1430	CB LYS 1 699	-0.839	20.695	3.531	1.00	0.51
ATOM	1431	CG LYS 1 699	-1.677	20.116	4.678	1.00	0.51
ATOM	1432	CD LYS 1 699	-0.960	19.104	5.576	1.00	0.51
ATOM	1433	CE LYS 1 699	-1.900	18.336	6.503	1.00	0.51
ATOM	1434	NZ LYS 1 699	-2.649	17.334	5.716	1.00	0.51
ATOM	1435	N ALA 1 700	2.147	20.088	4.116	1.00	0.30
ATOM	1436	CA ALA 1 700	3.064	19.273	4.856	1.00	0.30
ATOM	1437	C ALA 1 700	3.878	20.181	5.719	1.00	0.30
ATOM	1438	O ALA 1 700	4.070	19.912	6.901	1.00	0.30
ATOM	1439	CB ALA 1 700	4.032	18.493	3.951	1.00	0.30
ATOM	1440	N ILE 1 701	4.363	21.300	5.154	1.00	0.10
ATOM	1441	CA ILE 1 701	5.161	22.196	5.940	1.00	0.10
ATOM	1442	C ILE 1 701	4.318	22.798	7.019	1.00	0.10

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ATOM	1443	O	ILE	1	701	4.811	23.027	8.119	1.00	0.10
ATOM	1444	CB	ILE	1	701	5.779	23.316	5.157	1.00	0.10
ATOM	1445	CG1	ILE	1	701	6.800	22.756	4.156	1.00	0.10
ATOM	1446	CG2	ILE	1	701	6.380	24.319	6.154	1.00	0.10
ATOM	1447	CD1	ILE	1	701	7.389	23.822	3.239	1.00	0.10
ATOM	1448	N	VAL	1	702	3.027	23.067	6.751	1.00	0.25
ATOM	1449	CA	VAL	1	702	2.179	23.698	7.728	1.00	0.25
ATOM	1450	C	VAL	1	702	2.105	22.838	8.953	1.00	0.25
ATOM	1451	O	VAL	1	702	2.160	23.345	10.074	1.00	0.25
ATOM	1452	CB	VAL	1	702	0.773	23.893	7.237	1.00	0.25
ATOM	1453	CG1	VAL	1	702	-0.072	24.462	8.390	1.00	0.25
ATOM	1454	CG2	VAL	1	702	0.804	24.793	5.992	1.00	0.25
ATOM	1455	N	LYS	1	703	1.976	21.510	8.782	1.00	0.54
ATOM	1456	CA	LYS	1	703	1.907	20.638	9.921	1.00	0.54
ATOM	1457	C	LYS	1	703	3.202	20.763	10.655	1.00	0.54
ATOM	1458	O	LYS	1	703	3.252	20.709	11.882	1.00	0.54
ATOM	1459	CB	LYS	1	703	1.736	19.156	9.544	1.00	0.54
ATOM	1460	CG	LYS	1	703	0.302	18.767	9.175	1.00	0.54
ATOM	1461	CD	LYS	1	703	-0.678	18.913	10.343	1.00	0.54
ATOM	1462	CE	LYS	1	703	-2.115	18.520	9.997	1.00	0.54
ATOM	1463	NZ	LYS	1	703	-2.697	19.497	9.051	1.00	0.54
ATOM	1464	N	ARG	1	704	4.285	20.916	9.876	1.00	0.56
ATOM	1465	CA	ARG	1	704	5.649	21.052	10.296	1.00	0.56
ATOM	1466	C	ARG	1	704	5.826	22.375	10.975	1.00	0.56
ATOM	1467	O	ARG	1	704	6.790	22.569	11.706	1.00	0.56
ATOM	1468	CB	ARG	1	704	6.621	21.060	9.110	1.00	0.56
ATOM	1469	CG	ARG	1	704	6.476	19.841	8.203	1.00	0.56
ATOM	1470	CD	ARG	1	704	7.538	18.769	8.399	1.00	0.56
ATOM	1471	NE	ARG	1	704	7.227	17.677	7.435	1.00	0.56
ATOM	1472	CZ	ARG	1	704	7.577	17.824	6.126	1.00	0.56
ATOM	1473	NH1	ARG	1	704	8.094	19.016	5.707	1.00	0.56
ATOM	1474	NH2	ARG	1	704	7.393	16.800	5.241	1.00	0.56
ATOM	1475	N	GLU	1	705	4.943	23.351	10.703	1.00	0.33
ATOM	1476	CA	GLU	1	705	5.067	24.660	11.273	1.00	0.33
ATOM	1477	C	GLU	1	705	5.018	24.487	12.745	1.00	0.33
ATOM	1478	O	GLU	1	705	5.553	25.308	13.487	1.00	0.33
ATOM	1479	CB	GLU	1	705	3.927	25.610	10.865	1.00	0.33
ATOM	1480	CG	GLU	1	705	3.971	26.009	9.388	1.00	0.33
ATOM	1481	CD	GLU	1	705	2.801	26.945	9.116	1.00	0.33
ATOM	1482	OE1	GLU	1	705	1.661	26.599	9.526	1.00	0.33
ATOM	1483	OE2	GLU	1	705	3.033	28.020	8.502	1.00	0.33
ATOM	1484	N	GLY	1	706	4.349	23.411	13.199	1.00	0.32
ATOM	1485	CA	GLY	1	706	4.308	23.157	14.606	1.00	0.32
ATOM	1486	C	GLY	1	706	5.740	23.077	15.057	1.00	0.32
ATOM	1487	O	GLY	1	706	6.110	23.626	16.093	1.00	0.32
ATOM	1488	N	ASN	1	707	6.583	22.380	14.269	1.00	0.57
ATOM	1489	CA	ASN	1	707	8.003	22.293	14.495	1.00	0.57
ATOM	1490	C	ASN	1	707	8.678	23.518	13.914	1.00	0.57
ATOM	1491	O	ASN	1	707	8.123	24.615	13.978	1.00	0.57
ATOM	1492	CB	ASN	1	707	8.675	21.053	13.883	1.00	0.57
ATOM	1493	CG	ASN	1	707	8.450	19.896	14.845	1.00	0.57
ATOM	1494	OD1	ASN	1	707	8.562	20.061	16.059	1.00	0.57
ATOM	1495	ND2	ASN	1	707	8.128	18.695	14.295	1.00	0.57
ATOM	1496	N	SER	1	708	9.913	23.381	13.351	1.00	0.75
ATOM	1497	CA	SER	1	708	10.585	24.562	12.856	1.00	0.75
ATOM	1498	C	SER	1	708	11.409	24.261	11.624	1.00	0.75
ATOM	1499	O	SER	1	708	10.923	23.649	10.675	1.00	0.75
ATOM	1500	CB	SER	1	708	11.518	25.203	13.903	1.00	0.75
ATOM	1501	OG	SER	1	708	11.979	26.472	13.456	1.00	0.75
ATOM	1502	N	SER	1	709	12.701	24.680	11.637	1.00	0.78
ATOM	1503	CA	SER	1	709	13.639	24.623	10.539	1.00	0.78

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ATOM	1504	C	SER	1	709	13.812	23.206	10.131	1.00	0.78
ATOM	1505	O	SER	1	709	14.038	22.890	8.963	1.00	0.78
ATOM	1506	CB	SER	1	709	15.027	25.173	10.906	1.00	0.78
ATOM	1507	OG	SER	1	709	15.895	25.089	9.785	1.00	0.78
ATOM	1508	N	GLN	1	710	13.662	22.297	11.097	1.00	0.75
ATOM	1509	CA	GLN	1	710	13.776	20.896	10.850	1.00	0.75
ATOM	1510	C	GLN	1	710	12.756	20.537	9.812	1.00	0.75
ATOM	1511	O	GLN	1	710	12.848	19.490	9.176	1.00	0.75
ATOM	1512	CB	GLN	1	710	13.556	20.062	12.126	1.00	0.75
ATOM	1513	CG	GLN	1	710	12.186	20.243	12.786	1.00	0.75
ATOM	1514	CD	GLN	1	710	11.210	19.233	12.201	1.00	0.75
ATOM	1515	OE1	GLN	1	710	10.623	19.439	11.140	1.00	0.75
ATOM	1516	NE2	GLN	1	710	11.024	18.097	12.925	1.00	0.75
ATOM	1517	N	ASN	1	711	11.739	21.396	9.614	1.00	0.76
ATOM	1518	CA	ASN	1	711	10.693	21.096	8.687	1.00	0.76
ATOM	1519	C	ASN	1	711	11.273	20.783	7.340	1.00	0.76
ATOM	1520	O	ASN	1	711	10.878	19.797	6.721	1.00	0.76
ATOM	1521	CB	ASN	1	711	9.669	22.243	8.500	1.00	0.76
ATOM	1522	CG	ASN	1	711	10.266	23.392	7.691	1.00	0.76
ATOM	1523	OD1	ASN	1	711	9.671	23.816	6.701	1.00	0.76
ATOM	1524	ND2	ASN	1	711	11.464	23.898	8.088	1.00	0.76
ATOM	1525	N	TRP	1	712	12.239	21.579	6.841	1.00	0.75
ATOM	1526	CA	TRP	1	712	12.723	21.288	5.526	1.00	0.75
ATOM	1527	C	TRP	1	712	13.425	19.976	5.555	1.00	0.75
ATOM	1528	O	TRP	1	712	13.300	19.181	4.626	1.00	0.75
ATOM	1529	CB	TRP	1	712	13.655	22.361	4.925	1.00	0.75
ATOM	1530	CG	TRP	1	712	14.940	22.648	5.661	1.00	0.75
ATOM	1531	CD1	TRP	1	712	15.209	23.608	6.592	1.00	0.75
ATOM	1532	CD2	TRP	1	712	16.165	21.927	5.457	1.00	0.75
ATOM	1533	NE1	TRP	1	712	16.525	23.530	6.981	1.00	0.75
ATOM	1534	CE2	TRP	1	712	17.126	22.501	6.289	1.00	0.75
ATOM	1535	CE3	TRP	1	712	16.465	20.877	4.637	1.00	0.75
ATOM	1536	CZ2	TRP	1	712	18.406	22.030	6.315	1.00	0.75
ATOM	1537	CZ3	TRP	1	712	17.757	20.402	4.669	1.00	0.75
ATOM	1538	CH2	TRP	1	712	18.710	20.967	5.492	1.00	0.75
ATOM	1539	N	GLN	1	713	14.177	19.695	6.634	1.00	0.74
ATOM	1540	CA	GLN	1	713	14.891	18.457	6.634	1.00	0.74
ATOM	1541	C	GLN	1	713	13.930	17.308	6.637	1.00	0.74
ATOM	1542	O	GLN	1	713	14.136	16.347	5.898	1.00	0.74
ATOM	1543	CB	GLN	1	713	15.880	18.271	7.805	1.00	0.74
ATOM	1544	CG	GLN	1	713	15.253	18.190	9.195	1.00	0.74
ATOM	1545	CD	GLN	1	713	16.378	18.001	10.202	1.00	0.74
ATOM	1546	OE1	GLN	1	713	17.241	17.142	10.026	1.00	0.74
ATOM	1547	NE2	GLN	1	713	16.375	18.824	11.285	1.00	0.74
ATOM	1548	N	ARG	1	714	12.852	17.354	7.452	1.00	0.79
ATOM	1549	CA	ARG	1	714	12.025	16.180	7.441	1.00	0.79
ATOM	1550	C	ARG	1	714	11.270	16.111	6.153	1.00	0.79
ATOM	1551	O	ARG	1	714	10.972	15.018	5.677	1.00	0.79
ATOM	1552	CB	ARG	1	714	11.013	15.980	8.582	1.00	0.79
ATOM	1553	CG	ARG	1	714	9.787	16.880	8.603	1.00	0.79
ATOM	1554	CD	ARG	1	714	8.678	16.232	9.436	1.00	0.79
ATOM	1555	NE	ARG	1	714	8.479	14.866	8.866	1.00	0.79
ATOM	1556	CZ	ARG	1	714	8.281	13.792	9.687	1.00	0.79
ATOM	1557	NH1	ARG	1	714	8.141	13.974	11.032	1.00	0.79
ATOM	1558	NH2	ARG	1	714	8.236	12.531	9.163	1.00	0.79
ATOM	1559	N	PHE	1	715	10.938	17.275	5.557	1.00	0.65
ATOM	1560	CA	PHE	1	715	10.213	17.296	4.317	1.00	0.65
ATOM	1561	C	PHE	1	715	10.983	16.458	3.352	1.00	0.65
ATOM	1562	O	PHE	1	715	10.428	15.591	2.677	1.00	0.65
ATOM	1563	CB	PHE	1	715	10.144	18.722	3.732	1.00	0.65
ATOM	1564	CG	PHE	1	715	9.605	18.677	2.343	1.00	0.65

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ATOM	1565	CD1 PHE 1 715	10.456	18.485	1.279	1.00	0.65
ATOM	1566	CD2 PHE 1 715	8.261	18.839	2.098	1.00	0.65
ATOM	1567	CE1 PHE 1 715	9.980	18.442	-0.009	1.00	0.65
ATOM	1568	CE2 PHE 1 715	7.778	18.796	0.810	1.00	0.65
ATOM	1569	CZ PHE 1 715	8.636	18.600	-0.245	1.00	0.65
ATOM	1570	N TYR 1 716	12.304	16.684	3.293	1.00	0.39
ATOM	1571	CA TYR 1 716	13.139	15.973	2.374	1.00	0.39
ATOM	1572	C TYR 1 716	13.190	14.523	2.758	1.00	0.39
ATOM	1573	O TYR 1 716	13.166	13.645	1.898	1.00	0.39
ATOM	1574	CB TYR 1 716	14.574	16.527	2.358	1.00	0.39
ATOM	1575	CG TYR 1 716	15.270	15.962	1.170	1.00	0.39
ATOM	1576	CD1 TYR 1 716	14.998	16.459	-0.084	1.00	0.39
ATOM	1577	CD2 TYR 1 716	16.199	14.958	1.303	1.00	0.39
ATOM	1578	CE1 TYR 1 716	15.632	15.958	-1.196	1.00	0.39
ATOM	1579	CE2 TYR 1 716	16.835	14.453	0.193	1.00	0.39
ATOM	1580	CZ TYR 1 716	16.553	14.949	-1.057	1.00	0.39
ATOM	1581	OH TYR 1 716	17.210	14.426	-2.192	1.00	0.39
ATOM	1582	N GLN 1 717	13.246	14.226	4.069	1.00	0.36
ATOM	1583	CA GLN 1 717	13.376	12.867	4.515	1.00	0.36
ATOM	1584	C GLN 1 717	12.169	12.094	4.088	1.00	0.36
ATOM	1585	O GLN 1 717	12.266	10.940	3.674	1.00	0.36
ATOM	1586	CB GLN 1 717	13.486	12.774	6.047	1.00	0.36
ATOM	1587	CG GLN 1 717	14.732	13.473	6.595	1.00	0.36
ATOM	1588	CD GLN 1 717	14.729	13.344	8.112	1.00	0.36
ATOM	1589	OE1 GLN 1 717	13.812	12.773	8.699	1.00	0.36
ATOM	1590	NE2 GLN 1 717	15.784	13.899	8.767	1.00	0.36
ATOM	1591	N LEU 1 718	10.995	12.730	4.195	1.00	0.57
ATOM	1592	CA LEU 1 718	9.732	12.125	3.904	1.00	0.57
ATOM	1593	C LEU 1 718	9.666	11.818	2.429	1.00	0.57
ATOM	1594	O LEU 1 718	9.368	10.690	2.038	1.00	0.57
ATOM	1595	CB LEU 1 718	8.641	13.110	4.380	1.00	0.57
ATOM	1596	CG LEU 1 718	7.234	12.552	4.638	1.00	0.57
ATOM	1597	CD1 LEU 1 718	6.404	12.443	3.364	1.00	0.57
ATOM	1598	CD2 LEU 1 718	7.308	11.232	5.423	1.00	0.57
ATOM	1599	N THR 1 719	10.036	12.791	1.569	1.00	0.57
ATOM	1600	CA THR 1 719	9.946	12.619	0.142	1.00	0.57
ATOM	1601	C THR 1 719	10.827	11.486	-0.296	1.00	0.57
ATOM	1602	O THR 1 719	10.443	10.696	-1.157	1.00	0.57
ATOM	1603	CB THR 1 719	10.346	13.839	-0.634	1.00	0.57
ATOM	1604	OG1 THR 1 719	10.019	13.674	-2.006	1.00	0.57
ATOM	1605	CG2 THR 1 719	11.858	14.065	-0.477	1.00	0.57
ATOM	1606	N LYS 1 720	12.023	11.354	0.307	1.00	0.38
ATOM	1607	CA LYS 1 720	12.934	10.319	-0.099	1.00	0.38
ATOM	1608	C LYS 1 720	12.274	8.996	0.098	1.00	0.38
ATOM	1609	O LYS 1 720	12.531	8.055	-0.652	1.00	0.38
ATOM	1610	CB LYS 1 720	14.252	10.265	0.693	1.00	0.38
ATOM	1611	CG LYS 1 720	15.349	11.205	0.189	1.00	0.38
ATOM	1612	CD LYS 1 720	16.603	11.178	1.068	1.00	0.38
ATOM	1613	CE LYS 1 720	17.860	11.700	0.369	1.00	0.38
ATOM	1614	NZ LYS 1 720	19.019	11.637	1.288	1.00	0.38
ATOM	1615	N LEU 1 721	11.410	8.889	1.118	1.00	0.41
ATOM	1616	CA LEU 1 721	10.767	7.646	1.426	1.00	0.41
ATOM	1617	C LEU 1 721	9.983	7.235	0.221	1.00	0.41
ATOM	1618	O LEU 1 721	9.905	6.051	-0.104	1.00	0.41
ATOM	1619	CB LEU 1 721	9.819	7.794	2.641	1.00	0.41
ATOM	1620	CG LEU 1 721	9.144	6.513	3.195	1.00	0.41
ATOM	1621	CD1 LEU 1 721	8.249	6.867	4.393	1.00	0.41
ATOM	1622	CD2 LEU 1 721	8.357	5.719	2.139	1.00	0.41
ATOM	1623	N LEU 1 722	9.394	8.208	-0.496	1.00	0.46
ATOM	1624	CA LEU 1 722	8.576	7.876	-1.624	1.00	0.46
ATOM	1625	C LEU 1 722	9.408	7.127	-2.616	1.00	0.46

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ATOM 1626 O LEU 1 722	8.915	6.230	-3.299	1.00	0.46
ATOM 1627 CB LEU 1 722	7.969	9.106	-2.310	1.00	0.46
ATOM 1628 CG LEU 1 722	7.062	9.891	-1.348	1.00	0.46
ATOM 1629 CD1 LEU 1 722	5.991	8.978	-0.757	1.00	0.46
ATOM 1630 CD2 LEU 1 722	7.853	10.594	-0.247	1.00	0.46
ATOM 1631 N ASP 1 723	10.702	7.472	-2.713	1.00	0.32
ATOM 1632 CA ASP 1 723	11.577	6.833	-3.653	1.00	0.32
ATOM 1633 C ASP 1 723	11.612	5.365	-3.353	1.00	0.32
ATOM 1634 O ASP 1 723	11.535	4.538	-4.260	1.00	0.32
ATOM 1635 CB ASP 1 723	13.016	7.366	-3.553	1.00	0.32
ATOM 1636 CG ASP 1 723	13.820	6.816	-4.720	1.00	0.32
ATOM 1637 OD1 ASP 1 723	13.280	5.949	-5.460	1.00	0.32
ATOM 1638 OD2 ASP 1 723	14.986	7.261	-4.891	1.00	0.32
ATOM 1639 N SER 1 724	11.725	4.993	-2.064	1.00	0.37
ATOM 1640 CA SER 1 724	11.768	3.605	-1.698	1.00	0.37
ATOM 1641 C SER 1 724	10.451	2.992	-2.035	1.00	0.37
ATOM 1642 O SER 1 724	10.378	1.874	-2.545	1.00	0.37
ATOM 1643 CB SER 1 724	11.996	3.386	-0.193	1.00	0.37
ATOM 1644 OG SER 1 724	13.290	3.839	0.179	1.00	0.37
ATOM 1645 N MET 1 725	9.361	3.729	-1.762	1.00	0.66
ATOM 1646 CA MET 1 725	8.072	3.193	-2.052	1.00	0.66
ATOM 1647 C MET 1 725	7.970	2.854	-3.501	1.00	0.66
ATOM 1648 O MET 1 725	7.555	1.752	-3.852	1.00	0.66
ATOM 1649 CB MET 1 725	6.932	4.153	-1.772	1.00	0.66
ATOM 1650 CG MET 1 725	5.871	3.883	-2.820	1.00	0.66
ATOM 1651 SD MET 1 725	4.224	3.695	-2.158	1.00	0.66
ATOM 1652 CE MET 1 725	4.459	1.902	-2.141	1.00	0.66
ATOM 1653 N HIS 1 726	8.371	3.782	-4.387	1.00	0.61
ATOM 1654 CA HIS 1 726	8.237	3.502	-5.783	1.00	0.61
ATOM 1655 C HIS 1 726	9.095	2.305	-6.065	1.00	0.61
ATOM 1656 O HIS 1 726	8.780	1.475	-6.915	1.00	0.61
ATOM 1657 CB HIS 1 726	8.711	4.639	-6.711	1.00	0.61
ATOM 1658 CG HIS 1 726	10.055	4.399	-7.336	1.00	0.61
ATOM 1659 ND1 HIS 1 726	11.249	4.906	-6.875	1.00	0.61
ATOM 1660 CD2 HIS 1 726	10.368	3.665	-8.439	1.00	0.61
ATOM 1661 CE1 HIS 1 726	12.217	4.456	-7.713	1.00	0.61
ATOM 1662 NE2 HIS 1 726	11.731	3.696	-8.679	1.00	0.61
ATOM 1663 N GLU 1 727	10.225	2.180	-5.350	1.00	0.31
ATOM 1664 CA GLU 1 727	11.096	1.064	-5.583	1.00	0.31
ATOM 1665 C GLU 1 727	10.346	-0.202	-5.309	1.00	0.31
ATOM 1666 O GLU 1 727	10.375	-1.135	-6.109	1.00	0.31
ATOM 1667 CB GLU 1 727	12.319	1.061	-4.647	1.00	0.31
ATOM 1668 CG GLU 1 727	13.277	-0.115	-4.861	1.00	0.31
ATOM 1669 CD GLU 1 727	14.217	0.223	-6.009	1.00	0.31
ATOM 1670 OE1 GLU 1 727	14.052	1.322	-6.600	1.00	0.31
ATOM 1671 OE2 GLU 1 727	15.116	-0.610	-6.307	1.00	0.31
ATOM 1672 N VAL 1 728	9.625	-0.260	-4.173	1.00	0.24
ATOM 1673 CA VAL 1 728	8.946	-1.466	-3.797	1.00	0.24
ATOM 1674 C VAL 1 728	7.895	-1.812	-4.811	1.00	0.24
ATOM 1675 O VAL 1 728	7.779	-2.966	-5.215	1.00	0.24
ATOM 1676 CB VAL 1 728	8.270	-1.359	-2.460	1.00	0.24
ATOM 1677 CG1 VAL 1 728	7.544	-2.684	-2.179	1.00	0.24
ATOM 1678 CG2 VAL 1 728	9.328	-0.993	-1.403	1.00	0.24
ATOM 1679 N VAL 1 729	7.106	-0.824	-5.277	1.00	0.27
ATOM 1680 CA VAL 1 729	6.049	-1.153	-6.196	1.00	0.27
ATOM 1681 C VAL 1 729	6.627	-1.732	-7.446	1.00	0.27
ATOM 1682 O VAL 1 729	6.080	-2.685	-7.999	1.00	0.27
ATOM 1683 CB VAL 1 729	5.187	0.011	-6.578	1.00	0.27
ATOM 1684 CG1 VAL 1 729	6.083	1.141	-7.070	1.00	0.27
ATOM 1685 CG2 VAL 1 729	4.225	-0.450	-7.682	1.00	0.27
ATOM 1686 N GLU 1 730	7.755	-1.181	-7.930	1.00	0.20

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ATOM	1687	CA	GLU 1 730	8.331	-1.697	-9.137	1.00	0.20
ATOM	1688	C	GLU 1 730	8.701	-3.128	-8.906	1.00	0.20
ATOM	1689	O	GLU 1 730	8.432	-3.992	-9.739	1.00	0.20
ATOM	1690	CB	GLU 1 730	9.622	-0.967	-9.548	1.00	0.20
ATOM	1691	CG	GLU 1 730	9.411	0.480	-9.995	1.00	0.20
ATOM	1692	CD	GLU 1 730	10.775	1.052	-10.361	1.00	0.20
ATOM	1693	OE1	GLU 1 730	11.795	0.364	-10.089	1.00	0.20
ATOM	1694	OE2	GLU 1 730	10.815	2.182	-10.918	1.00	0.20
ATOM	1695	N	ASN 1 731	9.320	-3.425	-7.747	1.00	0.32
ATOM	1696	CA	ASN 1 731	9.750	-4.770	-7.476	1.00	0.32
ATOM	1697	C	ASN 1 731	8.540	-5.653	-7.428	1.00	0.32
ATOM	1698	O	ASN 1 731	8.524	-6.750	-7.984	1.00	0.32
ATOM	1699	CB	ASN 1 731	10.439	-4.911	-6.106	1.00	0.32
ATOM	1700	CG	ASN 1 731	11.757	-4.150	-6.131	1.00	0.32
ATOM	1701	OD1	ASN 1 731	11.966	-3.220	-5.353	1.00	0.32
ATOM	1702	ND2	ASN 1 731	12.677	-4.561	-7.043	1.00	0.32
ATOM	1703	N	LEU 1 732	7.485	-5.154	-6.767	1.00	0.58
ATOM	1704	CA	LEU 1 732	6.243	-5.819	-6.490	1.00	0.58
ATOM	1705	C	LEU 1 732	5.591	-6.183	-7.788	1.00	0.58
ATOM	1706	O	LEU 1 732	5.074	-7.284	-7.968	1.00	0.58
ATOM	1707	CB	LEU 1 732	5.328	-4.808	-5.758	1.00	0.58
ATOM	1708	CG	LEU 1 732	3.972	-5.281	-5.199	1.00	0.58
ATOM	1709	CD1	LEU 1 732	3.073	-5.879	-6.288	1.00	0.58
ATOM	1710	CD2	LEU 1 732	4.136	-6.139	-3.935	1.00	0.58
ATOM	1711	N	LEU 1 733	5.610	-5.243	-8.741	1.00	0.50
ATOM	1712	CA	LEU 1 733	4.987	-5.442	-10.012	1.00	0.50
ATOM	1713	C	LEU 1 733	5.675	-6.592	-10.665	1.00	0.50
ATOM	1714	O	LEU 1 733	5.035	-7.455	-11.264	1.00	0.50
ATOM	1715	CB	LEU 1 733	5.120	-4.169	-10.881	1.00	0.50
ATOM	1716	CG	LEU 1 733	4.505	-4.206	-12.297	1.00	0.50
ATOM	1717	CD1	LEU 1 733	4.515	-2.802	-12.923	1.00	0.50
ATOM	1718	CD2	LEU 1 733	5.231	-5.199	-13.215	1.00	0.50
ATOM	1719	N	ASN 1 734	7.011	-6.640	-10.542	1.00	0.49
ATOM	1720	CA	ASN 1 734	7.777	-7.666	-11.173	1.00	0.49
ATOM	1721	C	ASN 1 734	7.385	-8.993	-10.610	1.00	0.49
ATOM	1722	O	ASN 1 734	7.142	-9.935	-11.364	1.00	0.49
ATOM	1723	CB	ASN 1 734	9.285	-7.497	-10.929	1.00	0.49
ATOM	1724	CG	ASN 1 734	9.726	-6.207	-11.606	1.00	0.49
ATOM	1725	OD1	ASN 1 734	10.835	-5.724	-11.385	1.00	0.49
ATOM	1726	ND2	ASN 1 734	8.829	-5.626	-12.446	1.00	0.49
ATOM	1727	N	TYR 1 735	7.291	-9.120	-9.270	1.00	0.60
ATOM	1728	CA	TYR 1 735	7.005	-10.439	-8.801	1.00	0.60
ATOM	1729	C	TYR 1 735	5.599	-10.789	-9.177	1.00	0.60
ATOM	1730	O	TYR 1 735	5.313	-11.930	-9.530	1.00	0.60
ATOM	1731	CB	TYR 1 735	7.184	-10.691	-7.286	1.00	0.60
ATOM	1732	CG	TYR 1 735	6.309	-11.797	-6.820	1.00	0.60
ATOM	1733	CD1	TYR 1 735	6.817	-13.073	-6.700	1.00	0.60
ATOM	1734	CD2	TYR 1 735	5.000	-11.570	-6.487	1.00	0.60
ATOM	1735	CE1	TYR 1 735	6.032	-14.115	-6.271	1.00	0.60
ATOM	1736	CE2	TYR 1 735	4.213	-12.610	-6.058	1.00	0.60
ATOM	1737	CZ	TYR 1 735	4.720	-13.880	-5.945	1.00	0.60
ATOM	1738	OH	TYR 1 735	3.896	-14.937	-5.502	1.00	0.60
ATOM	1739	N	CYS 1 736	4.679	-9.807	-9.118	1.00	0.35
ATOM	1740	CA	CYS 1 736	3.307	-10.089	-9.430	1.00	0.35
ATOM	1741	C	CYS 1 736	3.190	-10.561	-10.845	1.00	0.35
ATOM	1742	O	CYS 1 736	2.445	-11.495	-11.129	1.00	0.35
ATOM	1743	CB	CYS 1 736	2.372	-8.880	-9.264	1.00	0.35
ATOM	1744	SG	CYS 1 736	0.657	-9.282	-9.704	1.00	0.35
ATOM	1745	N	PHE 1 737	3.916	-9.929	-11.781	1.00	0.23
ATOM	1746	CA	PHE 1 737	3.843	-10.330	-13.159	1.00	0.23
ATOM	1747	C	PHE 1 737	4.403	-11.702	-13.327	1.00	0.23

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ATOM 1748 O PHE 1 737	3.948 -12.460 -14.182	1.00 0.23
ATOM 1749 CB PHE 1 737	4.580 -9.375 -14.112	1.00 0.23
ATOM 1750 CG PHE 1 737	3.649 -8.243 -14.374	1.00 0.23
ATOM 1751 CD1 PHE 1 737	3.272 -7.390 -13.365	1.00 0.23
ATOM 1752 CD2 PHE 1 737	3.162 -8.024 -15.642	1.00 0.23
ATOM 1753 CE1 PHE 1 737	2.417 -6.343 -13.610	1.00 0.23
ATOM 1754 CE2 PHE 1 737	2.307 -6.979 -15.897	1.00 0.23
ATOM 1755 CZ PHE 1 737	1.932 -6.135 -14.879	1.00 0.23
ATOM 1756 N GLN 1 738	5.406 -12.066 -12.510	1.00 0.51
ATOM 1757 CA GLN 1 738	6.023 -13.349 -12.668	1.00 0.51
ATOM 1758 C GLN 1 738	4.972 -14.401 -12.517	1.00 0.51
ATOM 1759 O GLN 1 738	4.969 -15.382 -13.259	1.00 0.51
ATOM 1760 CB GLN 1 738	7.117 -13.623 -11.624	1.00 0.51
ATOM 1761 CG GLN 1 738	7.780 -14.992 -11.789	1.00 0.51
ATOM 1762 CD GLN 1 738	8.835 -15.134 -10.704	1.00 0.51
ATOM 1763 OE1 GLN 1 738	9.512 -16.157 -10.608	1.00 0.51
ATOM 1764 NE2 GLN 1 738	8.986 -14.076 -9.863	1.00 0.51
ATOM 1765 N THR 1 739	4.048 -14.244 -11.550	1.00 0.90
ATOM 1766 CA THR 1 739	3.029 -15.247 -11.419	1.00 0.90
ATOM 1767 C THR 1 739	2.174 -15.225 -12.654	1.00 0.90
ATOM 1768 O THR 1 739	1.803 -16.279 -13.166	1.00 0.90
ATOM 1769 CB THR 1 739	2.142 -15.068 -10.217	1.00 0.90
ATOM 1770 OG1 THR 1 739	1.347 -16.230 -10.027	1.00 0.90
ATOM 1771 CG2 THR 1 739	1.232 -13.847 -10.419	1.00 0.90
ATOM 1772 N PHE 1 740	1.885 -14.006 -13.162	1.00 1.13
ATOM 1773 CA PHE 1 740	1.060 -13.667 -14.296	1.00 1.13
ATOM 1774 C PHE 1 740	-0.092 -14.595 -14.496	1.00 1.13
ATOM 1775 O PHE 1 740	0.046 -15.748 -14.904	1.00 1.13
ATOM 1776 CB PHE 1 740	1.801 -13.428 -15.632	1.00 1.13
ATOM 1777 CG PHE 1 740	2.485 -14.665 -16.094	1.00 1.13
ATOM 1778 CD1 PHE 1 740	3.764 -14.948 -15.680	1.00 1.13
ATOM 1779 CD2 PHE 1 740	1.856 -15.534 -16.954	1.00 1.13
ATOM 1780 CE1 PHE 1 740	4.405 -16.086 -16.105	1.00 1.13
ATOM 1781 CE2 PHE 1 740	2.491 -16.675 -17.384	1.00 1.13
ATOM 1782 CZ PHE 1 740	3.768 -16.953 -16.960	1.00 1.13
ATOM 1783 N LEU 1 741	-1.299 -14.062 -14.231	1.00 0.91
ATOM 1784 CA LEU 1 741	-2.516 -14.800 -14.363	1.00 0.91
ATOM 1785 C LEU 1 741	-2.585 -15.245 -15.795	1.00 0.91
ATOM 1786 O LEU 1 741	-1.798 -14.796 -16.627	1.00 0.91
ATOM 1787 CB LEU 1 741	-3.734 -13.946 -13.914	1.00 0.91
ATOM 1788 CG LEU 1 741	-5.116 -14.632 -13.813	1.00 0.91
ATOM 1789 CD1 LEU 1 741	-6.063 -13.813 -12.921	1.00 0.91
ATOM 1790 CD2 LEU 1 741	-5.774 -14.842 -15.181	1.00 0.91
ATOM 1791 N ASP 1 742	-3.497 -16.191 -16.097	1.00 0.71
ATOM 1792 CA ASP 1 742	-3.666 -16.809 -17.383	1.00 0.71
ATOM 1793 C ASP 1 742	-3.861 -15.793 -18.466	1.00 0.71
ATOM 1794 O ASP 1 742	-3.692 -14.590 -18.274	1.00 0.71
ATOM 1795 CB ASP 1 742	-4.868 -17.767 -17.437	1.00 0.71
ATOM 1796 CG ASP 1 742	-4.569 -18.945 -16.523	1.00 0.71
ATOM 1797 OD1 ASP 1 742	-3.413 -19.028 -16.026	1.00 0.71
ATOM 1798 OD2 ASP 1 742	-5.488 -19.779 -16.312	1.00 0.71
ATOM 1799 N LYS 1 743	-4.243 -16.293 -19.661	1.00 0.84
ATOM 1800 CA LYS 1 743	-4.406 -15.475 -20.827	1.00 0.84
ATOM 1801 C LYS 1 743	-5.329 -14.369 -20.453	1.00 0.84
ATOM 1802 O LYS 1 743	-5.007 -13.196 -20.640	1.00 0.84
ATOM 1803 CB LYS 1 743	-5.006 -16.263 -22.010	1.00 0.84
ATOM 1804 CG LYS 1 743	-5.190 -15.460 -23.300	1.00 0.84
ATOM 1805 CD LYS 1 743	-6.291 -14.398 -23.237	1.00 0.84
ATOM 1806 CE LYS 1 743	-7.656 -14.917 -23.697	1.00 0.84
ATOM 1807 NZ LYS 1 743	-8.094 -16.034 -22.830	1.00 0.84
ATOM 1808 N THR 1 744	-6.500 -14.709 -19.892	1.00 0.84

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ATOM	1809	CA	THR	1744	-7.332	-13.651	-19.420	1.00	0.84
ATOM	1810	C	THR	1744	-6.812	-13.353	-18.055	1.00	0.84
ATOM	1811	O	THR	1744	-7.419	-13.704	-17.045	1.00	0.84
ATOM	1812	CB	THR	1744	-8.785	-14.025	-19.345	1.00	0.84
ATOM	1813	OG1	THR	1744	-8.976	-15.151	-18.500	1.00	0.84
ATOM	1814	CG2	THR	1744	-9.272	-14.343	-20.769	1.00	0.84
ATOM	1815	N	MET	1745	-5.662	-12.654	-18.017	1.00	0.84
ATOM	1816	CA	MET	1745	-4.952	-12.372	-16.808	1.00	0.84
ATOM	1817	C	MET	1745	-5.849	-11.640	-15.886	1.00	0.84
ATOM	1818	O	MET	1745	-5.684	-11.743	-14.673	1.00	0.84
ATOM	1819	CB	MET	1745	-3.711	-11.490	-17.017	1.00	0.84
ATOM	1820	CG	MET	1745	-2.968	-11.199	-15.713	1.00	0.84
ATOM	1821	SD	MET	1745	-1.485	-10.163	-15.900	1.00	0.84
ATOM	1822	CE	MET	1745	-1.092	-10.137	-14.128	1.00	0.84
ATOM	1823	N	SER	1746	-6.793	-10.877	-16.467	1.00	1.05
ATOM	1824	CA	SER	1746	-7.760	-10.055	-15.802	1.00	1.05
ATOM	1825	C	SER	1746	-7.333	-8.683	-16.106	1.00	1.05
ATOM	1826	O	SER	1746	-6.261	-8.265	-15.673	1.00	1.05
ATOM	1827	CB	SER	1746	-7.886	-10.209	-14.269	1.00	1.05
ATOM	1828	OG	SER	1746	-8.876	-9.333	-13.750	1.00	1.05
ATOM	1829	N	ILE	1747	-8.164	-8.021	-16.932	1.00	1.19
ATOM	1830	CA	ILE	1747	-8.108	-6.670	-17.393	1.00	1.19
ATOM	1831	C	ILE	1747	-8.073	-5.783	-16.187	1.00	1.19
ATOM	1832	O	ILE	1747	-9.044	-5.151	-15.774	1.00	1.19
ATOM	1833	CB	ILE	1747	-9.231	-6.532	-18.420	1.00	1.19
ATOM	1834	CG1	ILE	1747	-8.658	-6.825	-19.821	1.00	1.19
ATOM	1835	CG2	ILE	1747	-10.165	-5.327	-18.267	1.00	1.19
ATOM	1836	CD1	ILE	1747	-8.097	-8.235	-19.995	1.00	1.19
ATOM	1837	N	GLU	1748	-6.863	-5.764	-15.594	1.00	1.16
ATOM	1838	CA	GLU	1748	-6.527	-5.086	-14.392	1.00	1.16
ATOM	1839	C	GLU	1748	-6.244	-3.643	-14.601	1.00	1.16
ATOM	1840	O	GLU	1748	-6.780	-2.817	-13.867	1.00	1.16
ATOM	1841	CB	GLU	1748	-5.313	-5.690	-13.672	1.00	1.16
ATOM	1842	CG	GLU	1748	-4.996	-4.930	-12.388	1.00	1.16
ATOM	1843	CD	GLU	1748	-6.286	-4.866	-11.578	1.00	1.16
ATOM	1844	OE1	GLU	1748	-7.179	-5.725	-11.808	1.00	1.16
ATOM	1845	OE2	GLU	1748	-6.399	-3.946	-10.724	1.00	1.16
ATOM	1846	N	PHE	1749	-5.380	-3.260	-15.565	1.00	1.07
ATOM	1847	CA	PHE	1749	-5.167	-1.844	-15.542	1.00	1.07
ATOM	1848	C	PHE	1749	-6.057	-0.830	-16.231	1.00	1.07
ATOM	1849	O	PHE	1749	-6.666	-0.153	-15.426	1.00	1.07
ATOM	1850	CB	PHE	1749	-3.708	-1.384	-15.525	1.00	1.07
ATOM	1851	CG	PHE	1749	-3.490	-1.527	-14.058	1.00	1.07
ATOM	1852	CD1	PHE	1749	-4.079	-0.621	-13.203	1.00	1.07
ATOM	1853	CD2	PHE	1749	-2.740	-2.551	-13.532	1.00	1.07
ATOM	1854	CE1	PHE	1749	-3.924	-0.728	-11.843	1.00	1.07
ATOM	1855	CE2	PHE	1749	-2.580	-2.664	-12.172	1.00	1.07
ATOM	1856	CZ	PHE	1749	-3.175	-1.757	-11.330	1.00	1.07
ATOM	1857	N	PRO	1750	-6.247	-0.589	-17.529	1.00	0.90
ATOM	1858	CA	PRO	1750	-7.221	0.431	-17.979	1.00	0.90
ATOM	1859	C	PRO	1750	-8.771	0.442	-18.016	1.00	0.90
ATOM	1860	O	PRO	1750	-9.291	1.473	-17.605	1.00	0.90
ATOM	1861	CB	PRO	1750	-6.687	0.963	-19.305	1.00	0.90
ATOM	1862	CG	PRO	1750	-5.169	0.827	-19.170	1.00	0.90
ATOM	1863	CD	PRO	1750	-4.983	-0.372	-18.237	1.00	0.90
ATOM	1864	N	GLU	1751	-9.539	-0.588	-18.489	1.00	0.84
ATOM	1865	CA	GLU	1751	-11.014	-0.740	-18.539	1.00	0.84
ATOM	1866	C	GLU	1751	-11.479	-0.956	-17.136	1.00	0.84
ATOM	1867	O	GLU	1751	-12.611	-0.771	-16.702	1.00	0.84
ATOM	1868	CB	GLU	1751	-11.508	-2.071	-19.129	1.00	0.84
ATOM	1869	CG	GLU	1751	-11.246	-2.389	-20.592	1.00	0.84

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ATOM	1870	CD	GLU	1	751	-11.804	-3.799	-20.762	1.00	0.84
ATOM	1871	OE1	GLU	1	751	-12.632	-4.206	-19.902	1.00	0.84
ATOM	1872	OE2	GLU	1	751	-11.407	-4.491	-21.736	1.00	0.84
ATOM	1873	N	MET	1	752	-10.435	-1.330	-16.468	1.00	1.00
ATOM	1874	CA	MET	1	752	-9.749	-1.826	-15.370	1.00	1.00
ATOM	1875	C	MET	1	752	-9.587	-0.479	-14.739	1.00	1.00
ATOM	1876	O	MET	1	752	-9.038	0.421	-15.327	1.00	1.00
ATOM	1877	CB	MET	1	752	-8.464	-2.412	-15.976	1.00	1.00
ATOM	1878	CG	MET	1	752	-8.681	-2.977	-17.397	1.00	1.00
ATOM	1879	SD	MET	1	752	-7.488	-3.879	-18.478	1.00	1.00
ATOM	1880	CE	MET	1	752	-5.812	-3.234	-18.336	1.00	1.00
ATOM	1881	N	LEU	1	753	-10.177	-0.119	-13.608	1.00	0.82
ATOM	1882	CA	LEU	1	753	-10.723	1.132	-13.156	1.00	0.82
ATOM	1883	C	LEU	1	753	-11.151	2.199	-14.132	1.00	0.82
ATOM	1884	O	LEU	1	753	-11.750	3.146	-13.637	1.00	0.82
ATOM	1885	CB	LEU	1	753	-9.733	1.821	-12.206	1.00	0.82
ATOM	1886	CG	LEU	1	753	-9.134	0.865	-11.154	1.00	0.82
ATOM	1887	CD1	LEU	1	753	-8.168	1.601	-10.215	1.00	0.82
ATOM	1888	CD2	LEU	1	753	-10.213	0.066	-10.416	1.00	0.82
ATOM	1889	N	ALA	1	754	-10.833	2.252	-15.434	1.00	0.46
ATOM	1890	CA	ALA	1	754	-11.599	3.228	-16.176	1.00	0.46
ATOM	1891	C	ALA	1	754	-13.059	2.905	-15.999	1.00	0.46
ATOM	1892	O	ALA	1	754	-13.882	3.799	-15.806	1.00	0.46
ATOM	1893	CB	ALA	1	754	-11.365	3.231	-17.693	1.00	0.46
ATOM	1894	N	GLU	1	755	-13.440	1.617	-16.045	1.00	0.40
ATOM	1895	CA	GLU	1	755	-14.834	1.335	-15.868	1.00	0.40
ATOM	1896	C	GLU	1	755	-15.213	1.617	-14.439	1.00	0.40
ATOM	1897	O	GLU	1	755	-16.289	2.147	-14.167	1.00	0.40
ATOM	1898	CB	GLU	1	755	-15.219	-0.113	-16.213	1.00	0.40
ATOM	1899	CG	GLU	1	755	-16.662	-0.249	-16.703	1.00	0.40
ATOM	1900	CD	GLU	1	755	-16.704	0.257	-18.144	1.00	0.40
ATOM	1901	OE1	GLU	1	755	-15.627	0.649	-18.670	1.00	0.40
ATOM	1902	OE2	GLU	1	755	-17.815	0.259	-18.738	1.00	0.40
ATOM	1903	N	ILE	1	756	-14.344	1.276	-13.465	1.00	0.54
ATOM	1904	CA	ILE	1	756	-14.767	1.507	-12.107	1.00	0.54
ATOM	1905	C	ILE	1	756	-14.871	2.980	-11.844	1.00	0.54
ATOM	1906	O	ILE	1	756	-15.787	3.444	-11.166	1.00	0.54
ATOM	1907	CB	ILE	1	756	-13.882	0.897	-11.056	1.00	0.54
ATOM	1908	CG1	ILE	1	756	-14.628	0.842	-9.715	1.00	0.54
ATOM	1909	CG2	ILE	1	756	-12.589	1.712	-10.964	1.00	0.54
ATOM	1910	CD1	ILE	1	756	-13.948	-0.046	-8.675	1.00	0.54
ATOM	1911	N	ILE	1	757	-13.918	3.756	-12.381	1.00	0.68
ATOM	1912	CA	ILE	1	757	-13.860	5.171	-12.178	1.00	0.68
ATOM	1913	C	ILE	1	757	-15.065	5.770	-12.829	1.00	0.68
ATOM	1914	O	ILE	1	757	-15.686	6.676	-12.277	1.00	0.68
ATOM	1915	CB	ILE	1	757	-12.586	5.766	-12.730	1.00	0.68
ATOM	1916	CG1	ILE	1	757	-12.330	7.179	-12.179	1.00	0.68
ATOM	1917	CG2	ILE	1	757	-12.629	5.683	-14.261	1.00	0.68
ATOM	1918	CD1	ILE	1	757	-13.415	8.191	-12.530	1.00	0.68
ATOM	1919	N	THR	1	758	-15.440	5.275	-14.024	1.00	0.66
ATOM	1920	CA	THR	1	758	-16.587	5.825	-14.688	1.00	0.66
ATOM	1921	C	THR	1	758	-17.817	5.482	-13.909	1.00	0.66
ATOM	1922	O	THR	1	758	-18.720	6.305	-13.764	1.00	0.66
ATOM	1923	CB	THR	1	758	-16.759	5.334	-16.101	1.00	0.66
ATOM	1924	OG1	THR	1	758	-17.730	6.122	-16.773	1.00	0.66
ATOM	1925	CG2	THR	1	758	-17.208	3.866	-16.084	1.00	0.66
ATOM	1926	N	ASN	1	759	-17.878	4.251	-13.365	1.00	0.59
ATOM	1927	CA	ASN	1	759	-19.051	3.827	-12.658	1.00	0.59
ATOM	1928	C	ASN	1	759	-19.270	4.756	-11.512	1.00	0.59
ATOM	1929	O	ASN	1	759	-20.380	5.246	-11.304	1.00	0.59
ATOM	1930	CB	ASN	1	759	-18.912	2.404	-12.085	1.00	0.59

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ATOM	1931	CG ASN 1 759	-20.216	2.021	-11.396	1.00	0.59
ATOM	1932	OD1 ASN 1 759	-20.634	2.642	-10.421	1.00	0.59
ATOM	1933	ND2 ASN 1 759	-20.885	0.959	-11.921	1.00	0.59
ATOM	1934	N GLN 1 760	-18.207	5.047	-10.745	1.00	0.63
ATOM	1935	CA GLN 1 760	-18.377	5.911	-9.617	1.00	0.63
ATOM	1936	C GLN 1 760	-18.731	7.261	-10.147	1.00	0.63
ATOM	1937	O GLN 1 760	-18.410	7.597	-11.286	1.00	0.63
ATOM	1938	CB GLN 1 760	-17.108	6.042	-8.759	1.00	0.63
ATOM	1939	CG GLN 1 760	-17.262	6.958	-7.545	1.00	0.63
ATOM	1940	CD GLN 1 760	-15.928	6.970	-6.815	1.00	0.63
ATOM	1941	OE1 GLN 1 760	-15.008	6.239	-7.179	1.00	0.63
ATOM	1942	NE2 GLN 1 760	-15.814	7.819	-5.758	1.00	0.63
ATOM	1943	N ILE 1 761	-19.443	8.061	-9.333	1.00	0.75
ATOM	1944	CA ILE 1 761	-19.806	9.378	-9.765	1.00	0.75
ATOM	1945	C ILE 1 761	-18.957	10.329	-8.920	1.00	0.75
ATOM	1946	O ILE 1 761	-18.295	9.822	-7.976	1.00	0.75
ATOM	1947	CB ILE 1 761	-21.261	9.689	-9.526	1.00	0.75
ATOM	1948	CG1 ILE 1 761	-22.144	8.673	-10.271	1.00	0.75
ATOM	1949	CG2 ILE 1 761	-21.544	11.138	-9.954	1.00	0.75
ATOM	1950	CD1 ILE 1 761	-23.618	8.746	-9.878	1.00	0.75
ATOM	1951	OXT ILE 1 761	-18.946	11.557	-9.202	1.00	99.99
TER	1952	ILE 1 761					
HETATM	1953	C01 UNK 1	-2.020	-7.470	-3.975	1.00	-0.03
HETATM	1954	C08 UNK 1	-2.604	-8.499	-4.716	1.00	0.00
HETATM	1955	C07 UNK 1	-3.588	-8.239	-5.676	1.00	0.00
HETATM	1956	C04 UNK 1	-4.044	-6.938	-5.927	1.00	0.15
HETATM	1957	C03 UNK 1	-3.449	-5.887	-5.194	1.00	0.00
HETATM	1958	C02 UNK 1	-2.450	-6.150	-4.229	1.00	0.00
HETATM	1959	N05 UNK 1	-5.088	-6.741	-6.891	1.00	-0.69
HETATM	1960	C06 UNK 1	-5.500	-7.809	-7.786	1.00	0.27
HETATM	1961	C09 UNK 1	-5.841	-5.513	-7.030	1.00	0.27
HETATM	1962	C19 C 2	2.863	-9.728	-3.299	1.00	0.02
HETATM	1963	C22 C 2	3.237	-10.282	-2.296	1.00	-0.39
HETATM	1964	C22 C 2	3.714	-10.953	-1.093	1.00	0.30
HETATM	1965	H100C 2	2.874	-11.106	-0.400	1.00	0.00
HETATM	1966	H101C 2	4.482	-10.332	-0.607	1.00	0.00
HETATM	1967	H102C 2	4.148	-11.927	-1.363	1.00	0.00
HETATM	1968	C01 UNK 3	-2.100	-6.783	-0.557	1.00	0.03
HETATM	1969	C02 UNK 3	-0.922	-6.070	-1.201	1.00	-0.03
HETATM	1970	C17 UNK 3	-0.435	-4.794	-0.622	1.00	-0.03
HETATM	1971	C16 UNK 3	0.740	-4.085	-1.251	1.00	0.03
HETATM	1972	C15 UNK 3	1.664	-5.067	-1.960	1.00	0.00
HETATM	1973	C14 UNK 3	0.923	-5.996	-2.938	1.00	0.14
HETATM	1974	C03 UNK 3	-0.344	-6.602	-2.292	1.00	-0.27
HETATM	1975	C04 UNK 3	-0.997	-7.843	-2.908	1.00	0.17
HETATM	1976	C05 UNK 3	0.077	-8.825	-3.425	1.00	0.00
HETATM	1977	C06 UNK 3	1.195	-8.166	-4.241	1.00	0.00
HETATM	1978	C07 UNK 3	0.631	-7.623	-5.568	1.00	0.00
HETATM	1979	C08 UNK 3	2.441	-9.040	-4.505	1.00	0.31
HETATM	1980	O09 UNK 3	2.272	-9.992	-5.534	1.00	-0.55
HETATM	1981	H10 UNK 3	1.590	-10.610	-5.262	1.00	0.31
HETATM	1982	C11 UNK 3	3.536	-8.012	-4.833	1.00	0.00
HETATM	1983	C12 UNK 3	3.149	-6.736	-4.082	1.00	0.00
HETATM	1984	C13 UNK 3	1.875	-7.132	-3.336	1.00	0.00
HETATM	1985	C18 UNK 3	-1.069	-4.259	0.508	1.00	0.00
HETATM	1986	C19 UNK 3	-2.258	-4.896	1.089	1.00	0.40
HETATM	1987	C21 UNK 3	-3.030	-5.873	0.233	1.00	0.05
HETATM	1988	O20 UNK 3	-2.621	-4.644	2.227	1.00	-0.45
CONECT	1953	1954 1958 1975					
CONECT	1954	1953 1955					
CONECT	1955	1954 1956					

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HEADER PROTEIN  
 COMPND GR\_TR\_V1  
 AUTHOR GENERATED BY SYBYL, A PRODUCT OF TRIPOS, INC.  
 28-FEB-100  
 SEQRES 1 1 240 PRO ALA THR LEU PRO GLN LEU THR PRO THR LEU VAL SER  
 SEQRES 2 1 240 LEU LEU GLU VAL ILE GLU PRO GLU VAL LEU TYR ALA GLY  
 SEQRES 3 1 240 TYR ASP SER SER VAL PRO ASP SER THR TRP ARG ILE MET  
 SEQRES 4 1 240 THR THR LEU ASN MET LEU GLY GLY ARG GLN VAL ILE ALA  
 SEQRES 5 1 240 ALA VAL LYS TRP ALA LYS ALA ILE PRO GLY PHE ARG ASN  
 SEQRES 6 1 240 LEU HIS LEU ASP ASP GLN MET THR LEU LEU GLN TYR SER  
 SEQRES 7 1 240 TRP MET PHE LEU MET ALA PHE ALA LEU GLY TRP ARG SER  
 SEQRES 8 1 240 TYR ARG GLN SER SER ALA ASN LEU LEU CYS PHE ALA PRO  
 SEQRES 9 1 240 ASP LEU ILE ILE ASN GLU GLN ARG MET THR LEU PRO CYS  
 SEQRES 10 1 240 MET TYR ASP GLN CYS LYS HIS MET LEU TYR VAL SER SER  
 SEQRES 11 1 240 GLU LEU HIS ARG LEU GLN VAL SER TYR GLU GLU TYR LEU  
 SEQRES 12 1 240 CYS MET LYS THR LEU LEU LEU LEU SER SER VAL PRO LYS  
 SEQRES 13 1 240 ASP GLY LEU LYS SER GLN GLU LEU PHE ASP GLU ILE ARG  
 SEQRES 14 1 240 MET THR TYR ILE LYS GLU LEU GLY LYS ALA ILE VAL LYS  
 SEQRES 15 1 240 ARG GLU GLY ASN SER SER GLN ASN TRP GLN ARG PHE TYR  
 SEQRES 16 1 240 GLN LEU THR LYS LEU LEU ASP SER MET HIS GLU VAL VAL  
 SEQRES 17 1 240 GLU ASN LEU LEU ASN TYR CYS PHE GLN THR PHE LEU ASP  
 SEQRES 18 1 240 LYS THR MET SER ILE GLU PHE PRO GLU MET LEU ALA GLU  
 SEQRES 19 1 240 ILE ILE THR ASN GLN ILE  
 ATOM 1 N PRO 1 522 -0.627 29.241 5.806 1.00 5.52  
 ATOM 2 CA PRO 1 522 -1.732 29.968 5.121 1.00 5.52  
 ATOM 3 C PRO 1 522 -3.005 29.229 5.366 1.00 5.52  
 ATOM 4 O PRO 1 522 -2.966 28.016 5.546 1.00 5.52  
 ATOM 5 CB PRO 1 522 -1.324 30.082 3.655 1.00 5.52  
 ATOM 6 CG PRO 1 522 0.209 30.020 3.670 1.00 5.52  
 ATOM 7 CD PRO 1 522 0.557 29.143 4.882 1.00 5.52  
 ATOM 8 N ALA 1 523 -4.144 29.942 5.367 1.00 0.96  
 ATOM 9 CA ALA 1 523 -5.430 29.392 5.693 1.00 0.96  
 ATOM 10 C ALA 1 523 -5.899 28.334 4.745 1.00 0.96  
 ATOM 11 O ALA 1 523 -6.411 27.298 5.168 1.00 0.96  
 ATOM 12 CB ALA 1 523 -6.527 30.469 5.724 1.00 0.96  
 ATOM 13 N THR 1 524 -5.708 28.546 3.432 1.00 5.12  
 ATOM 14 CA THR 1 524 -6.270 27.645 2.469 1.00 5.12  
 ATOM 15 C THR 1 524 -5.769 26.255 2.661 1.00 5.12  
 ATOM 16 O THR 1 524 -6.508 25.289 2.476 1.00 5.12  
 ATOM 17 CB THR 1 524 -5.970 28.028 1.048 1.00 5.12  
 ATOM 18 OG1 THR 1 524 -6.738 27.228 0.161 1.00 5.12  
 ATOM 19 CG2 THR 1 524 -4.469 27.825 0.775 1.00 5.12  
 ATOM 20 N LEU 1 525 -4.495 26.116 3.050 1.00 4.05  
 ATOM 21 CA LEU 1 525 -3.904 24.817 3.148 1.00 4.05  
 ATOM 22 C LEU 1 525 -4.619 23.998 4.180 1.00 4.05  
 ATOM 23 O LEU 1 525 -4.846 22.807 3.975 1.00 4.05  
 ATOM 24 CB LEU 1 525 -2.406 24.884 3.473 1.00 4.05  
 ATOM 25 CG LEU 1 525 -1.624 25.796 2.496 1.00 4.05  
 ATOM 26 CD1 LEU 1 525 -1.808 25.375 1.030 1.00 4.05  
 ATOM 27 CD2 LEU 1 525 -1.952 27.279 2.714 1.00 4.05  
 ATOM 28 N PRO 1 526 -4.986 24.583 5.282 1.00 2.45  
 ATOM 29 CA PRO 1 526 -5.729 23.833 6.245 1.00 2.45  
 ATOM 30 C PRO 1 526 -7.071 23.501 5.695 1.00 2.45  
 ATOM 31 O PRO 1 526 -7.745 22.642 6.253 1.00 2.45  
 ATOM 32 CB PRO 1 526 -5.728 24.660 7.535 1.00 2.45  
 ATOM 33 CG PRO 1 526 -4.888 25.909 7.201 1.00 2.45  
 ATOM 34 CD PRO 1 526 -4.087 25.487 5.960 1.00 2.45  
 ATOM 35 N GLN 1 527 -7.532 24.178 4.638 1.00 6.73  
 ATOM 36 CA GLN 1 527 -8.784 23.731 4.111 1.00 6.73  
 ATOM 37 C GLN 1 527 -8.494 22.376 3.553 1.00 6.73  
 ATOM 38 O GLN 1 527 -9.217 21.409 3.789 1.00 6.73  
 ATOM 39 CB GLN 1 527 -9.294 24.611 2.957 1.00 6.73

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ATOM	40	CG	GLN 1 527	-10.650	24.176	2.394	1.00	6.73
ATOM	41	CD	GLN 1 527	-11.731	24.634	3.365	1.00	6.73
ATOM	42	OE1	GLN 1 527	-12.924	24.477	3.113	1.00	6.73
ATOM	43	NE2	GLN 1 527	-11.299	25.225	4.511	1.00	6.73
ATOM	44	N	LEU 1 528	-7.375	22.285	2.811	1.00	1.25
ATOM	45	CA	LEU 1 528	-6.989	21.077	2.149	1.00	1.25
ATOM	46	C	LEU 1 528	-6.605	19.985	3.099	1.00	1.25
ATOM	47	O	LEU 1 528	-6.949	18.826	2.873	1.00	1.25
ATOM	48	CB	LEU 1 528	-5.827	21.278	1.167	1.00	1.25
ATOM	49	CG	LEU 1 528	-5.404	19.980	0.459	1.00	1.25
ATOM	50	CD1	LEU 1 528	-6.589	19.354	-0.296	1.00	1.25
ATOM	51	CD2	LEU 1 528	-4.197	20.216	-0.460	1.00	1.25
ATOM	52	N	THR 1 529	-5.883	20.309	4.187	1.00	5.96
ATOM	53	CA	THR 1 529	-5.449	19.243	5.042	1.00	5.96
ATOM	54	C	THR 1 529	-6.567	18.468	5.692	1.00	5.96
ATOM	55	O	THR 1 529	-6.499	17.241	5.674	1.00	5.96
ATOM	56	CB	THR 1 529	-4.353	19.648	6.007	1.00	5.96
ATOM	57	OG1	THR 1 529	-4.145	18.629	6.974	1.00	5.96
ATOM	58	CG2	THR 1 529	-4.595	21.030	6.638	1.00	5.96
ATOM	59	N	PRO 1 530	-7.594	19.043	6.263	1.00	5.19
ATOM	60	CA	PRO 1 530	-8.631	18.171	6.732	1.00	5.19
ATOM	61	C	PRO 1 530	-9.396	17.473	5.656	1.00	5.19
ATOM	62	O	PRO 1 530	-9.961	16.419	5.940	1.00	5.19
ATOM	63	CB	PRO 1 530	-9.480	18.989	7.697	1.00	5.19
ATOM	64	CG	PRO 1 530	-8.446	19.924	8.336	1.00	5.19
ATOM	65	CD	PRO 1 530	-7.367	20.075	7.254	1.00	5.19
ATOM	66	N	THR 1 531	-9.457	18.027	4.431	1.00	0.64
ATOM	67	CA	THR 1 531	-10.190	17.352	3.401	1.00	0.64
ATOM	68	C	THR 1 531	-9.495	16.061	3.114	1.00	0.64
ATOM	69	O	THR 1 531	-10.110	14.995	3.091	1.00	0.64
ATOM	70	CB	THR 1 531	-10.231	18.143	2.127	1.00	0.64
ATOM	71	OG1	THR 1 531	-10.823	19.412	2.362	1.00	0.64
ATOM	72	CG2	THR 1 531	-11.054	17.364	1.088	1.00	0.64
ATOM	73	N	LEU 1 532	-8.165	16.133	2.924	1.00	6.54
ATOM	74	CA	LEU 1 532	-7.401	14.967	2.608	1.00	6.54
ATOM	75	C	LEU 1 532	-7.451	14.010	3.750	1.00	6.54
ATOM	76	O	LEU 1 532	-7.628	12.816	3.537	1.00	6.54
ATOM	77	CB	LEU 1 532	-5.939	15.288	2.227	1.00	6.54
ATOM	78	CG	LEU 1 532	-5.114	16.074	3.268	1.00	6.54
ATOM	79	CD1	LEU 1 532	-4.690	15.205	4.462	1.00	6.54
ATOM	80	CD2	LEU 1 532	-3.922	16.777	2.601	1.00	6.54
ATOM	81	N	VAL 1 533	-7.357	14.496	4.997	1.00	0.78
ATOM	82	CA	VAL 1 533	-7.312	13.615	6.132	1.00	0.78
ATOM	83	C	VAL 1 533	-8.569	12.811	6.247	1.00	0.78
ATOM	84	O	VAL 1 533	-8.524	11.602	6.475	1.00	0.78
ATOM	85	CB	VAL 1 533	-7.153	14.365	7.416	1.00	0.78
ATOM	86	CG1	VAL 1 533	-7.253	13.368	8.578	1.00	0.78
ATOM	87	CG2	VAL 1 533	-5.825	15.139	7.368	1.00	0.78
ATOM	88	N	SER 1 534	-9.730	13.465	6.071	1.00	2.96
ATOM	89	CA	SER 1 534	-10.989	12.790	6.208	1.00	2.96
ATOM	90	C	SER 1 534	-11.018	11.730	5.164	1.00	2.96
ATOM	91	O	SER 1 534	-11.546	10.637	5.366	1.00	2.96
ATOM	92	CB	SER 1 534	-12.192	13.718	5.971	1.00	2.96
ATOM	93	OG	SER 1 534	-13.404	12.993	6.116	1.00	2.96
ATOM	94	N	LEU 1 535	-10.418	12.049	4.013	1.00	7.50
ATOM	95	CA	LEU 1 535	-10.349	11.153	2.910	1.00	7.50
ATOM	96	C	LEU 1 535	-9.730	9.848	3.293	1.00	7.50
ATOM	97	O	LEU 1 535	-10.320	8.802	3.027	1.00	7.50
ATOM	98	CB	LEU 1 535	-9.471	11.746	1.819	1.00	7.50
ATOM	99	CG	LEU 1 535	-9.060	10.667	0.844	1.00	7.50
ATOM	100	CD1	LEU 1 535	-10.323	9.945	0.376	1.00	7.50

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ATOM	101	CD2 LEU 1 535	-8.144	11.236	-0.247	1.00	7.50
ATOM	102	N LEU 1 536	-8.535	9.854	3.922	1.00	5.15
ATOM	103	CA LEU 1 536	-7.959	8.579	4.258	1.00	5.15
ATOM	104	C LEU 1 536	-8.747	7.902	5.310	1.00	5.15
ATOM	105	O LEU 1 536	-8.938	6.691	5.244	1.00	5.15
ATOM	106	CB LEU 1 536	-6.518	8.550	4.791	1.00	5.15
ATOM	107	CG LEU 1 536	-5.926	7.169	5.143	1.00	5.15
ATOM	108	CD1 LEU 1 536	-6.389	6.648	6.514	1.00	5.15
ATOM	109	CD2 LEU 1 536	-6.182	6.173	4.004	1.00	5.15
ATOM	110	N GLU 1 537	-9.215	8.674	6.306	1.00	3.32
ATOM	111	CA GLU 1 537	-9.876	8.087	7.433	1.00	3.32
ATOM	112	C GLU 1 537	-11.004	7.253	6.936	1.00	3.32
ATOM	113	O GLU 1 537	-11.180	6.113	7.366	1.00	3.32
ATOM	114	CB GLU 1 537	-10.491	9.139	8.375	1.00	3.32
ATOM	115	CG GLU 1 537	-9.466	9.988	9.130	1.00	3.32
ATOM	116	CD GLU 1 537	-8.937	9.165	10.295	1.00	3.32
ATOM	117	OE1 GLU 1 537	-8.074	9.692	11.047	1.00	3.32
ATOM	118	OE2 GLU 1 537	-9.391	8.000	10.453	1.00	3.32
ATOM	119	N VAL 1 538	-11.787	7.791	5.989	1.00	4.21
ATOM	120	CA VAL 1 538	-12.906	7.043	5.514	1.00	4.21
ATOM	121	C VAL 1 538	-12.485	5.790	4.802	1.00	4.21
ATOM	122	O VAL 1 538	-13.042	4.726	5.058	1.00	4.21
ATOM	123	CB VAL 1 538	-13.781	7.832	4.581	1.00	4.21
ATOM	124	CG1 VAL 1 538	-14.337	9.043	5.348	1.00	4.21
ATOM	125	CG2 VAL 1 538	-12.978	8.204	3.325	1.00	4.21
ATOM	126	N ILE 1 539	-11.500	5.860	3.880	1.00	8.15
ATOM	127	CA ILE 1 539	-11.192	4.652	3.161	1.00	8.15
ATOM	128	C ILE 1 539	-10.371	3.670	3.930	1.00	8.15
ATOM	129	O ILE 1 539	-10.401	2.484	3.614	1.00	8.15
ATOM	130	CB ILE 1 539	-10.538	4.768	1.805	1.00	8.15
ATOM	131	CG1 ILE 1 539	-9.065	5.184	1.864	1.00	8.15
ATOM	132	CG2 ILE 1 539	-11.410	5.716	0.966	1.00	8.15
ATOM	133	CD1 ILE 1 539	-8.851	6.612	2.298	1.00	8.15
ATOM	134	N GLU 1 540	-9.571	4.137	4.909	1.00	4.12
ATOM	135	CA GLU 1 540	-8.724	3.247	5.654	1.00	4.12
ATOM	136	C GLU 1 540	-9.574	2.205	6.301	1.00	4.12
ATOM	137	O GLU 1 540	-10.537	2.507	7.004	1.00	4.12
ATOM	138	CB GLU 1 540	-7.933	3.953	6.769	1.00	4.12
ATOM	139	CG GLU 1 540	-7.018	3.017	7.560	1.00	4.12
ATOM	140	CD GLU 1 540	-6.307	3.845	8.622	1.00	4.12
ATOM	141	OE1 GLU 1 540	-5.440	3.273	9.335	1.00	4.12
ATOM	142	OE2 GLU 1 540	-6.626	5.058	8.737	1.00	4.12
ATOM	143	N PRO 1 541	-9.231	0.969	6.072	1.00	5.53
ATOM	144	CA PRO 1 541	-10.006	-0.080	6.661	1.00	5.53
ATOM	145	C PRO 1 541	-9.704	-0.127	8.111	1.00	5.53
ATOM	146	O PRO 1 541	-8.615	0.310	8.476	1.00	5.53
ATOM	147	CB PRO 1 541	-9.637	-1.354	5.904	1.00	5.53
ATOM	148	CG PRO 1 541	-9.217	-0.837	4.517	1.00	5.53
ATOM	149	CD PRO 1 541	-8.676	0.577	4.786	1.00	5.53
ATOM	150	N GLU 1 542	-10.669	-0.632	8.912	1.00	6.38
ATOM	151	CA GLU 1 542	-10.594	-0.794	10.337	1.00	6.38
ATOM	152	C GLU 1 542	-9.653	0.163	10.975	1.00	6.38
ATOM	153	O GLU 1 542	-8.445	-0.062	10.977	1.00	6.38
ATOM	154	CB GLU 1 542	-10.213	-2.215	10.784	1.00	6.38
ATOM	155	CG GLU 1 542	-11.367	-3.220	10.712	1.00	6.38
ATOM	156	CD GLU 1 542	-11.704	-3.495	9.254	1.00	6.38
ATOM	157	OE1 GLU 1 542	-12.351	-2.620	8.618	1.00	6.38
ATOM	158	OE2 GLU 1 542	-11.328	-4.590	8.758	1.00	6.38
ATOM	159	N VAL 1 543	-10.188	1.285	11.490	1.00	2.42
ATOM	160	CA VAL 1 543	-9.342	2.211	12.175	1.00	2.42
ATOM	161	C VAL 1 543	-8.738	1.383	13.264	1.00	2.42

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ATOM	162	O	VAL	1 543	-7.553	1.510	13.567	1.00	2.42
ATOM	163	CB	VAL	1 543	-10.100	3.338	12.810	1.00	2.42
ATOM	164	CG1	VAL	1 543	-9.104	4.218	13.584	1.00	2.42
ATOM	165	CG2	VAL	1 543	-10.870	4.089	11.711	1.00	2.42
ATOM	166	N	LEU	1 544	-9.546	0.467	13.843	1.00	7.00
ATOM	167	CA	LEU	1 544	-9.040	-0.416	14.851	1.00	7.00
ATOM	168	C	LEU	1 544	-7.965	-1.188	14.158	1.00	7.00
ATOM	169	O	LEU	1 544	-8.090	-1.557	12.992	1.00	7.00
ATOM	170	CB	LEU	1 544	-10.117	-1.354	15.443	1.00	7.00
ATOM	171	CG	LEU	1 544	-9.644	-2.308	16.564	1.00	7.00
ATOM	172	CD1	LEU	1 544	-10.842	-3.017	17.209	1.00	7.00
ATOM	173	CD2	LEU	1 544	-8.606	-3.330	16.075	1.00	7.00
ATOM	174	N	TYR	1 545	-6.872	-1.457	14.883	1.00	9.50
ATOM	175	CA	TYR	1 545	-5.668	-1.991	14.326	1.00	9.50
ATOM	176	C	TYR	1 545	-5.530	-3.441	14.662	1.00	9.50
ATOM	177	O	TYR	1 545	-6.141	-4.317	14.047	1.00	9.50
ATOM	178	CB	TYR	1 545	-4.490	-1.241	14.972	1.00	9.50
ATOM	179	CG	TYR	1 545	-3.181	-1.414	14.291	1.00	9.50
ATOM	180	CD1	TYR	1 545	-2.875	-0.615	13.212	1.00	9.50
ATOM	181	CD2	TYR	1 545	-2.157	-2.048	14.954	1.00	9.50
ATOM	182	CE1	TYR	1 545	-1.574	-0.459	12.796	1.00	9.50
ATOM	183	CE2	TYR	1 545	-0.854	-1.898	14.545	1.00	9.50
ATOM	184	CZ	TYR	1 545	-0.560	-1.084	13.481	1.00	9.50
ATOM	185	OH	TYR	1 545	0.787	-0.832	13.147	1.00	9.50
ATOM	186	N	ALA	1 546	-4.692	-3.708	15.676	1.00	1.35
ATOM	187	CA	ALA	1 546	-4.340	-5.025	16.109	1.00	1.35
ATOM	188	C	ALA	1 546	-5.523	-5.783	16.607	1.00	1.35
ATOM	189	O	ALA	1 546	-5.545	-7.007	16.515	1.00	1.35
ATOM	190	CB	ALA	1 546	-3.300	-5.025	17.242	1.00	1.35
ATOM	191	N	GLY	1 547	-6.535	-5.086	17.151	1.00	1.27
ATOM	192	CA	GLY	1 547	-7.639	-5.775	17.755	1.00	1.27
ATOM	193	C	GLY	1 547	-8.252	-6.802	16.851	1.00	1.27
ATOM	194	O	GLY	1 547	-8.407	-7.954	17.251	1.00	1.27
ATOM	195	N	TYR	1 548	-8.598	-6.437	15.601	1.00	2.17
ATOM	196	CA	TYR	1 548	-9.253	-7.419	14.782	1.00	2.17
ATOM	197	C	TYR	1 548	-8.395	-7.952	13.677	1.00	2.17
ATOM	198	O	TYR	1 548	-8.822	-7.969	12.525	1.00	2.17
ATOM	199	CB	TYR	1 548	-10.529	-6.897	14.101	1.00	2.17
ATOM	200	CG	TYR	1 548	-11.566	-6.699	15.150	1.00	2.17
ATOM	201	CD1	TYR	1 548	-11.629	-5.525	15.864	1.00	2.17
ATOM	202	CD2	TYR	1 548	-12.485	-7.689	15.406	1.00	2.17
ATOM	203	CE1	TYR	1 548	-12.607	-5.344	16.814	1.00	2.17
ATOM	204	CE2	TYR	1 548	-13.461	-7.513	16.357	1.00	2.17
ATOM	205	CZ	TYR	1 548	-13.525	-6.335	17.060	1.00	2.17
ATOM	206	OH	TYR	1 548	-14.517	-6.151	18.046	1.00	2.17
ATOM	207	N	ASP	1 549	-7.177	-8.436	13.981	1.00	5.55
ATOM	208	CA	ASP	1 549	-6.380	-8.969	12.912	1.00	5.55
ATOM	209	C	ASP	1 549	-6.134	-10.427	13.168	1.00	5.55
ATOM	210	O	ASP	1 549	-6.262	-10.894	14.297	1.00	5.55
ATOM	211	CB	ASP	1 549	-5.014	-8.281	12.761	1.00	5.55
ATOM	212	CG	ASP	1 549	-4.212	-8.527	14.029	1.00	5.55
ATOM	213	OD1	ASP	1 549	-2.972	-8.307	13.984	1.00	5.55
ATOM	214	OD2	ASP	1 549	-4.816	-8.944	15.053	1.00	5.55
ATOM	215	N	SER	1 550	-5.790	-11.196	12.113	1.00	0.80
ATOM	216	CA	SER	1 550	-5.537	-12.600	12.289	1.00	0.80
ATOM	217	C	SER	1 550	-4.246	-12.948	11.606	1.00	0.80
ATOM	218	O	SER	1 550	-3.812	-12.245	10.695	1.00	0.80
ATOM	219	CB	SER	1 550	-6.620	-13.499	11.672	1.00	0.80
ATOM	220	OG	SER	1 550	-6.619	-13.359	10.259	1.00	0.80
ATOM	221	N	SER	1 551	-3.594	-14.046	12.051	1.00	3.97
ATOM	222	CA	SER	1 551	-2.348	-14.482	11.474	1.00	3.97

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ATOM	223	C	SER	1	551	-2.628	-15.435	10.351	1.00	3.97
ATOM	224	O	SER	1	551	-3.668	-16.089	10.330	1.00	3.97
ATOM	225	CB	SER	1	551	-1.416	-15.187	12.477	1.00	3.97
ATOM	226	OG	SER	1	551	-2.010	-16.390	12.944	1.00	3.97
ATOM	227	N	VAL	1	552	-1.703	-15.526	9.363	1.00	2.63
ATOM	228	CA	VAL	1	552	-1.933	-16.318	8.175	1.00	2.63
ATOM	229	C	VAL	1	552	-0.573	-16.748	7.601	1.00	2.63
ATOM	230	O	VAL	1	552	0.265	-15.862	7.505	1.00	2.63
ATOM	231	CB	VAL	1	552	-2.676	-15.415	7.202	1.00	2.63
ATOM	232	CG1	VAL	1	552	-2.855	-16.023	5.823	1.00	2.63
ATOM	233	CG2	VAL	1	552	-4.042	-15.059	7.811	1.00	2.63
ATOM	234	N	PRO	1	553	-0.231	-18.027	7.329	1.00	9.93
ATOM	235	CA	PRO	1	553	1.065	-18.358	6.679	1.00	9.93
ATOM	236	C	PRO	1	553	1.126	-18.968	5.236	1.00	9.93
ATOM	237	O	PRO	1	553	0.475	-19.998	5.072	1.00	9.93
ATOM	238	CB	PRO	1	553	1.784	-19.288	7.649	1.00	9.93
ATOM	239	CG	PRO	1	553	0.631	-20.005	8.368	1.00	9.93
ATOM	240	CD	PRO	1	553	-0.490	-18.956	8.420	1.00	9.93
ATOM	241	N	ASP	1	554	1.928	-18.474	4.211	1.00	7.69
ATOM	242	CA	ASP	1	554	2.026	-19.177	2.915	1.00	7.69
ATOM	243	C	ASP	1	554	2.850	-18.555	1.745	1.00	7.69
ATOM	244	O	ASP	1	554	3.467	-17.502	1.910	1.00	7.69
ATOM	245	CB	ASP	1	554	0.671	-19.618	2.359	1.00	7.69
ATOM	246	CG	ASP	1	554	0.992	-20.935	1.676	1.00	7.69
ATOM	247	OD1	ASP	1	554	2.167	-21.375	1.764	1.00	7.69
ATOM	248	OD2	ASP	1	554	0.069	-21.531	1.072	1.00	7.69
ATOM	249	N	SER	1	555	2.873	-19.195	0.516	1.00	5.28
ATOM	250	CA	SER	1	555	3.725	-18.879	-0.634	1.00	5.28
ATOM	251	C	SER	1	555	2.970	-18.889	-1.948	1.00	5.28
ATOM	252	O	SER	1	555	1.762	-19.104	-1.955	1.00	5.28
ATOM	253	CB	SER	1	555	4.897	-19.883	-0.739	1.00	5.28
ATOM	254	OG	SER	1	555	5.767	-19.577	-1.819	1.00	5.28
ATOM	255	N	THR	1	556	3.665	-18.594	-3.079	1.00	9.81
ATOM	256	CA	THR	1	556	3.098	-18.498	-4.399	1.00	9.81
ATOM	257	C	THR	1	556	2.078	-19.549	-4.606	1.00	9.81
ATOM	258	O	THR	1	556	2.322	-20.712	-4.296	1.00	9.81
ATOM	259	CB	THR	1	556	4.110	-18.631	-5.498	1.00	9.81
ATOM	260	OG1	THR	1	556	4.727	-19.910	-5.444	1.00	9.81
ATOM	261	CG2	THR	1	556	5.165	-17.525	-5.339	1.00	9.81
ATOM	262	N	TRP	1	557	0.895	-19.108	-5.085	1.00	5.43
ATOM	263	CA	TRP	1	557	-0.253	-19.917	-5.357	1.00	5.43
ATOM	264	C	TRP	1	557	-1.190	-19.773	-4.203	1.00	5.43
ATOM	265	O	TRP	1	557	-2.096	-18.941	-4.231	1.00	5.43
ATOM	266	CB	TRP	1	557	0.057	-21.409	-5.621	1.00	5.43
ATOM	267	CG	TRP	1	557	0.908	-21.586	-6.860	1.00	5.43
ATOM	268	CD1	TRP	1	557	1.247	-20.638	-7.782	1.00	5.43
ATOM	269	CD2	TRP	1	557	1.570	-22.798	-7.266	1.00	5.43
ATOM	270	NE1	TRP	1	557	2.062	-21.184	-8.742	1.00	5.43
ATOM	271	CE2	TRP	1	557	2.273	-22.511	-8.437	1.00	5.43
ATOM	272	CE3	TRP	1	557	1.595	-24.046	-6.710	1.00	5.43
ATOM	273	CZ2	TRP	1	557	3.012	-23.468	-9.072	1.00	5.43
ATOM	274	CZ3	TRP	1	557	2.341	-25.008	-7.354	1.00	5.43
ATOM	275	CH2	TRP	1	557	3.037	-24.726	-8.512	1.00	5.43
ATOM	276	N	ARG	1	558	-0.986	-20.580	-3.147	1.00	4.12
ATOM	277	CA	ARG	1	558	-1.870	-20.583	-2.018	1.00	4.12
ATOM	278	C	ARG	1	558	-1.869	-19.291	-1.243	1.00	4.12
ATOM	279	O	ARG	1	558	-2.939	-18.741	-0.987	1.00	4.12
ATOM	280	CB	ARG	1	558	-1.570	-21.770	-1.089	1.00	4.12
ATOM	281	CG	ARG	1	558	-2.483	-21.915	0.132	1.00	4.12
ATOM	282	CD	ARG	1	558	-2.129	-23.147	0.976	1.00	4.12
ATOM	283	NE	ARG	1	558	-2.927	-23.111	2.231	1.00	4.12

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ATOM	284	CZ ARG 1 558	-4.086	-23.824	2.321	1.00	4.12
ATOM	285	NH1 ARG 1 558	-4.518	-24.562	1.258	1.00	4.12
ATOM	286	NH2 ARG 1 558	-4.799	-23.816	3.484	1.00	4.12
ATOM	287	N ILE 1 559	-0.695	-18.747	-0.843	1.00	7.58
ATOM	288	CA ILE 1 559	-0.761	-17.491	-0.136	1.00	7.58
ATOM	289	C ILE 1 559	-1.163	-16.455	-1.122	1.00	7.58
ATOM	290	O ILE 1 559	-1.922	-15.554	-0.783	1.00	7.58
ATOM	291	CB ILE 1 559	0.492	-17.071	0.590	1.00	7.58
ATOM	292	CG1 ILE 1 559	0.360	-15.803	1.440	1.00	7.58
ATOM	293	CG2 ILE 1 559	1.567	-16.870	-0.411	1.00	7.58
ATOM	294	CD1 ILE 1 559	-0.030	-14.472	0.828	1.00	7.58
ATOM	295	N MET 1 560	-0.726	-16.591	-2.389	1.00	1.02
ATOM	296	CA MET 1 560	-1.077	-15.624	-3.390	1.00	1.02
ATOM	297	C MET 1 560	-2.568	-15.530	-3.413	1.00	1.02
ATOM	298	O MET 1 560	-3.133	-14.446	-3.546	1.00	1.02
ATOM	299	CB MET 1 560	-0.619	-16.020	-4.805	1.00	1.02
ATOM	300	CG MET 1 560	-0.959	-14.967	-5.865	1.00	1.02
ATOM	301	SD MET 1 560	-0.338	-15.332	-7.535	1.00	1.02
ATOM	302	CE MET 1 560	-1.515	-16.668	-7.887	1.00	1.02
ATOM	303	N THR 1 561	-3.245	-16.676	-3.233	1.00	0.75
ATOM	304	CA THR 1 561	-4.675	-16.664	-3.213	1.00	0.75
ATOM	305	C THR 1 561	-5.142	-15.836	-2.058	1.00	0.75
ATOM	306	O THR 1 561	-6.070	-15.039	-2.189	1.00	0.75
ATOM	307	CB THR 1 561	-5.280	-18.020	-3.010	1.00	0.75
ATOM	308	OG1 THR 1 561	-4.864	-18.913	-4.033	1.00	0.75
ATOM	309	CG2 THR 1 561	-6.811	-17.868	-3.035	1.00	0.75
ATOM	310	N THR 1 562	-4.503	-15.997	-0.883	1.00	4.60
ATOM	311	CA THR 1 562	-4.985	-15.299	0.272	1.00	4.60
ATOM	312	C THR 1 562	-4.840	-13.814	0.133	1.00	4.60
ATOM	313	O THR 1 562	-5.749	-13.078	0.514	1.00	4.60
ATOM	314	CB THR 1 562	-4.347	-15.723	1.571	1.00	4.60
ATOM	315	OG1 THR 1 562	-5.143	-15.272	2.658	1.00	4.60
ATOM	316	CG2 THR 1 562	-2.945	-15.112	1.703	1.00	4.60
ATOM	317	N LEU 1 563	-3.710	-13.318	-0.419	1.00	3.84
ATOM	318	CA LEU 1 563	-3.589	-11.887	-0.483	1.00	3.84
ATOM	319	C LEU 1 563	-4.655	-11.438	-1.412	1.00	3.84
ATOM	320	O LEU 1 563	-5.340	-10.444	-1.182	1.00	3.84
ATOM	321	CB LEU 1 563	-2.329	-11.312	-1.161	1.00	3.84
ATOM	322	CG LEU 1 563	-0.992	-11.979	-0.831	1.00	3.84
ATOM	323	CD1 LEU 1 563	-0.839	-13.222	-1.707	1.00	3.84
ATOM	324	CD2 LEU 1 563	0.197	-11.014	-0.964	1.00	3.84
ATOM	325	N ASN 1 564	-4.818	-12.207	-2.499	1.00	3.56
ATOM	326	CA ASN 1 564	-5.696	-11.869	-3.572	1.00	3.56
ATOM	327	C ASN 1 564	-7.113	-11.760	-3.109	1.00	3.56
ATOM	328	O ASN 1 564	-7.853	-10.902	-3.586	1.00	3.56
ATOM	329	CB ASN 1 564	-5.638	-12.914	-4.692	1.00	3.56
ATOM	330	CG ASN 1 564	-6.061	-12.202	-5.953	1.00	3.56
ATOM	331	OD1 ASN 1 564	-7.106	-12.483	-6.539	1.00	3.56
ATOM	332	ND2 ASN 1 564	-5.205	-11.231	-6.370	1.00	3.56
ATOM	333	N MET 1 565	-7.531	-12.613	-2.155	1.00	5.34
ATOM	334	CA MET 1 565	-8.898	-12.577	-1.713	1.00	5.34
ATOM	335	C MET 1 565	-9.213	-11.199	-1.222	1.00	5.34
ATOM	336	O MET 1 565	-10.265	-10.646	-1.540	1.00	5.34
ATOM	337	CB MET 1 565	-9.165	-13.522	-0.524	1.00	5.34
ATOM	338	CG MET 1 565	-9.227	-15.013	-0.868	1.00	5.34
ATOM	339	SD MET 1 565	-10.846	-15.587	-1.472	1.00	5.34
ATOM	340	CE MET 1 565	-11.623	-15.702	0.166	1.00	5.34
ATOM	341	N LEU 1 566	-8.304	-10.627	-0.412	1.00	1.68
ATOM	342	CA LEU 1 566	-8.430	-9.317	0.170	1.00	1.68
ATOM	343	C LEU 1 566	-8.206	-8.166	-0.760	1.00	1.68
ATOM	344	O LEU 1 566	-8.694	-7.069	-0.497	1.00	1.68

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ATOM	345	CB	LEU 1 566	-7.494	-9.071	1.368	1.00	1.68
ATOM	346	CG	LEU 1 566	-7.870	-9.869	2.628	1.00	1.68
ATOM	347	CD1	LEU 1 566	-6.977	-9.475	3.815	1.00	1.68
ATOM	348	CD2	LEU 1 566	-9.368	-9.737	2.945	1.00	1.68
ATOM	349	N	GLY 1 567	-7.446	-8.371	-1.852	1.00	1.08
ATOM	350	CA	GLY 1 567	-7.005	-7.298	-2.704	1.00	1.08
ATOM	351	C	GLY 1 567	-8.083	-6.411	-3.249	1.00	1.08
ATOM	352	O	GLY 1 567	-7.882	-5.202	-3.354	1.00	1.08
ATOM	353	N	GLY 1 568	-9.245	-6.968	-3.633	1.00	0.69
ATOM	354	CA	GLY 1 568	-10.276	-6.151	-4.209	1.00	0.69
ATOM	355	C	GLY 1 568	-10.734	-5.095	-3.250	1.00	0.69
ATOM	356	O	GLY 1 568	-10.984	-3.958	-3.637	1.00	0.69
ATOM	357	N	ARG 1 569	-10.894	-5.421	-1.963	1.00	8.50
ATOM	358	CA	ARG 1 569	-11.347	-4.412	-1.049	1.00	8.50
ATOM	359	C	ARG 1 569	-10.311	-3.332	-0.953	1.00	8.50
ATOM	360	O	ARG 1 569	-10.625	-2.143	-0.913	1.00	8.50
ATOM	361	CB	ARG 1 569	-11.586	-4.953	0.372	1.00	8.50
ATOM	362	CG	ARG 1 569	-12.843	-5.819	0.536	1.00	8.50
ATOM	363	CD	ARG 1 569	-12.824	-7.141	-0.237	1.00	8.50
ATOM	364	NE	ARG 1 569	-13.206	-6.855	-1.650	1.00	8.50
ATOM	365	CZ	ARG 1 569	-12.718	-7.634	-2.660	1.00	8.50
ATOM	366	NH1	ARG 1 569	-11.861	-8.659	-2.377	1.00	8.50
ATOM	367	NH2	ARG 1 569	-13.087	-7.391	-3.951	1.00	8.50
ATOM	368	N	GLN 1 570	-9.030	-3.730	-0.922	1.00	0.65
ATOM	369	CA	GLN 1 570	-7.957	-2.791	-0.774	1.00	0.65
ATOM	370	C	GLN 1 570	-7.918	-1.860	-1.944	1.00	0.65
ATOM	371	O	GLN 1 570	-7.699	-0.660	-1.780	1.00	0.65
ATOM	372	CB	GLN 1 570	-6.584	-3.476	-0.703	1.00	0.65
ATOM	373	CG	GLN 1 570	-6.407	-4.379	0.518	1.00	0.65
ATOM	374	CD	GLN 1 570	-5.012	-4.978	0.446	1.00	0.65
ATOM	375	OE1	GLN 1 570	-4.262	-4.718	-0.494	1.00	0.65
ATOM	376	NE2	GLN 1 570	-4.651	-5.807	1.462	1.00	0.65
ATOM	377	N	VAL 1 571	-8.116	-2.396	-3.162	1.00	4.09
ATOM	378	CA	VAL 1 571	-8.061	-1.597	-4.350	1.00	4.09
ATOM	379	C	VAL 1 571	-9.161	-0.576	-4.319	1.00	4.09
ATOM	380	O	VAL 1 571	-8.904	0.612	-4.488	1.00	4.09
ATOM	381	CB	VAL 1 571	-8.180	-2.448	-5.611	1.00	4.09
ATOM	382	CG1	VAL 1 571	-9.582	-3.028	-5.750	1.00	4.09
ATOM	383	CG2	VAL 1 571	-7.855	-1.633	-6.856	1.00	4.09
ATOM	384	N	ILE 1 572	-10.419	-0.955	-4.025	1.00	7.34
ATOM	385	CA	ILE 1 572	-11.411	0.081	-4.132	1.00	7.34
ATOM	386	C	ILE 1 572	-11.182	1.164	-3.124	1.00	7.34
ATOM	387	O	ILE 1 572	-11.483	2.326	-3.386	1.00	7.34
ATOM	388	CB	ILE 1 572	-12.868	-0.317	-4.065	1.00	7.34
ATOM	389	CG1	ILE 1 572	-13.301	-0.901	-2.715	1.00	7.34
ATOM	390	CG2	ILE 1 572	-13.127	-1.259	-5.252	1.00	7.34
ATOM	391	CD1	ILE 1 572	-12.853	-2.332	-2.490	1.00	7.34
ATOM	392	N	ALA 1 573	-10.612	0.818	-1.957	1.00	0.75
ATOM	393	CA	ALA 1 573	-10.379	1.810	-0.949	1.00	0.75
ATOM	394	C	ALA 1 573	-9.475	2.880	-1.482	1.00	0.75
ATOM	395	O	ALA 1 573	-9.693	4.063	-1.229	1.00	0.75
ATOM	396	CB	ALA 1 573	-9.718	1.230	0.313	1.00	0.75
ATOM	397	N	ALA 1 574	-8.428	2.496	-2.236	1.00	0.63
ATOM	398	CA	ALA 1 574	-7.516	3.468	-2.772	1.00	0.63
ATOM	399	C	ALA 1 574	-8.244	4.342	-3.747	1.00	0.63
ATOM	400	O	ALA 1 574	-8.018	5.549	-3.802	1.00	0.63
ATOM	401	CB	ALA 1 574	-6.310	2.829	-3.482	1.00	0.63
ATOM	402	N	VAL 1 575	-9.147	3.744	-4.550	1.00	0.59
ATOM	403	CA	VAL 1 575	-9.902	4.488	-5.519	1.00	0.59
ATOM	404	C	VAL 1 575	-10.779	5.467	-4.804	1.00	0.59
ATOM	405	O	VAL 1 575	-10.914	6.615	-5.221	1.00	0.59

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ATOM	406	CB	VAL 1 575	-10.806	3.616	-6.340	1.00	0.59
ATOM	407	CG1	VAL 1 575	-11.582	4.505	-7.326	1.00	0.59
ATOM	408	CG2	VAL 1 575	-9.960	2.527	-7.019	1.00	0.59
ATOM	409	N	LYS 1 576	-11.392	5.025	-3.688	1.00	5.66
ATOM	410	CA	LYS 1 576	-12.292	5.853	-2.937	1.00	5.66
ATOM	411	C	LYS 1 576	-11.533	7.030	-2.426	1.00	5.66
ATOM	412	O	LYS 1 576	-12.029	8.155	-2.424	1.00	5.66
ATOM	413	CB	LYS 1 576	-12.875	5.132	-1.709	1.00	5.66
ATOM	414	CG	LYS 1 576	-13.748	3.926	-2.060	1.00	5.66
ATOM	415	CD	LYS 1 576	-14.972	4.279	-2.907	1.00	5.66
ATOM	416	CE	LYS 1 576	-15.839	3.066	-3.254	1.00	5.66
ATOM	417	NZ	LYS 1 576	-15.076	2.130	-4.109	1.00	5.66
ATOM	418	N	TRP 1 577	-10.288	6.789	-1.982	1.00	0.85
ATOM	419	CA	TRP 1 577	-9.473	7.831	-1.446	1.00	0.85
ATOM	420	C	TRP 1 577	-9.309	8.899	-2.481	1.00	0.85
ATOM	421	O	TRP 1 577	-9.578	10.076	-2.248	1.00	0.85
ATOM	422	CB	TRP 1 577	-8.070	7.313	-1.085	1.00	0.85
ATOM	423	CG	TRP 1 577	-7.130	8.338	-0.507	1.00	0.85
ATOM	424	CD1	TRP 1 577	-6.897	8.652	0.799	1.00	0.85
ATOM	425	CD2	TRP 1 577	-6.244	9.157	-1.286	1.00	0.85
ATOM	426	NE1	TRP 1 577	-5.917	9.608	0.878	1.00	0.85
ATOM	427	CE2	TRP 1 577	-5.505	9.931	-0.393	1.00	0.85
ATOM	428	CE3	TRP 1 577	-6.055	9.251	-2.634	1.00	0.85
ATOM	429	CZ2	TRP 1 577	-4.570	10.822	-0.833	1.00	0.85
ATOM	430	CZ3	TRP 1 577	-5.108	10.150	-3.074	1.00	0.85
ATOM	431	CH2	TRP 1 577	-4.381	10.922	-2.193	1.00	0.85
ATOM	432	N	ALA 1 578	-8.926	8.508	-3.699	1.00	1.04
ATOM	433	CA	ALA 1 578	-8.660	9.480	-4.717	1.00	1.04
ATOM	434	C	ALA 1 578	-9.883	10.278	-5.039	1.00	1.04
ATOM	435	O	ALA 1 578	-9.799	11.479	-5.289	1.00	1.04
ATOM	436	CB	ALA 1 578	-8.169	8.837	-6.026	1.00	1.04
ATOM	437	N	LYS 1 579	-11.062	9.636	-5.045	1.00	4.62
ATOM	438	CA	LYS 1 579	-12.259	10.335	-5.412	1.00	4.62
ATOM	439	C	LYS 1 579	-12.592	11.437	-4.454	1.00	4.62
ATOM	440	O	LYS 1 579	-13.125	12.471	-4.855	1.00	4.62
ATOM	441	CB	LYS 1 579	-13.477	9.411	-5.561	1.00	4.62
ATOM	442	CG	LYS 1 579	-13.391	8.576	-6.839	1.00	4.62
ATOM	443	CD	LYS 1 579	-14.419	7.452	-6.939	1.00	4.62
ATOM	444	CE	LYS 1 579	-14.310	6.661	-8.245	1.00	4.62
ATOM	445	NZ	LYS 1 579	-14.577	7.549	-9.399	1.00	4.62
ATOM	446	N	ALA 1 580	-12.288	11.248	-3.159	1.00	1.29
ATOM	447	CA	ALA 1 580	-12.598	12.223	-2.151	1.00	1.29
ATOM	448	C	ALA 1 580	-11.822	13.493	-2.321	1.00	1.29
ATOM	449	O	ALA 1 580	-12.196	14.518	-1.753	1.00	1.29
ATOM	450	CB	ALA 1 580	-12.371	11.733	-0.717	1.00	1.29
ATOM	451	N	ILE 1 581	-10.682	13.451	-3.042	1.00	3.84
ATOM	452	CA	ILE 1 581	-9.885	14.636	-3.206	1.00	3.84
ATOM	453	C	ILE 1 581	-10.346	15.411	-4.410	1.00	3.84
ATOM	454	O	ILE 1 581	-10.388	14.917	-5.536	1.00	3.84
ATOM	455	CB	ILE 1 581	-8.415	14.317	-3.325	1.00	3.84
ATOM	456	CG1	ILE 1 581	-7.541	15.562	-3.135	1.00	3.84
ATOM	457	CG2	ILE 1 581	-8.166	13.584	-4.651	1.00	3.84
ATOM	458	CD1	ILE 1 581	-6.071	15.199	-2.925	1.00	3.84
ATOM	459	N	PRO 1 582	-10.712	16.640	-4.160	1.00	3.26
ATOM	460	CA	PRO 1 582	-11.266	17.522	-5.155	1.00	3.26
ATOM	461	C	PRO 1 582	-10.417	17.677	-6.381	1.00	3.26
ATOM	462	O	PRO 1 582	-10.967	17.695	-7.481	1.00	3.26
ATOM	463	CB	PRO 1 582	-11.447	18.862	-4.446	1.00	3.26
ATOM	464	CG	PRO 1 582	-10.333	18.851	-3.381	1.00	3.26
ATOM	465	CD	PRO 1 582	-10.191	17.365	-3.012	1.00	3.26
ATOM	466	N	GLY 1 583	-9.088	17.794	-6.227	1.00	0.75

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ATOM	467	CA	GLY 1 583	-8.238	18.027	-7.358	1.00	0.75
ATOM	468	C	GLY 1 583	-8.296	16.878	-8.311	1.00	0.75
ATOM	469	O	GLY 1 583	-8.201	17.067	-9.521	1.00	0.75
ATOM	470	N	PHE 1 584	-8.420	15.655	-7.768	1.00	1.03
ATOM	471	CA	PHE 1 584	-8.409	14.430	-8.520	1.00	1.03
ATOM	472	C	PHE 1 584	-9.581	14.306	-9.446	1.00	1.03
ATOM	473	O	PHE 1 584	-9.430	13.931	-10.608	1.00	1.03
ATOM	474	CB	PHE 1 584	-8.422	13.217	-7.568	1.00	1.03
ATOM	475	CG	PHE 1 584	-8.361	11.929	-8.319	1.00	1.03
ATOM	476	CD1	PHE 1 584	-7.161	11.470	-8.810	1.00	1.03
ATOM	477	CD2	PHE 1 584	-9.444	11.078	-8.324	1.00	1.03
ATOM	478	CE1	PHE 1 584	-7.049	10.201	-9.323	1.00	1.03
ATOM	479	CE2	PHE 1 584	-9.337	9.805	-8.837	1.00	1.03
ATOM	480	CZ	PHE 1 584	-8.134	9.359	-9.328	1.00	1.03
ATOM	481	N	ARG 1 585	-10.782	14.653	-8.951	1.00	5.26
ATOM	482	CA	ARG 1 585	-11.990	14.486	-9.706	1.00	5.26
ATOM	483	C	ARG 1 585	-11.955	15.324	-10.940	1.00	5.26
ATOM	484	O	ARG 1 585	-12.483	14.934	-11.980	1.00	5.26
ATOM	485	CB	ARG 1 585	-13.247	14.881	-8.912	1.00	5.26
ATOM	486	CG	ARG 1 585	-14.548	14.666	-9.688	1.00	5.26
ATOM	487	CD	ARG 1 585	-15.802	15.056	-8.904	1.00	5.26
ATOM	488	NE	ARG 1 585	-16.977	14.796	-9.784	1.00	5.26
ATOM	489	CZ	ARG 1 585	-18.231	14.750	-9.249	1.00	5.26
ATOM	490	NH1	ARG 1 585	-19.307	14.502	-10.052	1.00	5.26
ATOM	491	NH2	ARG 1 585	-18.411	14.954	-7.910	1.00	5.26
ATOM	492	N	ASN 1 586	-11.322	16.506	-10.856	1.00	0.91
ATOM	493	CA	ASN 1 586	-11.280	17.411	-11.966	1.00	0.91
ATOM	494	C	ASN 1 586	-10.596	16.779	-13.138	1.00	0.91
ATOM	495	O	ASN 1 586	-10.973	17.026	-14.282	1.00	0.91
ATOM	496	CB	ASN 1 586	-10.529	18.714	-11.645	1.00	0.91
ATOM	497	CG	ASN 1 586	-11.381	19.523	-10.676	1.00	0.91
ATOM	498	OD1	ASN 1 586	-12.586	19.670	-10.867	1.00	0.91
ATOM	499	ND2	ASN 1 586	-10.739	20.060	-9.604	1.00	0.91
ATOM	500	N	LEU 1 587	-9.569	15.947	-12.892	1.00	4.04
ATOM	501	CA	LEU 1 587	-8.834	15.380	-13.988	1.00	4.04
ATOM	502	C	LEU 1 587	-9.724	14.592	-14.891	1.00	4.04
ATOM	503	O	LEU 1 587	-10.793	14.129	-14.499	1.00	4.04
ATOM	504	CB	LEU 1 587	-7.698	14.425	-13.571	1.00	4.04
ATOM	505	CG	LEU 1 587	-6.611	15.067	-12.690	1.00	4.04
ATOM	506	CD1	LEU 1 587	-7.107	15.257	-11.255	1.00	4.04
ATOM	507	CD2	LEU 1 587	-5.287	14.295	-12.751	1.00	4.04
ATOM	508	N	HIS 1 588	-9.290	14.422	-16.155	1.00	3.17
ATOM	509	CA	HIS 1 588	-10.079	13.664	-17.076	1.00	3.17
ATOM	510	C	HIS 1 588	-10.007	12.242	-16.633	1.00	3.17
ATOM	511	O	HIS 1 588	-9.091	11.842	-15.917	1.00	3.17
ATOM	512	CB	HIS 1 588	-9.598	13.754	-18.533	1.00	3.17
ATOM	513	CG	HIS 1 588	-9.688	15.146	-19.088	1.00	3.17
ATOM	514	ND1	HIS 1 588	-8.713	16.103	-18.921	1.00	3.17
ATOM	515	CD2	HIS 1 588	-10.655	15.730	-19.848	1.00	3.17
ATOM	516	CE1	HIS 1 588	-9.134	17.211	-19.581	1.00	3.17
ATOM	517	NE2	HIS 1 588	-10.309	17.033	-20.159	1.00	3.17
ATOM	518	N	LEU 1 589	-10.986	11.432	-17.066	1.00	6.31
ATOM	519	CA	LEU 1 589	-11.066	10.071	-16.633	1.00	6.31
ATOM	520	C	LEU 1 589	-9.832	9.331	-17.025	1.00	6.31
ATOM	521	O	LEU 1 589	-9.335	8.501	-16.267	1.00	6.31
ATOM	522	CB	LEU 1 589	-12.264	9.322	-17.240	1.00	6.31
ATOM	523	CG	LEU 1 589	-12.366	7.856	-16.779	1.00	6.31
ATOM	524	CD1	LEU 1 589	-12.605	7.759	-15.265	1.00	6.31
ATOM	525	CD2	LEU 1 589	-13.414	7.086	-17.599	1.00	6.31
ATOM	526	N	ASP 1 590	-9.298	9.614	-18.224	1.00	4.07
ATOM	527	CA	ASP 1 590	-8.153	8.874	-18.669	1.00	4.07

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ATOM	528	C	ASP	1	590	-6.992	9.057	-17.744	1.00	4.07
ATOM	529	O	ASP	1	590	-6.344	8.084	-17.365	1.00	4.07
ATOM	530	CB	ASP	1	590	-7.704	9.236	-20.099	1.00	4.07
ATOM	531	CG	ASP	1	590	-7.307	10.703	-20.151	1.00	4.07
ATOM	532	OD1	ASP	1	590	-7.873	11.496	-19.353	1.00	4.07
ATOM	533	OD2	ASP	1	590	-6.436	11.053	-20.992	1.00	4.07
ATOM	534	N	ASP	1	591	-6.691	10.304	-17.343	1.00	5.67
ATOM	535	CA	ASP	1	591	-5.581	10.496	-16.462	1.00	5.67
ATOM	536	C	ASP	1	591	-5.860	9.994	-15.078	1.00	5.67
ATOM	537	O	ASP	1	591	-4.955	9.560	-14.366	1.00	5.67
ATOM	538	CB	ASP	1	591	-4.982	11.914	-16.507	1.00	5.67
ATOM	539	CG	ASP	1	591	-6.017	12.981	-16.269	1.00	5.67
ATOM	540	OD1	ASP	1	591	-5.748	13.867	-15.419	1.00	5.67
ATOM	541	OD2	ASP	1	591	-7.067	12.957	-16.959	1.00	5.67
ATOM	542	N	GLN	1	592	-7.139	10.019	-14.668	1.00	3.91
ATOM	543	CA	GLN	1	592	-7.529	9.540	-13.376	1.00	3.91
ATOM	544	C	GLN	1	592	-7.134	8.098	-13.282	1.00	3.91
ATOM	545	O	GLN	1	592	-6.576	7.658	-12.277	1.00	3.91
ATOM	546	CB	GLN	1	592	-9.055	9.639	-13.213	1.00	3.91
ATOM	547	CG	GLN	1	592	-9.601	9.161	-11.873	1.00	3.91
ATOM	548	CD	GLN	1	592	-11.113	9.338	-11.900	1.00	3.91
ATOM	549	OE1	GLN	1	592	-11.867	8.413	-11.598	1.00	3.91
ATOM	550	NE2	GLN	1	592	-11.574	10.564	-12.269	1.00	3.91
ATOM	551	N	MET	1	593	-7.404	7.323	-14.351	1.00	7.01
ATOM	552	CA	MET	1	593	-7.112	5.919	-14.356	1.00	7.01
ATOM	553	C	MET	1	593	-5.636	5.669	-14.286	1.00	7.01
ATOM	554	O	MET	1	593	-5.177	4.839	-13.503	1.00	7.01
ATOM	555	CB	MET	1	593	-7.648	5.216	-15.618	1.00	7.01
ATOM	556	CG	MET	1	593	-7.623	3.686	-15.552	1.00	7.01
ATOM	557	SD	MET	1	593	-5.971	2.929	-15.626	1.00	7.01
ATOM	558	CE	MET	1	593	-6.578	1.220	-15.511	1.00	7.01
ATOM	559	N	THR	1	594	-4.845	6.403	-15.092	1.00	0.78
ATOM	560	CA	THR	1	594	-3.429	6.170	-15.146	1.00	0.78
ATOM	561	C	THR	1	594	-2.828	6.465	-13.814	1.00	0.78
ATOM	562	O	THR	1	594	-1.933	5.772	-13.335	1.00	0.78
ATOM	563	CB	THR	1	594	-2.739	7.045	-16.151	1.00	0.78
ATOM	564	OG1	THR	1	594	-3.268	6.813	-17.448	1.00	0.78
ATOM	565	CG2	THR	1	594	-1.234	6.727	-16.129	1.00	0.78
ATOM	566	N	LEU	1	595	-3.332	7.530	-13.187	1.00	6.73
ATOM	567	CA	LEU	1	595	-2.861	8.039	-11.943	1.00	6.73
ATOM	568	C	LEU	1	595	-3.069	7.019	-10.875	1.00	6.73
ATOM	569	O	LEU	1	595	-2.176	6.702	-10.090	1.00	6.73
ATOM	570	CB	LEU	1	595	-3.723	9.246	-11.624	1.00	6.73
ATOM	571	CG	LEU	1	595	-3.056	10.184	-10.664	1.00	6.73
ATOM	572	CD1	LEU	1	595	-1.680	10.521	-11.250	1.00	6.73
ATOM	573	CD2	LEU	1	595	-3.970	11.395	-10.435	1.00	6.73
ATOM	574	N	LEU	1	596	-4.286	6.462	-10.859	1.00	6.22
ATOM	575	CA	LEU	1	596	-4.726	5.531	-9.876	1.00	6.22
ATOM	576	C	LEU	1	596	-3.874	4.315	-10.036	1.00	6.22
ATOM	577	O	LEU	1	596	-3.404	3.721	-9.067	1.00	6.22
ATOM	578	CB	LEU	1	596	-6.201	5.209	-10.157	1.00	6.22
ATOM	579	CG	LEU	1	596	-6.995	4.659	-8.972	1.00	6.22
ATOM	580	CD1	LEU	1	596	-7.054	5.683	-7.827	1.00	6.22
ATOM	581	CD2	LEU	1	596	-8.393	4.211	-9.414	1.00	6.22
ATOM	582	N	GLN	1	597	-3.624	3.936	-11.296	1.00	3.34
ATOM	583	CA	GLN	1	597	-2.857	2.764	-11.591	1.00	3.34
ATOM	584	C	GLN	1	597	-1.445	2.904	-11.116	1.00	3.34
ATOM	585	O	GLN	1	597	-0.871	1.959	-10.580	1.00	3.34
ATOM	586	CB	GLN	1	597	-2.806	2.471	-13.097	1.00	3.34
ATOM	587	CG	GLN	1	597	-1.995	1.225	-13.456	1.00	3.34
ATOM	588	CD	GLN	1	597	-2.036	1.069	-14.968	1.00	3.34

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ATOM	589	OE1 GLN 1 597	-3.114	1.065	-15.570	1.00	3.34
ATOM	590	NE2 GLN 1 597	-0.844	0.946	-15.606	1.00	3.34
ATOM	591	N TYR 1 598	-0.840	4.086	-11.323	1.00	7.16
ATOM	592	CA TYR 1 598	0.539	4.275	-10.976	1.00	7.16
ATOM	593	C TYR 1 598	0.810	4.257	-9.501	1.00	7.16
ATOM	594	O TYR 1 598	1.769	3.635	-9.051	1.00	7.16
ATOM	595	CB TYR 1 598	1.093	5.591	-11.532	1.00	7.16
ATOM	596	CG TYR 1 598	2.525	5.717	-11.138	1.00	7.16
ATOM	597	CD1 TYR 1 598	3.517	5.120	-11.883	1.00	7.16
ATOM	598	CD2 TYR 1 598	2.881	6.510	-10.073	1.00	7.16
ATOM	599	CE1 TYR 1 598	4.842	5.306	-11.566	1.00	7.16
ATOM	600	CE2 TYR 1 598	4.205	6.712	-9.763	1.00	7.16
ATOM	601	CZ TYR 1 598	5.188	6.108	-10.506	1.00	7.16
ATOM	602	OH TYR 1 598	6.547	6.317	-10.185	1.00	7.16
ATOM	603	N SER 1 599	-0.013	4.975	-8.716	1.00	4.48
ATOM	604	CA SER 1 599	0.146	5.134	-7.293	1.00	4.48
ATOM	605	C SER 1 599	-0.364	3.986	-6.474	1.00	4.48
ATOM	606	O SER 1 599	-0.056	3.853	-5.291	1.00	4.48
ATOM	607	CB SER 1 599	-0.501	6.433	-6.784	1.00	4.48
ATOM	608	OG SER 1 599	0.029	6.770	-5.511	1.00	4.48
ATOM	609	N TRP 1 600	-1.166	3.123	-7.103	1.00	2.83
ATOM	610	CA TRP 1 600	-1.945	2.101	-6.479	1.00	2.83
ATOM	611	C TRP 1 600	-1.188	1.302	-5.467	1.00	2.83
ATOM	612	O TRP 1 600	-1.561	1.258	-4.294	1.00	2.83
ATOM	613	CB TRP 1 600	-2.341	1.109	-7.565	1.00	2.83
ATOM	614	CG TRP 1 600	-3.591	0.441	-7.181	1.00	2.83
ATOM	615	CD1 TRP 1 600	-3.942	-0.815	-6.793	1.00	2.83
ATOM	616	CD2 TRP 1 600	-4.693	1.293	-6.907	1.00	2.83
ATOM	617	NE1 TRP 1 600	-5.257	-0.809	-6.409	1.00	2.83
ATOM	618	CE2 TRP 1 600	-5.718	0.492	-6.479	1.00	2.83
ATOM	619	CE3 TRP 1 600	-4.818	2.647	-6.992	1.00	2.83
ATOM	620	CZ2 TRP 1 600	-6.916	1.047	-6.205	1.00	2.83
ATOM	621	CZ3 TRP 1 600	-6.018	3.201	-6.627	1.00	2.83
ATOM	622	CH2 TRP 1 600	-7.081	2.405	-6.290	1.00	2.83
ATOM	623	N MET 1 601	-0.100	0.641	-5.888	1.00	4.56
ATOM	624	CA MET 1 601	0.614	-0.167	-4.950	1.00	4.56
ATOM	625	C MET 1 601	1.324	0.717	-3.974	1.00	4.56
ATOM	626	O MET 1 601	1.564	0.322	-2.836	1.00	4.56
ATOM	627	CB MET 1 601	1.602	-1.163	-5.582	1.00	4.56
ATOM	628	CG MET 1 601	3.025	-0.654	-5.783	1.00	4.56
ATOM	629	SD MET 1 601	4.060	-0.617	-4.285	1.00	4.56
ATOM	630	CE MET 1 601	4.167	-2.419	-4.091	1.00	4.56
ATOM	631	N PHE 1 602	1.706	1.937	-4.408	1.00	6.98
ATOM	632	CA PHE 1 602	2.410	2.844	-3.542	1.00	6.98
ATOM	633	C PHE 1 602	1.582	3.074	-2.317	1.00	6.98
ATOM	634	O PHE 1 602	2.086	2.981	-1.200	1.00	6.98
ATOM	635	CB PHE 1 602	2.534	4.278	-4.096	1.00	6.98
ATOM	636	CG PHE 1 602	3.498	4.431	-5.217	1.00	6.98
ATOM	637	CD1 PHE 1 602	3.158	4.051	-6.495	1.00	6.98
ATOM	638	CD2 PHE 1 602	4.567	5.281	-5.046	1.00	6.98
ATOM	639	CE1 PHE 1 602	3.924	4.447	-7.564	1.00	6.98
ATOM	640	CE2 PHE 1 602	5.340	5.673	-6.109	1.00	6.98
ATOM	641	CZ PHE 1 602	5.042	5.221	-7.369	1.00	6.98
ATOM	642	N LEU 1 603	0.286	3.407	-2.501	1.00	3.79
ATOM	643	CA LEU 1 603	-0.551	3.686	-1.365	1.00	3.79
ATOM	644	C LEU 1 603	-0.740	2.459	-0.541	1.00	3.79
ATOM	645	O LEU 1 603	-0.676	2.509	0.685	1.00	3.79
ATOM	646	CB LEU 1 603	-1.995	4.128	-1.677	1.00	3.79
ATOM	647	CG LEU 1 603	-2.165	5.496	-2.352	1.00	3.79
ATOM	648	CD1 LEU 1 603	-1.536	6.626	-1.521	1.00	3.79
ATOM	649	CD2 LEU 1 603	-1.720	5.453	-3.813	1.00	3.79

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ATOM	650	N	MET	1 604	-0.978	1.317	-1.209	1.00	5.17
ATOM	651	CA	MET	1 604	-1.284	0.101	-0.519	1.00	5.17
ATOM	652	C	MET	1 604	-0.137	-0.248	0.370	1.00	5.17
ATOM	653	O	MET	1 604	-0.322	-0.589	1.537	1.00	5.17
ATOM	654	CB	MET	1 604	-1.430	-1.091	-1.479	1.00	5.17
ATOM	655	CG	MET	1 604	-2.428	-0.856	-2.612	1.00	5.17
ATOM	656	SD	MET	1 604	-4.150	-0.604	-2.106	1.00	5.17
ATOM	657	CE	MET	1 604	-4.639	-0.119	-3.784	1.00	5.17
ATOM	658	N	ALA	1 605	1.090	-0.153	-0.170	1.00	0.70
ATOM	659	CA	ALA	1 605	2.263	-0.519	0.565	1.00	0.70
ATOM	660	C	ALA	1 605	2.414	0.368	1.754	1.00	0.70
ATOM	661	O	ALA	1 605	2.793	-0.090	2.830	1.00	0.70
ATOM	662	CB	ALA	1 605	3.551	-0.397	-0.268	1.00	0.70
ATOM	663	N	PHE	1 606	2.133	1.673	1.590	1.00	4.22
ATOM	664	CA	PHE	1 606	2.309	2.548	2.707	1.00	4.22
ATOM	665	C	PHE	1 606	1.317	2.211	3.776	1.00	4.22
ATOM	666	O	PHE	1 606	1.648	2.206	4.960	1.00	4.22
ATOM	667	CB	PHE	1 606	2.157	4.042	2.396	1.00	4.22
ATOM	668	CG	PHE	1 606	2.785	4.728	3.563	1.00	4.22
ATOM	669	CD1	PHE	1 606	2.099	4.905	4.743	1.00	4.22
ATOM	670	CD2	PHE	1 606	4.109	5.095	3.513	1.00	4.22
ATOM	671	CE1	PHE	1 606	2.706	5.477	5.835	1.00	4.22
ATOM	672	CE2	PHE	1 606	4.725	5.668	4.600	1.00	4.22
ATOM	673	CZ	PHE	1 606	4.022	5.863	5.765	1.00	4.22
ATOM	674	N	ALA	1 607	0.069	1.893	3.381	1.00	0.92
ATOM	675	CA	ALA	1 607	-0.960	1.605	4.338	1.00	0.92
ATOM	676	C	ALA	1 607	-0.537	0.427	5.153	1.00	0.92
ATOM	677	O	ALA	1 607	-0.765	0.376	6.361	1.00	0.92
ATOM	678	CB	ALA	1 607	-2.302	1.253	3.676	1.00	0.92
ATOM	679	N	LEU	1 608	0.067	-0.568	4.487	1.00	4.26
ATOM	680	CA	LEU	1 608	0.559	-1.747	5.129	1.00	4.26
ATOM	681	C	LEU	1 608	1.704	-1.393	6.034	1.00	4.26
ATOM	682	O	LEU	1 608	1.779	-1.876	7.161	1.00	4.26
ATOM	683	CB	LEU	1 608	1.010	-2.780	4.068	1.00	4.26
ATOM	684	CG	LEU	1 608	1.578	-4.119	4.573	1.00	4.26
ATOM	685	CD1	LEU	1 608	1.752	-5.104	3.410	1.00	4.26
ATOM	686	CD2	LEU	1 608	2.921	-3.927	5.286	1.00	4.26
ATOM	687	N	GLY	1 609	2.631	-0.542	5.551	1.00	0.62
ATOM	688	CA	GLY	1 609	3.824	-0.209	6.281	1.00	0.62
ATOM	689	C	GLY	1 609	3.521	0.478	7.577	1.00	0.62
ATOM	690	O	GLY	1 609	4.164	0.210	8.589	1.00	0.62
ATOM	691	N	TRP	1 610	2.542	1.395	7.598	1.00	3.39
ATOM	692	CA	TRP	1 610	2.246	2.087	8.821	1.00	3.39
ATOM	693	C	TRP	1 610	1.768	1.108	9.843	1.00	3.39
ATOM	694	O	TRP	1 610	1.936	1.305	11.045	1.00	3.39
ATOM	695	CB	TRP	1 610	1.172	3.178	8.672	1.00	3.39
ATOM	696	CG	TRP	1 610	0.730	3.769	9.990	1.00	3.39
ATOM	697	CD1	TRP	1 610	-0.435	3.565	10.671	1.00	3.39
ATOM	698	CD2	TRP	1 610	1.575	4.541	10.858	1.00	3.39
ATOM	699	NE1	TRP	1 610	-0.391	4.210	11.884	1.00	3.39
ATOM	700	CE2	TRP	1 610	0.846	4.805	12.018	1.00	3.39
ATOM	701	CE3	TRP	1 610	2.860	4.981	10.709	1.00	3.39
ATOM	702	CZ2	TRP	1 610	1.388	5.525	13.044	1.00	3.39
ATOM	703	CZ3	TRP	1 610	3.408	5.692	11.754	1.00	3.39
ATOM	704	CH2	TRP	1 610	2.684	5.966	12.895	1.00	3.39
ATOM	705	N	ARG	1 611	1.110	0.045	9.366	1.00	4.02
ATOM	706	CA	ARG	1 611	0.550	-1.005	10.161	1.00	4.02
ATOM	707	C	ARG	1 611	1.493	-2.017	10.738	1.00	4.02
ATOM	708	O	ARG	1 611	1.046	-2.871	11.500	1.00	4.02
ATOM	709	CB	ARG	1 611	-0.632	-1.729	9.497	1.00	4.02
ATOM	710	CG	ARG	1 611	-1.429	-0.764	8.613	1.00	4.02

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ATOM	711	CD	ARG	1	611	-2.571	-1.408	7.827	1.00	4.02
ATOM	712	NE	ARG	1	611	-1.971	-2.364	6.856	1.00	4.02
ATOM	713	CZ	ARG	1	611	-2.100	-2.115	5.520	1.00	4.02
ATOM	714	NH1	ARG	1	611	-2.768	-1.002	5.099	1.00	4.02
ATOM	715	NH2	ARG	1	611	-1.570	-2.977	4.605	1.00	4.02
ATOM	716	N	SER	1	612	2.787	-2.048	10.363	1.00	4.05
ATOM	717	CA	SER	1	612	3.539	-3.105	10.979	1.00	4.05
ATOM	718	C	SER	1	612	3.668	-2.931	12.454	1.00	4.05
ATOM	719	O	SER	1	612	3.685	-1.817	12.976	1.00	4.05
ATOM	720	CB	SER	1	612	4.919	-3.410	10.387	1.00	4.05
ATOM	721	OG	SER	1	612	5.539	-4.473	11.094	1.00	4.05
ATOM	722	N	TYR	1	613	3.743	-4.074	13.163	1.00	4.51
ATOM	723	CA	TYR	1	613	3.792	-4.072	14.594	1.00	4.51
ATOM	724	C	TYR	1	613	5.133	-4.616	14.963	1.00	4.51
ATOM	725	O	TYR	1	613	5.519	-5.697	14.522	1.00	4.51
ATOM	726	CB	TYR	1	613	2.716	-4.995	15.193	1.00	4.51
ATOM	727	CG	TYR	1	613	2.510	-4.676	16.633	1.00	4.51
ATOM	728	CD1	TYR	1	613	3.337	-5.181	17.606	1.00	4.51
ATOM	729	CD2	TYR	1	613	1.402	-3.951	17.009	1.00	4.51
ATOM	730	CE1	TYR	1	613	3.064	-4.947	18.934	1.00	4.51
ATOM	731	CE2	TYR	1	613	1.125	-3.716	18.335	1.00	4.51
ATOM	732	CZ	TYR	1	613	1.959	-4.221	19.302	1.00	4.51
ATOM	733	OH	TYR	1	613	1.675	-4.003	20.667	1.00	4.51
ATOM	734	N	ARG	1	614	5.891	-3.866	15.783	1.00	6.30
ATOM	735	CA	ARG	1	614	7.211	-4.286	16.147	1.00	6.30
ATOM	736	C	ARG	1	614	7.154	-5.564	16.919	1.00	6.30
ATOM	737	O	ARG	1	614	7.863	-6.520	16.608	1.00	6.30
ATOM	738	CB	ARG	1	614	7.917	-3.260	17.047	1.00	6.30
ATOM	739	CG	ARG	1	614	8.166	-1.916	16.361	1.00	6.30
ATOM	740	CD	ARG	1	614	6.880	-1.217	15.918	1.00	6.30
ATOM	741	NE	ARG	1	614	6.009	-1.054	17.116	1.00	6.30
ATOM	742	CZ	ARG	1	614	4.734	-0.591	16.966	1.00	6.30
ATOM	743	NH1	ARG	1	614	4.264	-0.277	15.724	1.00	6.30
ATOM	744	NH2	ARG	1	614	3.928	-0.444	18.057	1.00	6.30
ATOM	745	N	GLN	1	615	6.284	-5.619	17.943	1.00	3.13
ATOM	746	CA	GLN	1	615	6.219	-6.789	18.769	1.00	3.13
ATOM	747	C	GLN	1	615	5.740	-7.940	17.956	1.00	3.13
ATOM	748	O	GLN	1	615	6.283	-9.042	18.030	1.00	3.13
ATOM	749	CB	GLN	1	615	5.251	-6.635	19.952	1.00	3.13
ATOM	750	CG	GLN	1	615	5.665	-5.548	20.943	1.00	3.13
ATOM	751	CD	GLN	1	615	6.925	-6.023	21.650	1.00	3.13
ATOM	752	OE1	GLN	1	615	7.457	-7.089	21.342	1.00	3.13
ATOM	753	NE2	GLN	1	615	7.419	-5.214	22.625	1.00	3.13
ATOM	754	N	SER	1	616	4.708	-7.696	17.134	1.00	4.46
ATOM	755	CA	SER	1	616	4.133	-8.738	16.345	1.00	4.46
ATOM	756	C	SER	1	616	5.206	-9.213	15.424	1.00	4.46
ATOM	757	O	SER	1	616	5.342	-10.416	15.200	1.00	4.46
ATOM	758	CB	SER	1	616	2.943	-8.225	15.520	1.00	4.46
ATOM	759	OG	SER	1	616	2.192	-9.316	15.016	1.00	4.46
ATOM	760	N	SER	1	617	5.978	-8.253	14.871	1.00	6.06
ATOM	761	CA	SER	1	617	7.119	-8.454	14.019	1.00	6.06
ATOM	762	C	SER	1	617	7.082	-7.438	12.943	1.00	6.06
ATOM	763	O	SER	1	617	6.016	-7.070	12.454	1.00	6.06
ATOM	764	CB	SER	1	617	7.235	-9.826	13.321	1.00	6.06
ATOM	765	OG	SER	1	617	7.691	-10.813	14.235	1.00	6.06
ATOM	766	N	ALA	1	618	8.272	-6.952	12.548	1.00	1.34
ATOM	767	CA	ALA	1	618	8.328	-6.034	11.458	1.00	1.34
ATOM	768	C	ALA	1	618	7.780	-6.872	10.363	1.00	1.34
ATOM	769	O	ALA	1	618	7.040	-6.399	9.503	1.00	1.34
ATOM	770	CB	ALA	1	618	9.763	-5.633	11.080	1.00	1.34
ATOM	771	N	ASN	1	619	8.117	-8.172	10.420	1.00	2.27

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ATOM	772	CA	ASN 1 619	7.655	-9.121	9.458	1.00	2.27
ATOM	773	C	ASN 1 619	6.170	-9.004	9.485	1.00	2.27
ATOM	774	O	ASN 1 619	5.521	-8.973	8.442	1.00	2.27
ATOM	775	CB	ASN 1 619	7.978	-10.575	9.852	1.00	2.27
ATOM	776	CG	ASN 1 619	9.489	-10.762	9.929	1.00	2.27
ATOM	777	OD1	ASN 1 619	8.505	-11.245	10.491	1.00	2.27
ATOM	778	ND2	ASN 1 619	9.749	-9.835	8.973	1.00	2.27
ATOM	779	N	LEU 1 620	5.590	-8.915	10.698	1.00	1.42
ATOM	780	CA	LEU 1 620	4.167	-8.832	10.788	1.00	1.42
ATOM	781	C	LEU 1 620	3.676	-7.466	10.447	1.00	1.42
ATOM	782	O	LEU 1 620	3.870	-6.484	11.166	1.00	1.42
ATOM	783	CB	LEU 1 620	3.611	-9.328	12.134	1.00	1.42
ATOM	784	CG	LEU 1 620	3.876	-10.842	12.293	1.00	1.42
ATOM	785	CD1	LEU 1 620	3.339	-11.415	13.612	1.00	1.42
ATOM	786	CD2	LEU 1 620	3.363	-11.618	11.071	1.00	1.42
ATOM	787	N	LEU 1 621	3.019	-7.413	9.278	1.00	1.28
ATOM	788	CA	LEU 1 621	2.463	-6.252	8.661	1.00	1.28
ATOM	789	C	LEU 1 621	1.007	-6.575	8.629	1.00	1.28
ATOM	790	O	LEU 1 621	0.629	-7.744	8.704	1.00	1.28
ATOM	791	CB	LEU 1 621	2.927	-6.155	7.203	1.00	1.28
ATOM	792	CG	LEU 1 621	4.463	-6.148	7.063	1.00	1.28
ATOM	793	CD1	LEU 1 621	4.910	-6.052	5.593	1.00	1.28
ATOM	794	CD2	LEU 1 621	5.093	-5.062	7.948	1.00	1.28
ATOM	795	N	CYS 1 622	0.131	-5.561	8.548	1.00	1.26
ATOM	796	CA	CYS 1 622	-1.253	-5.921	8.517	1.00	1.26
ATOM	797	C	CYS 1 622	-1.831	-5.468	7.213	1.00	1.26
ATOM	798	O	CYS 1 622	-1.836	-4.277	6.907	1.00	1.26
ATOM	799	CB	CYS 1 622	-2.053	-5.269	9.652	1.00	1.26
ATOM	800	SG	CYS 1 622	-3.717	-5.966	9.791	1.00	1.26
ATOM	801	N	PHE 1 623	-2.346	-6.415	6.402	1.00	4.97
ATOM	802	CA	PHE 1 623	-2.922	-6.047	5.139	1.00	4.97
ATOM	803	C	PHE 1 623	-4.365	-5.819	5.378	1.00	4.97
ATOM	804	O	PHE 1 623	-4.995	-6.711	5.951	1.00	4.97
ATOM	805	CB	PHE 1 623	-2.879	-7.140	4.054	1.00	4.97
ATOM	806	CG	PHE 1 623	-1.505	-7.278	3.496	1.00	4.97
ATOM	807	CD1	PHE 1 623	-0.586	-8.126	4.069	1.00	4.97
ATOM	808	CD2	PHE 1 623	-1.182	-6.645	2.317	1.00	4.97
ATOM	809	CE1	PHE 1 623	0.634	-8.337	3.468	1.00	4.97
ATOM	810	CE2	PHE 1 623	0.040	-6.846	1.721	1.00	4.97
ATOM	811	CZ	PHE 1 623	0.946	-7.707	2.290	1.00	4.97
ATOM	812	N	ALA 1 624	-4.872	-4.641	4.901	1.00	5.16
ATOM	813	CA	ALA 1 624	-6.224	-4.152	5.033	1.00	5.16
ATOM	814	C	ALA 1 624	-6.657	-4.675	6.332	1.00	5.16
ATOM	815	O	ALA 1 624	-7.324	-5.698	6.295	1.00	5.16
ATOM	816	CB	ALA 1 624	-7.182	-4.694	3.959	1.00	5.16
ATOM	817	N	PRO 1 625	-6.437	-3.914	7.376	1.00	4.05
ATOM	818	CA	PRO 1 625	-6.315	-4.317	8.776	1.00	4.05
ATOM	819	C	PRO 1 625	-6.730	-5.645	9.373	1.00	4.05
ATOM	820	O	PRO 1 625	-6.476	-5.826	10.559	1.00	4.05
ATOM	821	CB	PRO 1 625	-6.868	-3.160	9.606	1.00	4.05
ATOM	822	CG	PRO 1 625	-7.701	-2.347	8.614	1.00	4.05
ATOM	823	CD	PRO 1 625	-7.007	-2.584	7.272	1.00	4.05
ATOM	824	N	ASP 1 626	-7.415	-6.545	8.659	1.00	3.31
ATOM	825	CA	ASP 1 626	-7.765	-7.863	9.076	1.00	3.31
ATOM	826	C	ASP 1 626	-6.607	-8.827	9.191	1.00	3.31
ATOM	827	O	ASP 1 626	-6.482	-9.506	10.208	1.00	3.31
ATOM	828	CB	ASP 1 626	-8.752	-8.509	8.092	1.00	3.31
ATOM	829	CG	ASP 1 626	-10.028	-7.681	8.097	1.00	3.31
ATOM	830	OD1	ASP 1 626	-10.848	-7.855	7.156	1.00	3.31
ATOM	831	OD2	ASP 1 626	-10.199	-6.858	9.037	1.00	3.31
ATOM	832	N	LEU 1 627	-5.704	-8.921	8.184	1.00	5.46

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ATOM	833	CA	LEU	1	627	-4.737	-9.984	8.288	1.00	5.46
ATOM	834	C	LEU	1	627	-3.336	-9.532	8.542	1.00	5.46
ATOM	835	O	LEU	1	627	-2.848	-8.558	7.972	1.00	5.46
ATOM	836	CB	LEU	1	627	-4.741	-10.955	7.086	1.00	5.46
ATOM	837	CG	LEU	1	627	-4.364	-10.353	5.716	1.00	5.46
ATOM	838	CD1	LEU	1	627	-2.877	-9.976	5.633	1.00	5.46
ATOM	839	CD2	LEU	1	627	-4.785	-11.295	4.576	1.00	5.46
ATOM	840	N	ILE	1	628	-2.646	-10.255	9.447	1.00	3.87
ATOM	841	CA	ILE	1	628	-1.294	-9.909	9.743	1.00	3.87
ATOM	842	C	ILE	1	628	-0.443	-10.972	9.139	1.00	3.87
ATOM	843	O	ILE	1	628	-0.757	-12.158	9.228	1.00	3.87
ATOM	844	CB	ILE	1	628	-0.993	-9.828	11.209	1.00	3.87
ATOM	845	CG1	ILE	1	628	0.352	-9.122	11.429	1.00	3.87
ATOM	846	CG2	ILE	1	628	-1.070	-11.245	11.799	1.00	3.87
ATOM	847	CD1	ILE	1	628	0.558	-8.654	12.866	1.00	3.87
ATOM	848	N	ILE	1	629	0.654	-10.561	8.479	1.00	7.73
ATOM	849	CA	ILE	1	629	1.481	-11.529	7.822	1.00	7.73
ATOM	850	C	ILE	1	629	2.901	-11.255	8.179	1.00	7.73
ATOM	851	O	ILE	1	629	3.262	-10.131	8.521	1.00	7.73
ATOM	852	CB	ILE	1	629	1.408	-11.466	6.322	1.00	7.73
ATOM	853	CG1	ILE	1	629	1.985	-10.137	5.798	1.00	7.73
ATOM	854	CG2	ILE	1	629	-0.054	-11.708	5.914	1.00	7.73
ATOM	855	CD1	ILE	1	629	1.253	-8.890	6.291	1.00	7.73
ATOM	856	N	ASN	1	630	3.742	-12.304	8.121	1.00	3.80
ATOM	857	CA	ASN	1	630	5.137	-12.184	8.419	1.00	3.80
ATOM	858	C	ASN	1	630	5.869	-11.907	7.147	1.00	3.80
ATOM	859	O	ASN	1	630	5.289	-11.908	6.062	1.00	3.80
ATOM	860	CB	ASN	1	630	5.738	-13.461	9.031	1.00	3.80
ATOM	861	CG	ASN	1	630	5.595	-14.578	8.007	1.00	3.80
ATOM	862	OD1	ASN	1	630	4.673	-14.573	7.192	1.00	3.80
ATOM	863	ND2	ASN	1	630	6.526	-15.567	8.050	1.00	3.80
ATOM	864	N	GLU	1	631	7.187	-11.662	7.263	1.00	3.57
ATOM	865	CA	GLU	1	631	7.988	-11.375	6.109	1.00	3.57
ATOM	866	C	GLU	1	631	7.926	-12.536	5.169	1.00	3.57
ATOM	867	O	GLU	1	631	7.764	-12.366	3.961	1.00	3.57
ATOM	868	CB	GLU	1	631	9.475	-11.173	6.450	1.00	3.57
ATOM	869	CG	GLU	1	631	10.345	-10.866	5.228	1.00	3.57
ATOM	870	CD	GLU	1	631	11.786	-10.712	5.696	1.00	3.57
ATOM	871	OE1	GLU	1	631	12.099	-9.663	6.319	1.00	3.57
ATOM	872	OE2	GLU	1	631	12.594	-11.644	5.436	1.00	3.57
ATOM	873	N	GLN	1	632	8.037	-13.761	5.707	1.00	5.74
ATOM	874	CA	GLN	1	632	8.056	-14.926	4.874	1.00	5.74
ATOM	875	C	GLN	1	632	6.771	-15.100	4.112	1.00	5.74
ATOM	876	O	GLN	1	632	6.799	-15.379	2.915	1.00	5.74
ATOM	877	CB	GLN	1	632	8.307	-16.215	5.684	1.00	5.74
ATOM	878	CG	GLN	1	632	8.337	-17.501	4.853	1.00	5.74
ATOM	879	CD	GLN	1	632	6.906	-17.987	4.659	1.00	5.74
ATOM	880	OE1	GLN	1	632	6.206	-18.306	5.619	1.00	5.74
ATOM	881	NE2	GLN	1	632	6.451	-18.027	3.378	1.00	5.74
ATOM	882	N	ARG	1	633	5.604	-14.942	4.770	1.00	6.29
ATOM	883	CA	ARG	1	633	4.389	-15.210	4.043	1.00	6.29
ATOM	884	C	ARG	1	633	4.211	-14.188	2.992	1.00	6.29
ATOM	885	O	ARG	1	633	3.685	-14.524	1.937	1.00	6.29
ATOM	886	CB	ARG	1	633	3.055	-15.288	4.868	1.00	6.29
ATOM	887	CG	ARG	1	633	1.781	-15.671	4.039	1.00	6.29
ATOM	888	CD	ARG	1	633	0.503	-16.120	4.825	1.00	6.29
ATOM	889	NE	ARG	1	633	-0.537	-16.684	3.894	1.00	6.29
ATOM	890	CZ	ARG	1	633	-1.381	-17.769	3.971	1.00	6.29
ATOM	891	NH1	ARG	1	633	-1.669	-18.475	5.103	1.00	6.29
ATOM	892	NH2	ARG	1	633	-2.050	-18.131	2.839	1.00	6.29
ATOM	893	N	MET	1	634	4.592	-12.927	3.267	1.00	5.30

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ATOM	894	CA	MET	1	634	4.490	-11.824	2.355	1.00	5.30
ATOM	895	C	MET	1	634	5.504	-11.870	1.253	1.00	5.30
ATOM	896	O	MET	1	634	5.243	-11.342	0.176	1.00	5.30
ATOM	897	CB	MET	1	634	4.655	-10.467	3.043	1.00	5.30
ATOM	898	CG	MET	1	634	6.088	-10.242	3.497	1.00	5.30
ATOM	899	SD	MET	1	634	6.423	-8.596	4.165	1.00	5.30
ATOM	900	CE	MET	1	634	8.197	-8.946	4.143	1.00	5.30
ATOM	901	N	THR	1	635	6.704	-12.449	1.496	1.00	5.56
ATOM	902	CA	THR	1	635	7.691	-12.574	0.448	1.00	5.56
ATOM	903	C	THR	1	635	7.291	-13.593	-0.573	1.00	5.56
ATOM	904	O	THR	1	635	7.247	-13.321	-1.770	1.00	5.56
ATOM	905	CB	THR	1	635	9.057	-12.970	0.948	1.00	5.56
ATOM	906	OG1	THR	1	635	9.976	-13.019	-0.133	1.00	5.56
ATOM	907	CG2	THR	1	635	9.006	-14.304	1.693	1.00	5.56
ATOM	908	N	LEU	1	636	6.921	-14.809	-0.133	1.00	4.24
ATOM	909	CA	LEU	1	636	6.544	-15.813	-1.089	1.00	4.24
ATOM	910	C	LEU	1	636	5.264	-15.595	-1.893	1.00	4.24
ATOM	911	O	LEU	1	636	5.255	-16.010	-3.054	1.00	4.24
ATOM	912	CB	LEU	1	636	6.419	-17.222	-0.478	1.00	4.24
ATOM	913	CG	LEU	1	636	7.748	-17.820	0.028	1.00	4.24
ATOM	914	CD1	LEU	1	636	8.241	-17.113	1.295	1.00	4.24
ATOM	915	CD2	LEU	1	636	7.655	-19.343	0.208	1.00	4.24
ATOM	916	N	PRO	1	637	4.186	-15.012	-1.382	1.00	3.86
ATOM	917	CA	PRO	1	637	2.948	-14.924	-2.088	1.00	3.86
ATOM	918	C	PRO	1	637	3.115	-14.366	-3.410	1.00	3.86
ATOM	919	O	PRO	1	637	2.533	-14.923	-4.330	1.00	3.86
ATOM	920	CB	PRO	1	637	2.043	-14.013	-1.293	1.00	3.86
ATOM	921	CG	PRO	1	637	3.014	-12.991	-0.736	1.00	3.86
ATOM	922	CD	PRO	1	637	4.304	-13.807	-0.651	1.00	3.86
ATOM	923	N	CYS	1	638	3.829	-13.241	-3.498	1.00	3.09
ATOM	924	CA	CYS	1	638	4.111	-12.683	-4.764	1.00	3.09
ATOM	925	C	CYS	1	638	5.156	-11.654	-4.537	1.00	3.09
ATOM	926	O	CYS	1	638	6.022	-11.460	-5.376	1.00	3.09
ATOM	927	CB	CYS	1	638	2.939	-11.903	-5.397	1.00	3.09
ATOM	928	SG	CYS	1	638	1.629	-12.922	-6.146	1.00	3.09
ATOM	929	N	MET	1	639	5.197	-11.038	-3.350	1.00	6.02
ATOM	930	CA	MET	1	639	6.036	-9.884	-3.188	1.00	6.02
ATOM	931	C	MET	1	639	7.487	-10.110	-3.503	1.00	6.02
ATOM	932	O	MET	1	639	8.080	-9.347	-4.263	1.00	6.02
ATOM	933	CB	MET	1	639	5.971	-9.336	-1.753	1.00	6.02
ATOM	934	CG	MET	1	639	4.557	-8.953	-1.308	1.00	6.02
ATOM	935	SD	MET	1	639	3.806	-7.570	-2.217	1.00	6.02
ATOM	936	CE	MET	1	639	2.242	-7.588	-1.297	1.00	6.02
ATOM	937	N	TYR	1	640	8.110	-11.154	-2.931	1.00	5.37
ATOM	938	CA	TYR	1	640	9.491	-11.430	-3.201	1.00	5.37
ATOM	939	C	TYR	1	640	10.263	-10.413	-2.419	1.00	5.37
ATOM	940	O	TYR	1	640	9.991	-10.188	-1.245	1.00	5.37
ATOM	941	CB	TYR	1	640	9.826	-11.396	-4.717	1.00	5.37
ATOM	942	CG	TYR	1	640	11.224	-11.840	-5.002	1.00	5.37
ATOM	943	CD1	TYR	1	640	12.204	-10.952	-5.390	1.00	5.37
ATOM	944	CD2	TYR	1	640	11.555	-13.171	-4.890	1.00	5.37
ATOM	945	CE1	TYR	1	640	13.483	-11.373	-5.655	1.00	5.37
ATOM	946	CE2	TYR	1	640	12.830	-13.603	-5.162	1.00	5.37
ATOM	947	CZ	TYR	1	640	13.797	-12.705	-5.546	1.00	5.37
ATOM	948	OH	TYR	1	640	15.105	-13.146	-5.831	1.00	5.37
ATOM	949	N	ASP	1	641	11.239	-9.752	-3.053	1.00	4.19
ATOM	950	CA	ASP	1	641	12.078	-8.786	-2.414	1.00	4.19
ATOM	951	C	ASP	1	641	11.284	-7.584	-2.016	1.00	4.19
ATOM	952	O	ASP	1	641	11.648	-6.875	-1.080	1.00	4.19
ATOM	953	CB	ASP	1	641	13.244	-8.321	-3.306	1.00	4.19
ATOM	954	CG	ASP	1	641	12.688	-7.658	-4.559	1.00	4.19

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ATOM	955	OD1 ASP 1 641	11.502	-7.911	-4.902	1.00	4.19
ATOM	956	OD2 ASP 1 641	13.457	-6.891	-5.196	1.00	4.19
ATOM	957	N GLN 1 642	10.173	-7.320	-2.723	1.00	3.89
ATOM	958	CA GLN 1 642	9.398	-6.150	-2.438	1.00	3.89
ATOM	959	C GLN 1 642	8.913	-6.211	-1.024	1.00	3.89
ATOM	960	O GLN 1 642	8.788	-5.182	-0.361	1.00	3.89
ATOM	961	CB GLN 1 642	8.180	-5.965	-3.361	1.00	3.89
ATOM	962	CG GLN 1 642	7.354	-4.712	-3.086	1.00	3.89
ATOM	963	CD GLN 1 642	6.027	-4.871	-3.815	1.00	3.89
ATOM	964	OE1 GLN 1 642	5.823	-4.303	-4.883	1.00	3.89
ATOM	965	NE2 GLN 1 642	5.097	-5.669	-3.220	1.00	3.89
ATOM	966	N CYS 1 643	8.626	-7.425	-0.521	1.00	3.75
ATOM	967	CA CYS 1 643	8.132	-7.555	0.820	1.00	3.75
ATOM	968	C CYS 1 643	9.163	-7.043	1.775	1.00	3.75
ATOM	969	O CYS 1 643	8.832	-6.384	2.760	1.00	3.75
ATOM	970	CB CYS 1 643	7.811	-9.006	1.219	1.00	3.75
ATOM	971	SG CYS 1 643	9.300	-10.002	1.508	1.00	3.75
ATOM	972	N LYS 1 644	10.451	-7.320	1.500	1.00	8.40
ATOM	973	CA LYS 1 644	11.497	-6.922	2.387	1.00	8.40
ATOM	974	C LYS 1 644	11.477	-5.434	2.423	1.00	8.40
ATOM	975	O LYS 1 644	11.625	-4.826	3.481	1.00	8.40
ATOM	976	CB LYS 1 644	12.884	-7.374	1.899	1.00	8.40
ATOM	977	CG LYS 1 644	13.980	-7.257	2.959	1.00	8.40
ATOM	978	CD LYS 1 644	13.803	-8.232	4.126	1.00	8.40
ATOM	979	CE LYS 1 644	13.697	-9.696	3.689	1.00	8.40
ATOM	980	NZ LYS 1 644	15.006	-10.177	3.191	1.00	8.40
ATOM	981	N HIS 1 645	11.256	-4.811	1.251	1.00	2.06
ATOM	982	CA HIS 1 645	11.262	-3.382	1.157	1.00	2.06
ATOM	983	C HIS 1 645	10.183	-2.804	2.017	1.00	2.06
ATOM	984	O HIS 1 645	10.409	-1.832	2.734	1.00	2.06
ATOM	985	CB HIS 1 645	11.040	-2.882	-0.279	1.00	2.06
ATOM	986	CG HIS 1 645	11.300	-1.414	-0.432	1.00	2.06
ATOM	987	ND1 HIS 1 645	11.608	-0.808	-1.630	1.00	2.06
ATOM	988	CD2 HIS 1 645	11.279	-0.416	0.493	1.00	2.06
ATOM	989	CE1 HIS 1 645	11.762	0.515	-1.371	1.00	2.06
ATOM	990	NE2 HIS 1 645	11.572	0.801	-0.096	1.00	2.06
ATOM	991	N MET 1 646	8.976	-3.394	1.970	1.00	2.52
ATOM	992	CA MET 1 646	7.880	-2.894	2.749	1.00	2.52
ATOM	993	C MET 1 646	8.163	-3.056	4.213	1.00	2.52
ATOM	994	O MET 1 646	7.864	-2.167	5.008	1.00	2.52
ATOM	995	CB MET 1 646	6.557	-3.626	2.455	1.00	2.52
ATOM	996	CG MET 1 646	6.032	-3.396	1.036	1.00	2.52
ATOM	997	SD MET 1 646	4.470	-4.249	0.661	1.00	2.52
ATOM	998	CE MET 1 646	4.358	-3.638	-1.046	1.00	2.52
ATOM	999	N LEU 1 647	8.741	-4.200	4.623	1.00	1.01
ATOM	1000	CA LEU 1 647	8.998	-4.389	6.025	1.00	1.01
ATOM	1001	C LEU 1 647	9.958	-3.366	6.506	1.00	1.01
ATOM	1002	O LEU 1 647	9.743	-2.749	7.548	1.00	1.01
ATOM	1003	CB LEU 1 647	9.690	-5.708	6.383	1.00	1.01
ATOM	1004	CG LEU 1 647	8.838	-6.958	6.180	1.00	1.01
ATOM	1005	CD1 LEU 1 647	9.605	-8.211	6.620	1.00	1.01
ATOM	1006	CD2 LEU 1 647	7.461	-6.831	6.834	1.00	1.01
ATOM	1007	N TYR 1 648	11.063	-3.160	5.767	1.00	6.90
ATOM	1008	CA TYR 1 648	11.990	-2.202	6.272	1.00	6.90
ATOM	1009	C TYR 1 648	11.426	-0.823	6.265	1.00	6.90
ATOM	1010	O TYR 1 648	11.736	-0.029	7.153	1.00	6.90
ATOM	1011	CB TYR 1 648	13.429	-2.259	5.705	1.00	6.90
ATOM	1012	CG TYR 1 648	13.499	-2.469	4.232	1.00	6.90
ATOM	1013	CD1 TYR 1 648	13.274	-1.450	3.336	1.00	6.90
ATOM	1014	CD2 TYR 1 648	14.075	-3.633	3.776	1.00	6.90
ATOM	1015	CE1 TYR 1 648	13.566	-1.623	2.002	1.00	6.90

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ATOM	1016	CE2 TYR 1 648	14.368	-3.814	2.447	1.00	6.90
ATOM	1017	CZ TYR 1 648	14.122	-2.800	1.556	1.00	6.90
ATOM	1018	OH TYR 1 648	14.436	-2.970	0.191	1.00	6.90
ATOM	1019	N VAL 1 649	10.571	-0.484	5.282	1.00	3.24
ATOM	1020	CA VAL 1 649	10.016	0.835	5.329	1.00	3.24
ATOM	1021	C VAL 1 649	9.185	0.944	6.569	1.00	3.24
ATOM	1022	O VAL 1 649	9.226	1.955	7.268	1.00	3.24
ATOM	1023	CB VAL 1 649	9.165	1.206	4.143	1.00	3.24
ATOM	1024	CG1 VAL 1 649	7.840	0.434	4.182	1.00	3.24
ATOM	1025	CG2 VAL 1 649	8.973	2.732	4.155	1.00	3.24
ATOM	1026	N SER 1 650	8.423	-0.116	6.895	1.00	3.01
ATOM	1027	CA SER 1 650	7.588	-0.062	8.057	1.00	3.01
ATOM	1028	C SER 1 650	8.382	0.080	9.315	1.00	3.01
ATOM	1029	O SER 1 650	7.972	0.789	10.232	1.00	3.01
ATOM	1030	CB SER 1 650	6.728	-1.292	8.289	1.00	3.01
ATOM	1031	OG SER 1 650	6.141	-1.100	9.562	1.00	3.01
ATOM	1032	N SER 1 651	9.529	-0.615	9.408	1.00	3.21
ATOM	1033	CA SER 1 651	10.305	-0.555	10.611	1.00	3.21
ATOM	1034	C SER 1 651	10.788	0.846	10.809	1.00	3.21
ATOM	1035	O SER 1 651	10.753	1.373	11.919	1.00	3.21
ATOM	1036	CB SER 1 651	11.543	-1.467	10.566	1.00	3.21
ATOM	1037	OG SER 1 651	12.442	-1.019	9.562	1.00	3.21
ATOM	1038	N GLU 1 652	11.247	1.482	9.715	1.00	3.30
ATOM	1039	CA GLU 1 652	11.786	2.811	9.744	1.00	3.30
ATOM	1040	C GLU 1 652	10.741	3.828	10.087	1.00	3.30
ATOM	1041	O GLU 1 652	11.018	4.810	10.772	1.00	3.30
ATOM	1042	CB GLU 1 652	12.417	3.215	8.399	1.00	3.30
ATOM	1043	CG GLU 1 652	13.164	4.548	8.446	1.00	3.30
ATOM	1044	CD GLU 1 652	13.852	4.745	7.102	1.00	3.30
ATOM	1045	OE1 GLU 1 652	14.492	3.772	6.620	1.00	3.30
ATOM	1046	OE2 GLU 1 652	13.746	5.866	6.538	1.00	3.30
ATOM	1047	N LEU 1 653	9.502	3.601	9.613	1.00	1.22
ATOM	1048	CA LEU 1 653	8.382	4.490	9.772	1.00	1.22
ATOM	1049	C LEU 1 653	7.999	4.675	11.205	1.00	1.22
ATOM	1050	O LEU 1 653	7.473	5.722	11.576	1.00	1.22
ATOM	1051	CB LEU 1 653	7.121	3.976	9.055	1.00	1.22
ATOM	1052	CG LEU 1 653	7.274	3.871	7.529	1.00	1.22
ATOM	1053	CD1 LEU 1 653	5.985	3.356	6.869	1.00	1.22
ATOM	1054	CD2 LEU 1 653	7.759	5.198	6.931	1.00	1.22
ATOM	1055	N HIS 1 654	8.239	3.664	12.056	1.00	0.94
ATOM	1056	CA HIS 1 654	7.780	3.733	13.412	1.00	0.94
ATOM	1057	C HIS 1 654	8.305	4.961	14.097	1.00	0.94
ATOM	1058	O HIS 1 654	7.566	5.632	14.816	1.00	0.94
ATOM	1059	CB HIS 1 654	8.210	2.509	14.238	1.00	0.94
ATOM	1060	CG HIS 1 654	7.684	1.227	13.664	1.00	0.94
ATOM	1061	ND1 HIS 1 654	6.369	0.824	13.747	1.00	0.94
ATOM	1062	CD2 HIS 1 654	8.323	0.263	12.946	1.00	0.94
ATOM	1063	CE1 HIS 1 654	6.279	-0.354	13.078	1.00	0.94
ATOM	1064	NE2 HIS 1 654	7.440	-0.735	12.578	1.00	0.94
ATOM	1065	N ARG 1 655	9.588	5.300	13.882	1.00	4.48
ATOM	1066	CA ARG 1 655	10.187	6.440	14.522	1.00	4.48
ATOM	1067	C ARG 1 655	9.540	7.715	14.072	1.00	4.48
ATOM	1068	O ARG 1 655	9.425	8.669	14.840	1.00	4.48
ATOM	1069	CB ARG 1 655	11.691	6.574	14.233	1.00	4.48
ATOM	1070	CG ARG 1 655	12.538	5.463	14.856	1.00	4.48
ATOM	1071	CD ARG 1 655	14.043	5.712	14.741	1.00	4.48
ATOM	1072	NE ARG 1 655	14.368	6.866	15.627	1.00	4.48
ATOM	1073	CZ ARG 1 655	15.669	7.202	15.868	1.00	4.48
ATOM	1074	NH1 ARG 1 655	15.961	8.258	16.682	1.00	4.48
ATOM	1075	NH2 ARG 1 655	16.677	6.484	15.293	1.00	4.48
ATOM	1076	N LEU 1 656	9.101	7.757	12.802	1.00	6.60

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ATOM 1077 CA LEU 1 656	8.539	8.936	12.207	1.00	6.60
ATOM 1078 C LEU 1 656	7.300	9.335	12.952	1.00	6.60
ATOM 1079 O LEU 1 656	6.991	10.521	13.063	1.00	6.60
ATOM 1080 CB LEU 1 656	8.207	8.718	10.718	1.00	6.60
ATOM 1081 CG LEU 1 656	7.801	9.993	9.959	1.00	6.60
ATOM 1082 CD1 LEU 1 656	8.927	11.038	9.999	1.00	6.60
ATOM 1083 CD2 LEU 1 656	7.394	9.665	8.514	1.00	6.60
ATOM 1084 N GLN 1 657	6.552	8.349	13.484	1.00	4.61
ATOM 1085 CA GLN 1 657	5.373	8.650	14.248	1.00	4.61
ATOM 1086 C GLN 1 657	4.426	9.452	13.422	1.00	4.61
ATOM 1087 O GLN 1 657	4.006	10.537	13.822	1.00	4.61
ATOM 1088 CB GLN 1 657	5.670	9.464	15.521	1.00	4.61
ATOM 1089 CG GLN 1 657	6.537	8.726	16.543	1.00	4.61
ATOM 1090 CD GLN 1 657	5.673	7.683	17.234	1.00	4.61
ATOM 1091 OE1 GLN 1 657	6.155	6.910	18.062	1.00	4.61
ATOM 1092 NE2 GLN 1 657	4.358	7.659	16.892	1.00	4.61
ATOM 1093 N VAL 1 658	4.057	8.932	12.237	1.00	4.09
ATOM 1094 CA VAL 1 658	3.151	9.662	11.405	1.00	4.09
ATOM 1095 C VAL 1 658	1.751	9.432	11.857	1.00	4.09
ATOM 1096 O VAL 1 658	1.415	8.383	12.406	1.00	4.09
ATOM 1097 CB VAL 1 658	3.196	9.282	9.954	1.00	4.09
ATOM 1098 CG1 VAL 1 658	4.593	9.604	9.412	1.00	4.09
ATOM 1099 CG2 VAL 1 658	2.781	7.811	9.803	1.00	4.09
ATOM 1100 N SER 1 659	0.893	10.447	11.648	1.00	5.48
ATOM 1101 CA SER 1 659	-0.487	10.313	11.998	1.00	5.48
ATOM 1102 C SER 1 659	-1.244	10.189	10.719	1.00	5.48
ATOM 1103 O SER 1 659	-0.664	10.146	9.635	1.00	5.48
ATOM 1104 CB SER 1 659	-1.056	11.510	12.768	1.00	5.48
ATOM 1105 OG SER 1 659	-0.398	11.640	14.020	1.00	5.48
ATOM 1106 N TYR 1 660	-2.582	10.134	10.816	1.00	4.14
ATOM 1107 CA TYR 1 660	-3.380	9.977	9.642	1.00	4.14
ATOM 1108 C TYR 1 660	-3.203	11.111	8.680	1.00	4.14
ATOM 1109 O TYR 1 660	-3.173	10.886	7.474	1.00	4.14
ATOM 1110 CB TYR 1 660	-4.869	9.731	9.952	1.00	4.14
ATOM 1111 CG TYR 1 660	-5.313	10.667	11.021	1.00	4.14
ATOM 1112 CD1 TYR 1 660	-4.992	10.401	12.333	1.00	4.14
ATOM 1113 CD2 TYR 1 660	-6.192	11.686	10.751	1.00	4.14
ATOM 1114 CE1 TYR 1 660	-5.513	11.159	13.354	1.00	4.14
ATOM 1115 CE2 TYR 1 660	-6.718	12.451	11.766	1.00	4.14
ATOM 1116 CZ TYR 1 660	-6.383	12.184	13.071	1.00	4.14
ATOM 1117 OH TYR 1 660	-6.940	12.949	14.117	1.00	4.14
ATOM 1118 N GLU 1 661	-3.055	12.357	9.166	1.00	3.59
ATOM 1119 CA GLU 1 661	-2.906	13.461	8.257	1.00	3.59
ATOM 1120 C GLU 1 661	-1.654	13.326	7.442	1.00	3.59
ATOM 1121 O GLU 1 661	-1.658	13.567	6.235	1.00	3.59
ATOM 1122 CB GLU 1 661	-2.847	14.820	8.973	1.00	3.59
ATOM 1123 CG GLU 1 661	-1.677	14.957	9.948	1.00	3.59
ATOM 1124 CD GLU 1 661	-1.767	16.345	10.567	1.00	3.59
ATOM 1125 OE1 GLU 1 661	-1.886	17.329	9.790	1.00	3.59
ATOM 1126 OE2 GLU 1 661	-1.728	16.440	11.822	1.00	3.59
ATOM 1127 N GLU 1 662	-0.542	12.935	8.085	1.00	1.15
ATOM 1128 CA GLU 1 662	0.708	12.809	7.393	1.00	1.15
ATOM 1129 C GLU 1 662	0.611	11.716	6.372	1.00	1.15
ATOM 1130 O GLU 1 662	1.114	11.856	5.259	1.00	1.15
ATOM 1131 CB GLU 1 662	1.866	12.534	8.369	1.00	1.15
ATOM 1132 CG GLU 1 662	2.138	13.747	9.268	1.00	1.15
ATOM 1133 CD GLU 1 662	3.040	13.341	10.425	1.00	1.15
ATOM 1134 OE1 GLU 1 662	2.691	12.356	11.130	1.00	1.15
ATOM 1135 OE2 GLU 1 662	4.085	14.016	10.624	1.00	1.15
ATOM 1136 N TYR 1 663	-0.048	10.591	6.720	1.00	6.52
ATOM 1137 CA TYR 1 663	-0.196	9.526	5.767	1.00	6.52

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ATOM 1138 C TYR 1 663	-1.042	9.982	4.620	1.00	6.52
ATOM 1139 O TYR 1 663	-0.767	9.640	3.472	1.00	6.52
ATOM 1140 CB TYR 1 663	-0.819	8.241	6.339	1.00	6.52
ATOM 1141 CG TYR 1 663	-1.054	7.337	5.175	1.00	6.52
ATOM 1142 CD1 TYR 1 663	-0.005	6.939	4.378	1.00	6.52
ATOM 1143 CD2 TYR 1 663	-2.288	6.761	4.971	1.00	6.52
ATOM 1144 CE1 TYR 1 663	-0.205	6.071	3.331	1.00	6.52
ATOM 1145 CE2 TYR 1 663	-2.484	5.855	3.955	1.00	6.52
ATOM 1146 CZ TYR 1 663	-1.445	5.526	3.115	1.00	6.52
ATOM 1147 OH TYR 1 663	-1.644	4.624	2.049	1.00	6.52
ATOM 1148 N LEU 1 664	-2.101	10.772	4.896	1.00	4.94
ATOM 1149 CA LEU 1 664	-2.936	11.261	3.833	1.00	4.94
ATOM 1150 C LEU 1 664	-2.160	12.062	2.863	1.00	4.94
ATOM 1151 O LEU 1 664	-2.253	11.872	1.652	1.00	4.94
ATOM 1152 CB LEU 1 664	-3.980	12.302	4.252	1.00	4.94
ATOM 1153 CG LEU 1 664	-5.336	11.712	4.558	1.00	4.94
ATOM 1154 CD1 LEU 1 664	-5.727	10.909	3.315	1.00	4.94
ATOM 1155 CD2 LEU 1 664	-5.408	11.006	5.915	1.00	4.94
ATOM 1156 N CYS 1 665	-1.380	12.996	3.409	1.00	0.94
ATOM 1157 CA CYS 1 665	-0.635	13.934	2.643	1.00	0.94
ATOM 1158 C CYS 1 665	0.294	13.182	1.757	1.00	0.94
ATOM 1159 O CYS 1 665	0.441	13.492	0.576	1.00	0.94
ATOM 1160 CB CYS 1 665	0.222	14.789	3.581	1.00	0.94
ATOM 1161 SG CYS 1 665	-0.788	15.819	4.692	1.00	0.94
ATOM 1162 N MET 1 666	0.948	12.155	2.317	1.00	4.36
ATOM 1163 CA MET 1 666	1.880	11.401	1.544	1.00	4.36
ATOM 1164 C MET 1 666	1.150	10.699	0.442	1.00	4.36
ATOM 1165 O MET 1 666	1.642	10.625	-0.683	1.00	4.36
ATOM 1166 CB MET 1 666	2.668	10.379	2.382	1.00	4.36
ATOM 1167 CG MET 1 666	1.864	9.172	2.858	1.00	4.36
ATOM 1168 SD MET 1 666	2.829	8.023	3.882	1.00	4.36
ATOM 1169 CE MET 1 666	4.183	7.920	2.678	1.00	4.36
ATOM 1170 N LYS 1 667	-0.059	10.178	0.729	1.00	2.57
ATOM 1171 CA LYS 1 667	-0.804	9.480	-0.281	1.00	2.57
ATOM 1172 C LYS 1 667	-1.119	10.417	-1.402	1.00	2.57
ATOM 1173 O LYS 1 667	-1.000	10.056	-2.572	1.00	2.57
ATOM 1174 CB LYS 1 667	-2.168	8.953	0.189	1.00	2.57
ATOM 1175 CG LYS 1 667	-2.117	7.815	1.204	1.00	2.57
ATOM 1176 CD LYS 1 667	-3.513	7.385	1.660	1.00	2.57
ATOM 1177 CE LYS 1 667	-4.251	6.536	0.622	1.00	2.57
ATOM 1178 NZ LYS 1 667	-5.555	6.092	1.163	1.00	2.57
ATOM 1179 N THR 1 668	-1.533	11.654	-1.069	1.00	5.21
ATOM 1180 CA THR 1 668	-1.916	12.584	-2.089	1.00	5.21
ATOM 1181 C THR 1 668	-0.743	12.889	-2.960	1.00	5.21
ATOM 1182 O THR 1 668	-0.876	12.992	-4.177	1.00	5.21
ATOM 1183 CB THR 1 668	-2.435	13.893	-1.555	1.00	5.21
ATOM 1184 OG1 THR 1 668	-1.418	14.575	-0.837	1.00	5.21
ATOM 1185 CG2 THR 1 668	-3.633	13.612	-0.634	1.00	5.21
ATOM 1186 N LEU 1 669	0.456	13.042	-2.378	1.00	0.92
ATOM 1187 CA LEU 1 669	1.555	13.381	-3.230	1.00	0.92
ATOM 1188 C LEU 1 669	1.838	12.252	-4.172	1.00	0.92
ATOM 1189 O LEU 1 669	2.136	12.473	-5.344	1.00	0.92
ATOM 1190 CB LEU 1 669	2.847	13.743	-2.480	1.00	0.92
ATOM 1191 CG LEU 1 669	3.977	14.146	-3.444	1.00	0.92
ATOM 1192 CD1 LEU 1 669	3.543	15.317	-4.339	1.00	0.92
ATOM 1193 CD2 LEU 1 669	5.270	14.473	-2.686	1.00	0.92
ATOM 1194 N LEU 1 670	1.738	11.000	-3.686	1.00	0.69
ATOM 1195 CA LEU 1 670	2.018	9.865	-4.520	1.00	0.69
ATOM 1196 C LEU 1 670	1.049	9.837	-5.661	1.00	0.69
ATOM 1197 O LEU 1 670	1.430	9.611	-6.810	1.00	0.69
ATOM 1198 CB LEU 1 670	1.861	8.535	-3.763	1.00	0.69

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ATOM	1199	CG	LEU	1	670	2.854	8.365	-2.599	1.00	0.69
ATOM	1200	CD1	LEU	1	670	2.651	7.018	-1.890	1.00	0.69
ATOM	1201	CD2	LEU	1	670	4.305	8.572	-3.066	1.00	0.69
ATOM	1202	N	LEU	1	671	-0.240	10.082	-5.368	1.00	3.54
ATOM	1203	CA	LEU	1	671	-1.272	10.024	-6.364	1.00	3.54
ATOM	1204	C	LEU	1	671	-1.070	11.102	-7.383	1.00	3.54
ATOM	1205	O	LEU	1	671	-1.261	10.883	-8.577	1.00	3.54
ATOM	1206	CB	LEU	1	671	-2.678	10.108	-5.728	1.00	3.54
ATOM	1207	CG	LEU	1	671	-3.861	10.063	-6.716	1.00	3.54
ATOM	1208	CD1	LEU	1	671	-5.177	9.741	-5.994	1.00	3.54
ATOM	1209	CD2	LEU	1	671	-3.993	11.377	-7.493	1.00	3.54
ATOM	1210	N	LEU	1	672	-0.642	12.284	-6.918	1.00	5.01
ATOM	1211	CA	LEU	1	672	-0.396	13.478	-7.671	1.00	5.01
ATOM	1212	C	LEU	1	672	0.765	13.403	-8.606	1.00	5.01
ATOM	1213	O	LEU	1	672	1.018	14.367	-9.325	1.00	5.01
ATOM	1214	CB	LEU	1	672	-0.250	14.727	-6.797	1.00	5.01
ATOM	1215	CG	LEU	1	672	-1.602	15.358	-6.418	1.00	5.01
ATOM	1216	CD1	LEU	1	672	-2.591	14.356	-5.807	1.00	5.01
ATOM	1217	CD2	LEU	1	672	-1.363	16.565	-5.508	1.00	5.01
ATOM	1218	N	SER	1	673	1.564	12.322	-8.549	1.00	4.46
ATOM	1219	CA	SER	1	673	2.677	12.205	-9.450	1.00	4.46
ATOM	1220	C	SER	1	673	2.229	12.452	-10.854	1.00	4.46
ATOM	1221	O	SER	1	673	1.485	11.670	-11.444	1.00	4.46
ATOM	1222	CB	SER	1	673	3.371	10.834	-9.381	1.00	4.46
ATOM	1223	OG	SER	1	673	2.450	9.808	-9.715	1.00	4.46
ATOM	1224	N	SER	1	674	2.710	13.573	-11.422	1.00	4.03
ATOM	1225	CA	SER	1	674	2.324	14.023	-12.726	1.00	4.03
ATOM	1226	C	SER	1	674	3.197	13.391	-13.750	1.00	4.03
ATOM	1227	O	SER	1	674	2.937	12.281	-14.209	1.00	4.03
ATOM	1228	CB	SER	1	674	2.464	15.545	-12.902	1.00	4.03
ATOM	1229	OG	SER	1	674	1.589	16.226	-12.016	1.00	4.03
ATOM	1230	N	VAL	1	675	4.265	14.110	-14.135	1.00	4.27
ATOM	1231	CA	VAL	1	675	5.158	13.662	-15.158	1.00	4.27
ATOM	1232	C	VAL	1	675	5.648	12.258	-14.953	1.00	4.27
ATOM	1233	O	VAL	1	675	6.039	11.636	-15.940	1.00	4.27
ATOM	1234	CB	VAL	1	675	6.348	14.565	-15.353	1.00	4.27
ATOM	1235	CG1	VAL	1	675	7.204	14.599	-14.077	1.00	4.27
ATOM	1236	CG2	VAL	1	675	7.113	14.081	-16.596	1.00	4.27
ATOM	1237	N	PRO	1	676	5.668	11.678	-13.779	1.00	2.47
ATOM	1238	CA	PRO	1	676	6.142	10.328	-13.718	1.00	2.47
ATOM	1239	C	PRO	1	676	5.180	9.425	-14.410	1.00	2.47
ATOM	1240	O	PRO	1	676	5.538	8.290	-14.721	1.00	2.47
ATOM	1241	CB	PRO	1	676	6.368	10.014	-12.235	1.00	2.47
ATOM	1242	CG	PRO	1	676	5.825	11.241	-11.479	1.00	2.47
ATOM	1243	CD	PRO	1	676	5.899	12.365	-12.518	1.00	2.47
ATOM	1244	N	LYS	1	677	3.953	9.909	-14.647	1.00	7.09
ATOM	1245	CA	LYS	1	677	2.953	9.130	-15.305	1.00	7.09
ATOM	1246	C	LYS	1	677	3.295	9.075	-16.754	1.00	7.09
ATOM	1247	O	LYS	1	677	3.876	10.009	-17.301	1.00	7.09
ATOM	1248	CB	LYS	1	677	1.565	9.786	-15.268	1.00	7.09
ATOM	1249	CG	LYS	1	677	0.945	9.990	-13.886	1.00	7.09
ATOM	1250	CD	LYS	1	677	0.660	8.694	-13.134	1.00	7.09
ATOM	1251	CE	LYS	1	677	1.641	8.443	-11.994	1.00	7.09
ATOM	1252	NZ	LYS	1	677	3.004	8.241	-12.528	1.00	7.09
ATOM	1253	N	ASP	1	678	2.936	7.960	-17.414	1.00	3.66
ATOM	1254	CA	ASP	1	678	3.159	7.842	-18.822	1.00	3.66
ATOM	1255	C	ASP	1	678	1.804	7.942	-19.448	1.00	3.66
ATOM	1256	O	ASP	1	678	0.919	7.138	-19.154	1.00	3.66
ATOM	1257	CB	ASP	1	678	3.754	6.479	-19.221	1.00	3.66
ATOM	1258	CG	ASP	1	678	4.010	6.465	-20.722	1.00	3.66
ATOM	1259	OD1	ASP	1	678	3.687	7.483	-21.392	1.00	3.66

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ATOM	1260	OD2 ASP	1 678	4.529	5.431	-21.220	1.00	3.66
ATOM	1261	N GLY	1 679	1.600	8.946	-20.323	1.00	0.72
ATOM	1262	CA GLY	1 679	0.337	9.069	-20.992	1.00	0.72
ATOM	1263	C GLY	1 679	-0.557	10.104	-20.372	1.00	0.72
ATOM	1264	O GLY	1 679	-1.593	10.440	-20.942	1.00	0.72
ATOM	1265	N LEU	1 680	-0.195	10.641	-19.189	1.00	3.91
ATOM	1266	CA LEU	1 680	-1.015	11.655	-18.577	1.00	3.91
ATOM	1267	C LEU	1 680	-1.041	12.859	-19.453	1.00	3.91
ATOM	1268	O LEU	1 680	0.005	13.396	-19.817	1.00	3.91
ATOM	1269	CB LEU	1 680	-0.504	12.083	-17.185	1.00	3.91
ATOM	1270	CG LEU	1 680	-0.962	11.201	-16.007	1.00	3.91
ATOM	1271	CD1 LEU	1 680	-2.274	11.711	-15.404	1.00	3.91
ATOM	1272	CD2 LEU	1 680	-1.132	9.738	-16.439	1.00	3.91
ATOM	1273	N LYS	1 681	-2.252	13.279	-19.873	1.00	9.62
ATOM	1274	CA LYS	1 681	-2.324	14.444	-20.700	1.00	9.62
ATOM	1275	C LYS	1 681	-2.135	15.726	-19.952	1.00	9.62
ATOM	1276	O LYS	1 681	-1.432	16.617	-20.426	1.00	9.62
ATOM	1277	CB LYS	1 681	-3.605	14.566	-21.542	1.00	9.62
ATOM	1278	CG LYS	1 681	-4.874	14.922	-20.780	1.00	9.62
ATOM	1279	CD LYS	1 681	-5.342	13.847	-19.810	1.00	9.62
ATOM	1280	CE LYS	1 681	-6.817	14.021	-19.474	1.00	9.62
ATOM	1281	NZ LYS	1 681	-7.616	13.820	-20.704	1.00	9.62
ATOM	1282	N SER	1 682	-2.741	15.867	-18.753	1.00	3.76
ATOM	1283	CA SER	1 682	-2.629	17.141	-18.102	1.00	3.76
ATOM	1284	C SER	1 682	-1.576	17.102	-17.041	1.00	3.76
ATOM	1285	O SER	1 682	-1.874	17.009	-15.851	1.00	3.76
ATOM	1286	CB SER	1 682	-3.935	17.597	-17.438	1.00	3.76
ATOM	1287	OG SER	1 682	-3.752	18.895	-16.898	1.00	3.76
ATOM	1288	N GLN	1 683	-0.300	17.189	-17.456	1.00	3.60
ATOM	1289	CA GLN	1 683	0.774	17.152	-16.511	1.00	3.60
ATOM	1290	C GLN	1 683	0.808	18.390	-15.668	1.00	3.60
ATOM	1291	O GLN	1 683	1.001	18.313	-14.457	1.00	3.60
ATOM	1292	CB GLN	1 683	2.158	17.009	-17.167	1.00	3.60
ATOM	1293	CG GLN	1 683	2.560	18.199	-18.039	1.00	3.60
ATOM	1294	CD GLN	1 683	3.940	17.908	-18.610	1.00	3.60
ATOM	1295	OE1 GLN	1 683	4.530	16.864	-18.336	1.00	3.60
ATOM	1296	NE2 GLN	1 683	4.475	18.857	-19.425	1.00	3.60
ATOM	1297	N GLU	1 684	0.603	19.567	-16.290	1.00	3.13
ATOM	1298	CA GLU	1 684	0.756	20.811	-15.586	1.00	3.13
ATOM	1299	C GLU	1 684	-0.201	21.003	-14.452	1.00	3.13
ATOM	1300	O GLU	1 684	0.216	21.351	-13.349	1.00	3.13
ATOM	1301	CB GLU	1 684	0.622	22.033	-16.511	1.00	3.13
ATOM	1302	CG GLU	1 684	1.772	22.148	-17.513	1.00	3.13
ATOM	1303	CD GLU	1 684	3.054	22.373	-16.723	1.00	3.13
ATOM	1304	OE1 GLU	1 684	2.967	22.482	-15.472	1.00	3.13
ATOM	1305	OE2 GLU	1 684	4.139	22.436	-17.362	1.00	3.13
ATOM	1306	N LEU	1 685	-1.509	20.769	-14.668	1.00	7.18
ATOM	1307	CA LEU	1 685	-2.427	21.022	-13.593	1.00	7.18
ATOM	1308	C LEU	1 685	-2.104	20.082	-12.491	1.00	7.18
ATOM	1309	O LEU	1 685	-2.183	20.414	-11.310	1.00	7.18
ATOM	1310	CB LEU	1 685	-3.919	20.860	-13.977	1.00	7.18
ATOM	1311	CG LEU	1 685	-4.434	19.429	-14.259	1.00	7.18
ATOM	1312	CD1 LEU	1 685	-4.558	18.563	-12.993	1.00	7.18
ATOM	1313	CD2 LEU	1 685	-5.752	19.480	-15.047	1.00	7.18
ATOM	1314	N PHE	1 686	-1.737	18.859	-12.885	1.00	3.83
ATOM	1315	CA PHE	1 686	-1.447	17.791	-11.989	1.00	3.83
ATOM	1316	C PHE	1 686	-0.251	18.129	-11.151	1.00	3.83
ATOM	1317	O PHE	1 686	-0.213	17.840	-9.954	1.00	3.83
ATOM	1318	CB PHE	1 686	-1.208	16.527	-12.809	1.00	3.83
ATOM	1319	CG PHE	1 686	-1.341	15.429	-11.852	1.00	3.83
ATOM	1320	CD1 PHE	1 686	-2.481	15.350	-11.090	1.00	3.83

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ATOM	1321	CD2 PHE 1 686	-0.486	14.369	-11.931	1.00	3.83
ATOM	1322	CE1 PHE 1 686	-2.676	14.293	-10.247	1.00	3.83
ATOM	1323	CE2 PHE 1 686	-0.708	13.282	-11.144	1.00	3.83
ATOM	1324	CZ PHE 1 686	-1.751	13.284	-10.258	1.00	3.83
ATOM	1325	N ASP 1 687	0.768	18.753	-11.768	1.00	4.20
ATOM	1326	CA ASP 1 687	1.949	19.143	-11.056	1.00	4.20
ATOM	1327	C ASP 1 687	1.566	20.206	-10.078	1.00	4.20
ATOM	1328	O ASP 1 687	2.041	20.230	-8.943	1.00	4.20
ATOM	1329	CB ASP 1 687	3.032	19.728	-11.978	1.00	4.20
ATOM	1330	CG ASP 1 687	4.308	19.892	-11.165	1.00	4.20
ATOM	1331	OD1 ASP 1 687	5.331	20.338	-11.752	1.00	4.20
ATOM	1332	OD2 ASP 1 687	4.279	19.570	-9.948	1.00	4.20
ATOM	1333	N GLU 1 688	0.669	21.115	-10.499	1.00	1.12
ATOM	1334	CA GLU 1 688	0.259	22.192	-9.649	1.00	1.12
ATOM	1335	C GLU 1 688	-0.378	21.601	-8.437	1.00	1.12
ATOM	1336	O GLU 1 688	-0.161	22.052	-7.313	1.00	1.12
ATOM	1337	CB GLU 1 688	-0.788	23.103	-10.312	1.00	1.12
ATOM	1338	CG GLU 1 688	-0.249	23.904	-11.497	1.00	1.12
ATOM	1339	CD GLU 1 688	-1.408	24.693	-12.086	1.00	1.12
ATOM	1340	OE1 GLU 1 688	-1.157	25.526	-12.997	1.00	1.12
ATOM	1341	OE2 GLU 1 688	-2.563	24.470	-11.635	1.00	1.12
ATOM	1342	N ILE 1 689	-1.196	20.559	-8.634	1.00	3.95
ATOM	1343	CA ILE 1 689	-1.864	19.967	-7.519	1.00	3.95
ATOM	1344	C ILE 1 689	-0.849	19.371	-6.598	1.00	3.95
ATOM	1345	O ILE 1 689	-0.917	19.555	-5.385	1.00	3.95
ATOM	1346	CB ILE 1 689	-2.812	18.880	-7.932	1.00	3.95
ATOM	1347	CG1 ILE 1 689	-3.859	19.434	-8.913	1.00	3.95
ATOM	1348	CG2 ILE 1 689	-3.448	18.299	-6.659	1.00	3.95
ATOM	1349	CD1 ILE 1 689	-4.718	20.551	-8.321	1.00	3.95
ATOM	1350	N ARG 1 690	0.153	18.658	-7.135	1.00	7.53
ATOM	1351	CA ARG 1 690	1.086	18.025	-6.251	1.00	7.53
ATOM	1352	C ARG 1 690	1.845	19.026	-5.444	1.00	7.53
ATOM	1353	O ARG 1 690	2.016	18.847	-4.239	1.00	7.53
ATOM	1354	CB ARG 1 690	2.112	17.131	-6.970	1.00	7.53
ATOM	1355	CG ARG 1 690	3.021	17.870	-7.953	1.00	7.53
ATOM	1356	CD ARG 1 690	4.037	16.952	-8.632	1.00	7.53
ATOM	1357	NE ARG 1 690	4.936	16.430	-7.564	1.00	7.53
ATOM	1358	CZ ARG 1 690	5.289	15.111	-7.550	1.00	7.53
ATOM	1359	NH1 ARG 1 690	6.109	14.637	-6.566	1.00	7.53
ATOM	1360	NH2 ARG 1 690	4.819	14.267	-8.514	1.00	7.53
ATOM	1361	N MET 1 691	2.310	20.127	-6.064	1.00	8.51
ATOM	1362	CA MET 1 691	3.098	21.007	-5.254	1.00	8.51
ATOM	1363	C MET 1 691	2.254	21.587	-4.169	1.00	8.51
ATOM	1364	O MET 1 691	2.743	21.819	-3.064	1.00	8.51
ATOM	1365	CB MET 1 691	3.846	22.155	-5.971	1.00	8.51
ATOM	1366	CG MET 1 691	3.084	23.466	-6.180	1.00	8.51
ATOM	1367	SD MET 1 691	2.189	23.618	-7.747	1.00	8.51
ATOM	1368	CE MET 1 691	3.673	23.884	-8.758	1.00	8.51
ATOM	1369	N THR 1 692	0.958	21.838	-4.439	1.00	4.62
ATOM	1370	CA THR 1 692	0.168	22.427	-3.398	1.00	4.62
ATOM	1371	C THR 1 692	0.124	21.491	-2.231	1.00	4.62
ATOM	1372	O THR 1 692	0.213	21.924	-1.083	1.00	4.62
ATOM	1373	CB THR 1 692	-1.245	22.771	-3.789	1.00	4.62
ATOM	1374	OG1 THR 1 692	-1.808	23.642	-2.819	1.00	4.62
ATOM	1375	CG2 THR 1 692	-2.094	21.496	-3.868	1.00	4.62
ATOM	1376	N TYR 1 693	-0.014	20.175	-2.487	1.00	1.13
ATOM	1377	CA TYR 1 693	-0.051	19.248	-1.393	1.00	1.13
ATOM	1378	C TYR 1 693	1.261	19.240	-0.685	1.00	1.13
ATOM	1379	O TYR 1 693	1.294	19.257	0.542	1.00	1.13
ATOM	1380	CB TYR 1 693	-0.396	17.808	-1.809	1.00	1.13
ATOM	1381	CG TYR 1 693	-1.845	17.808	-2.157	1.00	1.13

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ATOM 1382	CD1 TYR 1 693	-2.271	18.338	-3.348	1.00	1.13
ATOM 1383	CD2 TYR 1 693	-2.785	17.299	-1.293	1.00	1.13
ATOM 1384	CE1 TYR 1 693	-3.600	18.367	-3.687	1.00	1.13
ATOM 1385	CE2 TYR 1 693	-4.123	17.333	-1.616	1.00	1.13
ATOM 1386	CZ TYR 1 693	-4.532	17.869	-2.814	1.00	1.13
ATOM 1387	OH TYR 1 693	-5.904	17.965	-3.131	1.00	1.13
ATOM 1388	N ILE 1 694	2.381	19.263	-1.426	1.00	0.61
ATOM 1389	CA ILE 1 694	3.674	19.185	-0.803	1.00	0.61
ATOM 1390	C ILE 1 694	3.869	20.332	0.139	1.00	0.61
ATOM 1391	O ILE 1 694	4.382	20.153	1.244	1.00	0.61
ATOM 1392	CB ILE 1 694	4.797	19.235	-1.797	1.00	0.61
ATOM 1393	CG1 ILE 1 694	4.708	18.050	-2.772	1.00	0.61
ATOM 1394	CG2 ILE 1 694	6.121	19.294	-1.016	1.00	0.61
ATOM 1395	CD1 ILE 1 694	5.631	18.187	-3.983	1.00	0.61
ATOM 1396	N LYS 1 695	3.463	21.547	-0.271	1.00	8.13
ATOM 1397	CA LYS 1 695	3.654	22.702	0.559	1.00	8.13
ATOM 1398	C LYS 1 695	2.868	22.556	1.822	1.00	8.13
ATOM 1399	O LYS 1 695	3.366	22.835	2.912	1.00	8.13
ATOM 1400	CB LYS 1 695	3.189	23.998	-0.126	1.00	8.13
ATOM 1401	CG LYS 1 695	3.567	25.267	0.640	1.00	8.13
ATOM 1402	CD LYS 1 695	5.066	25.573	0.615	1.00	8.13
ATOM 1403	CE LYS 1 695	5.917	24.542	1.359	1.00	8.13
ATOM 1404	NZ LYS 1 695	5.642	24.610	2.811	1.00	8.13
ATOM 1405	N GLU 1 696	1.609	22.098	1.705	1.00	1.25
ATOM 1406	CA GLU 1 696	0.766	21.945	2.853	1.00	1.25
ATOM 1407	C GLU 1 696	1.349	20.908	3.750	1.00	1.25
ATOM 1408	O GLU 1 696	1.299	21.027	4.973	1.00	1.25
ATOM 1409	CB GLU 1 696	-0.655	21.486	2.498	1.00	1.25
ATOM 1410	CG GLU 1 696	-1.425	22.546	1.722	1.00	1.25
ATOM 1411	CD GLU 1 696	-2.816	22.018	1.423	1.00	1.25
ATOM 1412	OE1 GLU 1 696	-3.532	22.684	0.629	1.00	1.25
ATOM 1413	OE2 GLU 1 696	-3.181	20.951	1.982	1.00	1.25
ATOM 1414	N LEU 1 697	1.913	19.842	3.161	1.00	8.40
ATOM 1415	CA LEU 1 697	2.441	18.787	3.970	1.00	8.40
ATOM 1416	C LEU 1 697	3.586	19.306	4.776	1.00	8.40
ATOM 1417	O LEU 1 697	3.701	19.017	5.967	1.00	8.40
ATOM 1418	CB LEU 1 697	2.977	17.603	3.151	1.00	8.40
ATOM 1419	CG LEU 1 697	1.981	17.123	2.084	1.00	8.40
ATOM 1420	CD1 LEU 1 697	2.257	15.678	1.640	1.00	8.40
ATOM 1421	CD2 LEU 1 697	0.530	17.468	2.462	1.00	8.40
ATOM 1422	N GLY 1 698	4.466	20.103	4.143	1.00	0.45
ATOM 1423	CA GLY 1 698	5.622	20.592	4.835	1.00	0.45
ATOM 1424	C GLY 1 698	5.201	21.455	5.979	1.00	0.45
ATOM 1425	O GLY 1 698	5.741	21.351	7.080	1.00	0.45
ATOM 1426	N LYS 1 699	4.211	22.333	5.748	1.00	5.59
ATOM 1427	CA LYS 1 699	3.791	23.224	6.787	1.00	5.59
ATOM 1428	C LYS 1 699	3.230	22.419	7.911	1.00	5.59
ATOM 1429	O LYS 1 699	3.441	22.737	9.079	1.00	5.59
ATOM 1430	CB LYS 1 699	2.680	24.193	6.357	1.00	5.59
ATOM 1431	CG LYS 1 699	1.342	23.489	6.155	1.00	5.59
ATOM 1432	CD LYS 1 699	0.150	24.428	6.129	1.00	5.59
ATOM 1433	CE LYS 1 699	0.256	25.462	5.020	1.00	5.59
ATOM 1434	NZ LYS 1 699	-0.767	26.488	5.248	1.00	5.59
ATOM 1435	N ALA 1 700	2.489	21.346	7.580	1.00	0.65
ATOM 1436	CA ALA 1 700	1.876	20.550	8.598	1.00	0.65
ATOM 1437	C ALA 1 700	2.941	19.933	9.443	1.00	0.65
ATOM 1438	O ALA 1 700	2.831	19.901	10.667	1.00	0.65
ATOM 1439	CB ALA 1 700	1.015	19.412	8.026	1.00	0.65
ATOM 1440	N ILE 1 701	4.017	19.433	8.810	1.00	3.82
ATOM 1441	CA ILE 1 701	5.036	18.790	9.585	1.00	3.82
ATOM 1442	C ILE 1 701	5.693	19.794	10.475	1.00	3.82

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ATOM	1443	O	ILE	1	701	6.075	19.481	11.602	1.00	3.82
ATOM	1444	CB	ILE	1	701	6.075	18.082	8.764	1.00	3.82
ATOM	1445	CG1	ILE	1	701	6.839	17.095	9.659	1.00	3.82
ATOM	1446	CG2	ILE	1	701	6.979	19.119	8.079	1.00	3.82
ATOM	1447	CD1	ILE	1	701	7.626	16.051	8.874	1.00	3.82
ATOM	1448	N	VAL	1	702	5.845	21.039	9.986	1.00	0.51
ATOM	1449	CA	VAL	1	702	6.428	22.062	10.798	1.00	0.51
ATOM	1450	C	VAL	1	702	5.517	22.229	11.968	1.00	0.51
ATOM	1451	O	VAL	1	702	5.964	22.385	13.104	1.00	0.51
ATOM	1452	CB	VAL	1	702	6.515	23.385	10.096	1.00	0.51
ATOM	1453	CG1	VAL	1	702	7.095	24.420	11.074	1.00	0.51
ATOM	1454	CG2	VAL	1	702	7.344	23.206	8.812	1.00	0.51
ATOM	1455	N	LYS	1	703	4.197	22.165	11.712	1.00	9.37
ATOM	1456	CA	LYS	1	703	3.230	22.326	12.756	1.00	9.37
ATOM	1457	C	LYS	1	703	3.514	21.258	13.752	1.00	9.37
ATOM	1458	O	LYS	1	703	3.431	21.497	14.955	1.00	9.37
ATOM	1459	CB	LYS	1	703	1.780	22.143	12.269	1.00	9.37
ATOM	1460	CG	LYS	1	703	0.715	22.521	13.305	1.00	9.37
ATOM	1461	CD	LYS	1	703	0.716	21.657	14.570	1.00	9.37
ATOM	1462	CE	LYS	1	703	0.197	20.237	14.342	1.00	9.37
ATOM	1463	NZ	LYS	1	703	-1.226	20.280	13.937	1.00	9.37
ATOM	1464	N	ARG	1	704	3.839	20.043	13.267	1.00	8.04
ATOM	1465	CA	ARG	1	704	4.206	18.988	14.163	1.00	8.04
ATOM	1466	C	ARG	1	704	5.501	19.453	14.723	1.00	8.04
ATOM	1467	O	ARG	1	704	6.557	19.224	14.134	1.00	8.04
ATOM	1468	CB	ARG	1	704	4.479	17.646	13.467	1.00	8.04
ATOM	1469	CG	ARG	1	704	3.235	17.002	12.861	1.00	8.04
ATOM	1470	CD	ARG	1	704	2.385	16.248	13.882	1.00	8.04
ATOM	1471	NE	ARG	1	704	1.223	15.686	13.146	1.00	8.04
ATOM	1472	CZ	ARG	1	704	0.363	14.832	13.771	1.00	8.04
ATOM	1473	NH1	ARG	1	704	0.560	14.486	15.077	1.00	8.04
ATOM	1474	NH2	ARG	1	704	-0.703	14.331	13.084	1.00	8.04
ATOM	1475	N	GLU	1	705	5.433	20.112	15.891	1.00	6.89
ATOM	1476	CA	GLU	1	705	6.571	20.722	16.502	1.00	6.89
ATOM	1477	C	GLU	1	705	7.717	19.793	16.543	1.00	6.89
ATOM	1478	O	GLU	1	705	7.541	18.584	16.667	1.00	6.89
ATOM	1479	CB	GLU	1	705	6.312	21.210	17.939	1.00	6.89
ATOM	1480	CG	GLU	1	705	5.415	22.446	18.000	1.00	6.89
ATOM	1481	CD	GLU	1	705	6.174	23.576	17.320	1.00	6.89
ATOM	1482	OE1	GLU	1	705	5.603	24.693	17.201	1.00	6.89
ATOM	1483	OE2	GLU	1	705	7.339	23.332	16.906	1.00	6.89
ATOM	1484	N	GLY	1	706	8.927	20.362	16.413	1.00	2.21
ATOM	1485	CA	GLY	1	706	10.141	19.610	16.420	1.00	2.21
ATOM	1486	C	GLY	1	706	10.330	19.086	17.800	1.00	2.21
ATOM	1487	O	GLY	1	706	11.162	18.208	18.022	1.00	2.21
ATOM	1488	N	ASN	1	707	9.576	19.640	18.769	1.00	3.74
ATOM	1489	CA	ASN	1	707	9.717	19.183	20.118	1.00	3.74
ATOM	1490	C	ASN	1	707	9.444	17.717	20.094	1.00	3.74
ATOM	1491	O	ASN	1	707	10.295	16.908	20.458	1.00	3.74
ATOM	1492	CB	ASN	1	707	8.712	19.832	21.086	1.00	3.74
ATOM	1493	CG	ASN	1	707	9.135	19.488	22.509	1.00	3.74
ATOM	1494	OD1	ASN	1	707	8.484	19.885	23.475	1.00	3.74
ATOM	1495	ND2	ASN	1	707	10.260	18.739	22.647	1.00	3.74
ATOM	1496	N	SER	1	708	8.238	17.327	19.649	1.00	3.07
ATOM	1497	CA	SER	1	708	7.976	15.927	19.536	1.00	3.07
ATOM	1498	C	SER	1	708	8.722	15.483	18.319	1.00	3.07
ATOM	1499	O	SER	1	708	9.414	14.466	18.325	1.00	3.07
ATOM	1500	CB	SER	1	708	6.487	15.607	19.324	1.00	3.07
ATOM	1501	OG	SER	1	708	6.299	14.204	19.220	1.00	3.07
ATOM	1502	N	SER	1	709	8.607	16.282	17.242	1.00	4.34
ATOM	1503	CA	SER	1	709	9.228	15.993	15.988	1.00	4.34

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ATOM	1504	C	SER	1 709	10.693	16.280	16.079	1.00	4.34
ATOM	1505	O	SER	1 709	11.242	16.982	15.230	1.00	4.34
ATOM	1506	CB	SER	1 709	8.652	16.859	14.853	1.00	4.34
ATOM	1507	OG	SER	1 709	9.278	16.563	13.617	1.00	4.34
ATOM	1508	N	GLN	1 710	11.389	15.761	17.111	1.00	3.96
ATOM	1509	CA	GLN	1 710	12.803	15.981	17.041	1.00	3.96
ATOM	1510	C	GLN	1 710	13.402	14.857	16.284	1.00	3.96
ATOM	1511	O	GLN	1 710	13.900	13.888	16.857	1.00	3.96
ATOM	1512	CB	GLN	1 710	13.607	16.084	18.355	1.00	3.96
ATOM	1513	CG	GLN	1 710	13.732	17.498	18.931	1.00	3.96
ATOM	1514	CD	GLN	1 710	12.928	17.617	20.209	1.00	3.96
ATOM	1515	OE1	GLN	1 710	12.380	18.674	20.514	1.00	3.96
ATOM	1516	NE2	GLN	1 710	12.875	16.511	20.998	1.00	3.96
ATOM	1517	N	ASN	1 711	13.342	14.967	14.951	1.00	4.08
ATOM	1518	CA	ASN	1 711	13.976	14.014	14.103	1.00	4.08
ATOM	1519	C	ASN	1 711	14.772	14.907	13.220	1.00	4.08
ATOM	1520	O	ASN	1 711	14.246	15.879	12.682	1.00	4.08
ATOM	1521	CB	ASN	1 711	12.996	13.224	13.218	1.00	4.08
ATOM	1522	CG	ASN	1 711	13.739	12.049	12.597	1.00	4.08
ATOM	1523	OD1	ASN	1 711	13.346	10.895	12.759	1.00	4.08
ATOM	1524	ND2	ASN	1 711	14.845	12.343	11.864	1.00	4.08
ATOM	1525	N	TRP	1 712	16.076	14.630	13.069	1.00	4.56
ATOM	1526	CA	TRP	1 712	16.846	15.510	12.249	1.00	4.56
ATOM	1527	C	TRP	1 712	16.558	15.188	10.823	1.00	4.56
ATOM	1528	O	TRP	1 712	16.349	14.030	10.466	1.00	4.56
ATOM	1529	CB	TRP	1 712	18.366	15.377	12.449	1.00	4.56
ATOM	1530	CG	TRP	1 712	18.903	13.991	12.181	1.00	4.56
ATOM	1531	CD1	TRP	1 712	19.096	13.350	10.992	1.00	4.56
ATOM	1532	CD2	TRP	1 712	19.394	13.108	13.202	1.00	4.56
ATOM	1533	NE1	TRP	1 712	19.650	12.111	11.211	1.00	4.56
ATOM	1534	CE2	TRP	1 712	19.844	11.952	12.567	1.00	4.56
ATOM	1535	CE3	TRP	1 712	19.471	13.253	14.559	1.00	4.56
ATOM	1536	CZ2	TRP	1 712	20.375	10.915	13.280	1.00	4.56
ATOM	1537	CZ3	TRP	1 712	20.010	12.208	15.275	1.00	4.56
ATOM	1538	CH2	TRP	1 712	20.452	11.061	14.648	1.00	4.56
ATOM	1539	N	GLN	1 713	16.527	16.223	9.966	1.00	4.63
ATOM	1540	CA	GLN	1 713	16.349	15.980	8.566	1.00	4.63
ATOM	1541	C	GLN	1 713	14.980	15.395	8.370	1.00	4.63
ATOM	1542	O	GLN	1 713	14.782	14.579	7.474	1.00	4.63
ATOM	1543	CB	GLN	1 713	17.343	14.909	8.068	1.00	4.63
ATOM	1544	CG	GLN	1 713	18.778	15.071	8.596	1.00	4.63
ATOM	1545	CD	GLN	1 713	19.638	15.895	7.648	1.00	4.63
ATOM	1546	OE1	GLN	1 713	19.889	15.497	6.512	1.00	4.63
ATOM	1547	NE2	GLN	1 713	20.121	17.070	8.134	1.00	4.63
ATOM	1548	N	ARG	1 714	13.987	15.802	9.188	1.00	3.83
ATOM	1549	CA	ARG	1 714	12.701	15.167	9.100	1.00	3.83
ATOM	1550	C	ARG	1 714	11.971	15.323	7.801	1.00	3.83
ATOM	1551	O	ARG	1 714	11.537	14.331	7.218	1.00	3.83
ATOM	1552	CB	ARG	1 714	11.716	15.608	10.193	1.00	3.83
ATOM	1553	CG	ARG	1 714	10.353	14.928	10.041	1.00	3.83
ATOM	1554	CD	ARG	1 714	9.426	15.134	11.235	1.00	3.83
ATOM	1555	NE	ARG	1 714	9.949	14.285	12.341	1.00	3.83
ATOM	1556	CZ	ARG	1 714	9.284	13.149	12.699	1.00	3.83
ATOM	1557	NH1	ARG	1 714	9.786	12.343	13.678	1.00	3.83
ATOM	1558	NH2	ARG	1 714	8.109	12.828	12.083	1.00	3.83
ATOM	1559	N	PHE	1 715	11.811	16.556	7.285	1.00	7.35
ATOM	1560	CA	PHE	1 715	10.994	16.649	6.108	1.00	7.35
ATOM	1561	C	PHE	1 715	11.615	15.939	4.948	1.00	7.35
ATOM	1562	O	PHE	1 715	10.968	15.128	4.287	1.00	7.35
ATOM	1563	CB	PHE	1 715	10.643	18.095	5.701	1.00	7.35
ATOM	1564	CG	PHE	1 715	11.864	18.861	5.318	1.00	7.35

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ATOM	1565	CD1 PHE	1 715	12.296	18.874	4.011	1.00	7.35
ATOM	1566	CD2 PHE	1 715	12.497	19.665	6.236	1.00	7.35
ATOM	1567	CE1 PHE	1 715	13.350	19.671	3.630	1.00	7.35
ATOM	1568	CE2 PHE	1 715	13.555	20.459	5.862	1.00	7.35
ATOM	1569	CZ PHE	1 715	13.977	20.472	4.554	1.00	7.35
ATOM	1570	N TYR	1 716	12.905	16.199	4.687	1.00	4.17
ATOM	1571	CA TYR	1 716	13.554	15.554	3.588	1.00	4.17
ATOM	1572	C TYR	1 716	13.721	14.089	3.821	1.00	4.17
ATOM	1573	O TYR	1 716	13.701	13.300	2.878	1.00	4.17
ATOM	1574	CB TYR	1 716	14.874	16.225	3.162	1.00	4.17
ATOM	1575	CG TYR	1 716	15.608	16.683	4.370	1.00	4.17
ATOM	1576	CD1 TYR	1 716	15.188	17.824	5.012	1.00	4.17
ATOM	1577	CD2 TYR	1 716	16.814	16.131	4.723	1.00	4.17
ATOM	1578	CE1 TYR	1 716	15.914	18.386	6.031	1.00	4.17
ATOM	1579	CE2 TYR	1 716	17.552	16.698	5.733	1.00	4.17
ATOM	1580	CZ TYR	1 716	17.109	17.820	6.391	1.00	4.17
ATOM	1581	OH TYR	1 716	17.871	18.391	7.430	1.00	4.17
ATOM	1582	N GLN	1 717	13.892	13.661	5.083	1.00	4.45
ATOM	1583	CA GLN	1 717	14.034	12.252	5.290	1.00	4.45
ATOM	1584	C GLN	1 717	12.760	11.597	4.856	1.00	4.45
ATOM	1585	O GLN	1 717	12.790	10.543	4.227	1.00	4.45
ATOM	1586	CB GLN	1 717	14.289	11.853	6.756	1.00	4.45
ATOM	1587	CG GLN	1 717	13.128	12.151	7.705	1.00	4.45
ATOM	1588	CD GLN	1 717	13.537	11.704	9.101	1.00	4.45
ATOM	1589	OE1 GLN	1 717	12.744	11.748	10.041	1.00	4.45
ATOM	1590	NE2 GLN	1 717	14.812	11.253	9.242	1.00	4.45
ATOM	1591	N LEU	1 718	11.612	12.225	5.182	1.00	0.89
ATOM	1592	CA LEU	1 718	10.315	11.703	4.853	1.00	0.89
ATOM	1593	C LEU	1 718	10.116	11.696	3.366	1.00	0.89
ATOM	1594	O LEU	1 718	9.529	10.760	2.823	1.00	0.89
ATOM	1595	CB LEU	1 718	9.173	12.524	5.478	1.00	0.89
ATOM	1596	CG LEU	1 718	7.772	11.987	5.137	1.00	0.89
ATOM	1597	CD1 LEU	1 718	7.570	10.569	5.700	1.00	0.89
ATOM	1598	CD2 LEU	1 718	6.674	12.963	5.589	1.00	0.89
ATOM	1599	N THR	1 719	10.607	12.736	2.666	1.00	4.49
ATOM	1600	CA THR	1 719	10.417	12.802	1.244	1.00	4.49
ATOM	1601	C THR	1 719	11.120	11.627	0.650	1.00	4.49
ATOM	1602	O THR	1 719	10.716	11.101	-0.385	1.00	4.49
ATOM	1603	CB THR	1 719	10.957	14.047	0.599	1.00	4.49
ATOM	1604	OG1 THR	1 719	10.426	14.178	-0.712	1.00	4.49
ATOM	1605	CG2 THR	1 719	12.487	13.952	0.516	1.00	4.49
ATOM	1606	N LYS	1 720	12.203	11.191	1.313	1.00	8.13
ATOM	1607	CA LYS	1 720	12.989	10.077	0.874	1.00	8.13
ATOM	1608	C LYS	1 720	12.109	8.864	0.840	1.00	8.13
ATOM	1609	O LYS	1 720	12.278	7.996	-0.013	1.00	8.13
ATOM	1610	CB LYS	1 720	14.177	9.812	1.819	1.00	8.13
ATOM	1611	CG LYS	1 720	15.149	8.724	1.356	1.00	8.13
ATOM	1612	CD LYS	1 720	14.561	7.313	1.350	1.00	8.13
ATOM	1613	CE LYS	1 720	14.315	6.750	2.752	1.00	8.13
ATOM	1614	NZ LYS	1 720	13.746	5.387	2.658	1.00	8.13
ATOM	1615	N LEU	1 721	11.139	8.777	1.770	1.00	3.53
ATOM	1616	CA LEU	1 721	10.246	7.652	1.836	1.00	3.53
ATOM	1617	C LEU	1 721	9.467	7.564	0.564	1.00	3.53
ATOM	1618	O LEU	1 721	9.163	6.476	0.080	1.00	3.53
ATOM	1619	CB LEU	1 721	9.203	7.760	2.965	1.00	3.53
ATOM	1620	CG LEU	1 721	9.775	7.642	4.388	1.00	3.53
ATOM	1621	CD1 LEU	1 721	10.758	8.774	4.697	1.00	3.53
ATOM	1622	CD2 LEU	1 721	8.647	7.568	5.426	1.00	3.53
ATOM	1623	N LEU	1 722	9.113	8.720	-0.014	1.00	4.47
ATOM	1624	CA LEU	1 722	8.339	8.721	-1.217	1.00	4.47
ATOM	1625	C LEU	1 722	9.128	7.983	-2.250	1.00	4.47

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ATOM 1626 O LEU 1 722	8.576	7.213	-3.035	1.00	4.47
ATOM 1627 CB LEU 1 722	8.075	10.143	-1.733	1.00	4.47
ATOM 1628 CG LEU 1 722	7.237	10.990	-0.759	1.00	4.47
ATOM 1629 CD1 LEU 1 722	7.970	11.234	0.569	1.00	4.47
ATOM 1630 CD2 LEU 1 722	6.785	12.297	-1.417	1.00	4.47
ATOM 1631 N ASP 1 723	10.455	8.197	-2.256	1.00	4.04
ATOM 1632 CA ASP 1 723	11.333	7.563	-3.195	1.00	4.04
ATOM 1633 C ASP 1 723	11.247	6.081	-3.008	1.00	4.04
ATOM 1634 O ASP 1 723	11.102	5.331	-3.973	1.00	4.04
ATOM 1635 CB ASP 1 723	12.801	7.981	-2.965	1.00	4.04
ATOM 1636 CG ASP 1 723	13.697	7.406	-4.055	1.00	4.04
ATOM 1637 OD1 ASP 1 723	14.413	8.214	-4.705	1.00	4.04
ATOM 1638 OD2 ASP 1 723	13.684	6.163	-4.258	1.00	4.04
ATOM 1639 N SER 1 724	11.308	5.619	-1.747	1.00	3.24
ATOM 1640 CA SER 1 724	11.287	4.209	-1.498	1.00	3.24
ATOM 1641 C SER 1 724	9.986	3.653	-1.977	1.00	3.24
ATOM 1642 O SER 1 724	9.938	2.558	-2.534	1.00	3.24
ATOM 1643 CB SER 1 724	11.446	3.845	-0.009	1.00	3.24
ATOM 1644 OG SER 1 724	10.310	4.264	0.732	1.00	3.24
ATOM 1645 N MET 1 725	8.890	4.407	-1.776	1.00	0.77
ATOM 1646 CA MET 1 725	7.590	3.949	-2.165	1.00	0.77
ATOM 1647 C MET 1 725	7.516	3.774	-3.652	1.00	0.77
ATOM 1648 O MET 1 725	6.920	2.815	-4.138	1.00	0.77
ATOM 1649 CB MET 1 725	6.465	4.916	-1.756	1.00	0.77
ATOM 1650 CG MET 1 725	6.331	5.076	-0.241	1.00	0.77
ATOM 1651 SD MET 1 725	4.967	6.152	0.289	1.00	0.77
ATOM 1652 CE MET 1 725	3.672	4.931	-0.072	1.00	0.77
ATOM 1653 N HIS 1 726	8.098	4.697	-4.438	1.00	3.69
ATOM 1654 CA HIS 1 726	8.018	4.491	-5.855	1.00	3.69
ATOM 1655 C HIS 1 726	8.835	3.300	-6.224	1.00	3.69
ATOM 1656 O HIS 1 726	8.536	2.585	-7.177	1.00	3.69
ATOM 1657 CB HIS 1 726	8.434	5.689	-6.730	1.00	3.69
ATOM 1658 CG HIS 1 726	9.861	6.124	-6.617	1.00	3.69
ATOM 1659 ND1 HIS 1 726	10.251	7.298	-6.014	1.00	3.69
ATOM 1660 CD2 HIS 1 726	10.990	5.583	-7.148	1.00	3.69
ATOM 1661 CE1 HIS 1 726	11.586	7.412	-6.215	1.00	3.69
ATOM 1662 NE2 HIS 1 726	12.083	6.392	-6.892	1.00	3.69
ATOM 1663 N GLU 1 727	9.922	3.054	-5.483	1.00	3.10
ATOM 1664 CA GLU 1 727	10.722	1.912	-5.796	1.00	3.10
ATOM 1665 C GLU 1 727	9.893	0.682	-5.611	1.00	3.10
ATOM 1666 O GLU 1 727	9.911	-0.216	-6.453	1.00	3.10
ATOM 1667 CB GLU 1 727	11.945	1.794	-4.872	1.00	3.10
ATOM 1668 CG GLU 1 727	12.968	2.911	-5.081	1.00	3.10
ATOM 1669 CD GLU 1 727	13.728	2.599	-6.360	1.00	3.10
ATOM 1670 OE1 GLU 1 727	14.682	3.355	-6.684	1.00	3.10
ATOM 1671 OE2 GLU 1 727	13.365	1.595	-7.029	1.00	3.10
ATOM 1672 N VAL 1 728	9.116	0.615	-4.512	1.00	3.54
ATOM 1673 CA VAL 1 728	8.362	-0.578	-4.262	1.00	3.54
ATOM 1674 C VAL 1 728	7.337	-0.786	-5.333	1.00	3.54
ATOM 1675 O VAL 1 728	7.119	-1.913	-5.772	1.00	3.54
ATOM 1676 CB VAL 1 728	7.677	-0.623	-2.919	1.00	3.54
ATOM 1677 CG1 VAL 1 728	8.755	-0.522	-1.828	1.00	3.54
ATOM 1678 CG2 VAL 1 728	6.576	0.440	-2.837	1.00	3.54
ATOM 1679 N VAL 1 729	6.684	0.294	-5.803	1.00	3.39
ATOM 1680 CA VAL 1 729	5.675	0.117	-6.810	1.00	3.39
ATOM 1681 C VAL 1 729	6.279	-0.428	-8.067	1.00	3.39
ATOM 1682 O VAL 1 729	5.694	-1.291	-8.720	1.00	3.39
ATOM 1683 CB VAL 1 729	4.943	1.375	-7.186	1.00	3.39
ATOM 1684 CG1 VAL 1 729	5.919	2.329	-7.879	1.00	3.39
ATOM 1685 CG2 VAL 1 729	3.762	1.002	-8.099	1.00	3.39
ATOM 1686 N GLU 1 730	7.477	0.063	-8.441	1.00	1.12

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ATOM 1687	CA	GLU 1 730	8.090	-0.357	-9.663	1.00	1.12
ATOM 1688	C	GLU 1 730	8.377	-1.815	-9.564	1.00	1.12
ATOM 1689	O	GLU 1 730	8.113	-2.579	-10.490	1.00	1.12
ATOM 1690	CB	GLU 1 730	9.431	0.350	-9.936	1.00	1.12
ATOM 1691	CG	GLU 1 730	9.310	1.849	-10.229	1.00	1.12
ATOM 1692	CD	GLU 1 730	10.714	2.390	-10.474	1.00	1.12
ATOM 1693	OE1	GLU 1 730	10.842	3.618	-10.731	1.00	1.12
ATOM 1694	OE2	GLU 1 730	11.680	1.583	-10.410	1.00	1.12
ATOM 1695	N	ASN 1 731	8.908	-2.238	-8.405	1.00	3.09
ATOM 1696	CA	ASN 1 731	9.277	-3.607	-8.203	1.00	3.09
ATOM 1697	C	ASN 1 731	8.062	-4.472	-8.272	1.00	3.09
ATOM 1698	O	ASN 1 731	8.100	-5.581	-8.801	1.00	3.09
ATOM 1699	CB	ASN 1 731	9.937	-3.838	-6.836	1.00	3.09
ATOM 1700	CG	ASN 1 731	10.529	-5.236	-6.849	1.00	3.09
ATOM 1701	OD1	ASN 1 731	9.829	-6.227	-7.053	1.00	3.09
ATOM 1702	ND2	ASN 1 731	11.870	-5.318	-6.641	1.00	3.09
ATOM 1703	N	LEU 1 732	6.935	-3.981	-7.738	1.00	1.26
ATOM 1704	CA	LEU 1 732	5.742	-4.771	-7.713	1.00	1.26
ATOM 1705	C	LEU 1 732	5.349	-5.051	-9.132	1.00	1.26
ATOM 1706	O	LEU 1 732	4.895	-6.146	-9.456	1.00	1.26
ATOM 1707	CB	LEU 1 732	4.593	-4.049	-6.971	1.00	1.26
ATOM 1708	CG	LEU 1 732	3.312	-4.871	-6.685	1.00	1.26
ATOM 1709	CD1	LEU 1 732	2.279	-4.010	-5.941	1.00	1.26
ATOM 1710	CD2	LEU 1 732	2.700	-5.502	-7.945	1.00	1.26
ATOM 1711	N	LEU 1 733	5.537	-4.073	-10.034	1.00	6.33
ATOM 1712	CA	LEU 1 733	5.142	-4.289	-11.394	1.00	6.33
ATOM 1713	C	LEU 1 733	5.868	-5.480	-11.943	1.00	6.33
ATOM 1714	O	LEU 1 733	5.287	-6.307	-12.642	1.00	6.33
ATOM 1715	CB	LEU 1 733	5.480	-3.096	-12.307	1.00	6.33
ATOM 1716	CG	LEU 1 733	5.063	-3.298	-13.777	1.00	6.33
ATOM 1717	CD1	LEU 1 733	3.536	-3.380	-13.924	1.00	6.33
ATOM 1718	CD2	LEU 1 733	5.696	-2.234	-14.689	1.00	6.33
ATOM 1719	N	ASN 1 734	7.172	-5.615	-11.663	1.00	4.20
ATOM 1720	CA	ASN 1 734	7.856	-6.750	-12.213	1.00	4.20
ATOM 1721	C	ASN 1 734	7.377	-8.043	-11.629	1.00	4.20
ATOM 1722	O	ASN 1 734	7.196	-9.035	-12.335	1.00	4.20
ATOM 1723	CB	ASN 1 734	9.398	-6.679	-12.092	1.00	4.20
ATOM 1724	CG	ASN 1 734	9.854	-6.616	-10.639	1.00	4.20
ATOM 1725	OD1	ASN 1 734	10.239	-5.552	-10.159	1.00	4.20
ATOM 1726	ND2	ASN 1 734	9.831	-7.775	-9.927	1.00	4.20
ATOM 1727	N	TYR 1 735	7.136	-8.093	-10.314	1.00	7.65
ATOM 1728	CA	TYR 1 735	6.749	-9.366	-9.802	1.00	7.65
ATOM 1729	C	TYR 1 735	5.394	-9.717	-10.306	1.00	7.65
ATOM 1730	O	TYR 1 735	5.118	-10.881	-10.597	1.00	7.65
ATOM 1731	CB	TYR 1 735	6.652	-9.443	-8.283	1.00	7.65
ATOM 1732	CG	TYR 1 735	6.449	-10.889	-7.992	1.00	7.65
ATOM 1733	CD1	TYR 1 735	7.537	-11.677	-7.696	1.00	7.65
ATOM 1734	CD2	TYR 1 735	5.188	-11.455	-7.945	1.00	7.65
ATOM 1735	CE1	TYR 1 735	7.377	-12.989	-7.317	1.00	7.65
ATOM 1736	CE2	TYR 1 735	5.026	-12.770	-7.578	1.00	7.65
ATOM 1737	CZ	TYR 1 735	6.118	-13.531	-7.238	1.00	7.65
ATOM 1738	OH	TYR 1 735	5.951	-14.875	-6.842	1.00	7.65
ATOM 1739	N	CYS 1 736	4.507	-8.714	-10.433	1.00	4.30
ATOM 1740	CA	CYS 1 736	3.158	-9.054	-10.756	1.00	4.30
ATOM 1741	C	CYS 1 736	3.081	-9.771	-12.053	1.00	4.30
ATOM 1742	O	CYS 1 736	2.369	-10.767	-12.164	1.00	4.30
ATOM 1743	CB	CYS 1 736	2.192	-7.856	-10.780	1.00	4.30
ATOM 1744	SG	CYS 1 736	2.518	-6.684	-12.120	1.00	4.30
ATOM 1745	N	PHE 1 737	3.823	-9.323	-13.075	1.00	7.73
ATOM 1746	CA	PHE 1 737	3.655	-10.052	-14.290	1.00	7.73
ATOM 1747	C	PHE 1 737	4.160	-11.453	-14.158	1.00	7.73

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ATOM 1748	O PHE 1 737	3.507 -12.390 -14.611	1.00	7.73
ATOM 1749	CB PHE 1 737	4.273 -9.389 -15.540	1.00	7.73
ATOM 1750	CG PHE 1 737	5.754 -9.302 -15.437	1.00	7.73
ATOM 1751	CD1 PHE 1 737	6.355 -8.226 -14.824	1.00	7.73
ATOM 1752	CD2 PHE 1 737	6.542 -10.220 -16.092	1.00	7.73
ATOM 1753	CE1 PHE 1 737	7.722 -8.082 -14.847	1.00	7.73
ATOM 1754	CE2 PHE 1 737	7.911 -10.092 -16.101	1.00	7.73
ATOM 1755	CZ PHE 1 737	8.503 -9.023 -15.476	1.00	7.73
ATOM 1756	N GLN 1 738	5.315 -11.656 -13.493	1.00	7.23
ATOM 1757	CA GLN 1 738	5.836 -12.990 -13.454	1.00	7.23
ATOM 1758	C GLN 1 738	4.860 -13.857 -12.729	1.00	7.23
ATOM 1759	O GLN 1 738	4.605 -14.996 -13.114	1.00	7.23
ATOM 1760	CB GLN 1 738	7.208 -13.107 -12.762	1.00	7.23
ATOM 1761	CG GLN 1 738	7.177 -12.981 -11.240	1.00	7.23
ATOM 1762	CD GLN 1 738	7.120 -14.405 -10.704	1.00	7.23
ATOM 1763	OE1 GLN 1 738	7.186 -14.645 -9.500	1.00	7.23
ATOM 1764	NE2 GLN 1 738	7.013 -15.395 -11.631	1.00	7.23
ATOM 1765	N THR 1 739	4.283 -13.340 -11.637	1.00	5.24
ATOM 1766	CA THR 1 739	3.338 -14.132 -10.912	1.00	5.24
ATOM 1767	C THR 1 739	2.092 -14.330 -11.715	1.00	5.24
ATOM 1768	O THR 1 739	1.507 -15.413 -11.725	1.00	5.24
ATOM 1769	CB THR 1 739	2.953 -13.519 -9.596	1.00	5.24
ATOM 1770	OG1 THR 1 739	2.945 -12.102 -9.699	1.00	5.24
ATOM 1771	CG2 THR 1 739	3.949 -13.970 -8.515	1.00	5.24
ATOM 1772	N PHE 1 740	1.665 -13.276 -12.430	1.00	6.82
ATOM 1773	CA PHE 1 740	0.434 -13.258 -13.161	1.00	6.82
ATOM 1774	C PHE 1 740	0.463 -14.242 -14.278	1.00	6.82
ATOM 1775	O PHE 1 740	-0.558 -14.842 -14.609	1.00	6.82
ATOM 1776	CB PHE 1 740	0.130 -11.872 -13.756	1.00	6.82
ATOM 1777	CG PHE 1 740	-1.308 -11.852 -14.142	1.00	6.82
ATOM 1778	CD1 PHE 1 740	-1.724 -12.340 -15.358	1.00	6.82
ATOM 1779	CD2 PHE 1 740	-2.246 -11.343 -13.272	1.00	6.82
ATOM 1780	CE1 PHE 1 740	-3.055 -12.316 -15.701	1.00	6.82
ATOM 1781	CE2 PHE 1 740	-3.577 -11.318 -13.609	1.00	6.82
ATOM 1782	CZ PHE 1 740	-3.985 -11.804 -14.827	1.00	6.82
ATOM 1783	N LEU 1 741	1.647 -14.447 -14.877	1.00	5.17
ATOM 1784	CA LEU 1 741	1.718 -15.298 -16.022	1.00	5.17
ATOM 1785	C LEU 1 741	1.219 -16.654 -15.648	1.00	5.17
ATOM 1786	O LEU 1 741	0.458 -17.260 -16.398	1.00	5.17
ATOM 1787	CB LEU 1 741	3.155 -15.433 -16.573	1.00	5.17
ATOM 1788	CG LEU 1 741	3.290 -16.235 -17.890	1.00	5.17
ATOM 1789	CD1 LEU 1 741	3.002 -17.735 -17.715	1.00	5.17
ATOM 1790	CD2 LEU 1 741	2.455 -15.594 -19.010	1.00	5.17
ATOM 1791	N ASP 1 742	1.605 -17.172 -14.469	1.00	6.55
ATOM 1792	CA ASP 1 742	1.164 -18.507 -14.199	1.00	6.55
ATOM 1793	C ASP 1 742	0.007 -18.588 -13.252	1.00	6.55
ATOM 1794	O ASP 1 742	0.168 -18.330 -12.059	1.00	6.55
ATOM 1795	CB ASP 1 742	2.282 -19.432 -13.678	1.00	6.55
ATOM 1796	CG ASP 1 742	2.836 -18.875 -12.374	1.00	6.55
ATOM 1797	OD1 ASP 1 742	2.616 -17.665 -12.100	1.00	6.55
ATOM 1798	OD2 ASP 1 742	3.494 -19.654 -11.634	1.00	6.55
ATOM 1799	N LYS 1 743	-1.188 -18.919 -13.811	1.00	7.11
ATOM 1800	CA LYS 1 743	-2.427 -19.213 -13.129	1.00	7.11
ATOM 1801	C LYS 1 743	-3.536 -18.292 -13.532	1.00	7.11
ATOM 1802	O LYS 1 743	-3.327 -17.101 -13.755	1.00	7.11
ATOM 1803	CB LYS 1 743	-2.353 -19.214 -11.590	1.00	7.11
ATOM 1804	CG LYS 1 743	-3.579 -19.800 -10.895	1.00	7.11
ATOM 1805	CD LYS 1 743	-3.308 -20.161 -9.434	1.00	7.11
ATOM 1806	CE LYS 1 743	-2.225 -21.231 -9.278	1.00	7.11
ATOM 1807	NZ LYS 1 743	-2.007 -21.537 -7.847	1.00	7.11
ATOM 1808	N THR 1 744	-4.764 -18.848 -13.631	1.00	3.77

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ATOM	1809	CA	THR	1 744	-5.932	-18.071	-13.934	1.00	3.77
ATOM	1810	C	THR	1 744	-6.606	-18.018	-12.601	1.00	3.77
ATOM	1811	O	THR	1 744	-5.925	-17.857	-11.590	1.00	3.77
ATOM	1812	CB	THR	1 744	-6.839	-18.721	-14.948	1.00	3.77
ATOM	1813	OG1	THR	1 744	-6.106	-18.987	-16.136	1.00	3.77
ATOM	1814	CG2	THR	1 744	-7.995	-17.762	-15.299	1.00	3.77
ATOM	1815	N	MET	1 745	-7.948	-18.136	-12.517	1.00	12.59
ATOM	1816	CA	MET	1 745	-8.413	-18.065	-11.172	1.00	12.59
ATOM	1817	C	MET	1 745	-9.878	-18.181	-10.986	1.00	12.59
ATOM	1818	O	MET	1 745	-10.676	-17.804	-11.842	1.00	12.59
ATOM	1819	CB	MET	1 745	-8.183	-16.711	-10.536	1.00	12.59
ATOM	1820	CG	MET	1 745	-9.189	-15.659	-11.022	1.00	12.59
ATOM	1821	SD	MET	1 745	-9.788	-14.502	-9.750	1.00	12.59
ATOM	1822	CE	MET	1 745	-10.941	-13.605	-10.832	1.00	12.59
ATOM	1823	N	SER	1 746	-10.262	-18.777	-9.844	1.00	4.73
ATOM	1824	CA	SER	1 746	-11.605	-18.590	-9.414	1.00	4.73
ATOM	1825	C	SER	1 746	-11.447	-17.285	-8.692	1.00	4.73
ATOM	1826	O	SER	1 746	-11.988	-16.252	-9.084	1.00	4.73
ATOM	1827	CB	SER	1 746	-12.061	-19.649	-8.395	1.00	4.73
ATOM	1828	OG	SER	1 746	-13.407	-19.413	-8.007	1.00	4.73
ATOM	1829	N	ILE	1 747	-10.646	-17.343	-7.603	1.00	6.94
ATOM	1830	CA	ILE	1 747	-10.266	-16.253	-6.747	1.00	6.94
ATOM	1831	C	ILE	1 747	-8.902	-15.708	-7.066	1.00	6.94
ATOM	1832	O	ILE	1 747	-8.586	-14.569	-6.729	1.00	6.94
ATOM	1833	CB	ILE	1 747	-10.217	-16.660	-5.303	1.00	6.94
ATOM	1834	CG1	ILE	1 747	-9.984	-15.428	-4.414	1.00	6.94
ATOM	1835	CG2	ILE	1 747	-9.141	-17.749	-5.149	1.00	6.94
ATOM	1836	CD1	ILE	1 747	-11.153	-14.445	-4.422	1.00	6.94
ATOM	1837	N	GLU	1 748	-8.062	-16.506	-7.750	1.00	5.83
ATOM	1838	CA	GLU	1 748	-6.665	-16.191	-7.900	1.00	5.83
ATOM	1839	C	GLU	1 748	-6.317	-14.839	-8.467	1.00	5.83
ATOM	1840	O	GLU	1 748	-5.542	-14.112	-7.851	1.00	5.83
ATOM	1841	CB	GLU	1 748	-5.904	-17.242	-8.728	1.00	5.83
ATOM	1842	CG	GLU	1 748	-4.393	-17.188	-8.502	1.00	5.83
ATOM	1843	CD	GLU	1 748	-4.115	-17.849	-7.157	1.00	5.83
ATOM	1844	OE1	GLU	1 748	-4.360	-19.080	-7.041	1.00	5.83
ATOM	1845	OE2	GLU	1 748	-3.656	-17.133	-6.228	1.00	5.83
ATOM	1846	N	PHE	1 749	-6.846	-14.431	-9.636	1.00	0.97
ATOM	1847	CA	PHE	1 749	-6.471	-13.137	-10.126	1.00	0.97
ATOM	1848	C	PHE	1 749	-7.707	-12.328	-10.320	1.00	0.97
ATOM	1849	O	PHE	1 749	-8.441	-12.492	-11.293	1.00	0.97
ATOM	1850	CB	PHE	1 749	-5.729	-13.184	-11.471	1.00	0.97
ATOM	1851	CG	PHE	1 749	-4.441	-13.886	-11.218	1.00	0.97
ATOM	1852	CD1	PHE	1 749	-4.391	-15.260	-11.210	1.00	0.97
ATOM	1853	CD2	PHE	1 749	-3.294	-13.173	-10.959	1.00	0.97
ATOM	1854	CE1	PHE	1 749	-3.209	-15.915	-10.956	1.00	0.97
ATOM	1855	CE2	PHE	1 749	-2.109	-13.822	-10.701	1.00	0.97
ATOM	1856	CZ	PHE	1 749	-2.066	-15.196	-10.702	1.00	0.97
ATOM	1857	N	PRO	1 750	-7.925	-11.440	-9.397	1.00	2.67
ATOM	1858	CA	PRO	1 750	-9.095	-10.620	-9.417	1.00	2.67
ATOM	1859	C	PRO	1 750	-9.079	-9.888	-10.712	1.00	2.67
ATOM	1860	O	PRO	1 750	-7.998	-9.566	-11.200	1.00	2.67
ATOM	1861	CB	PRO	1 750	-8.924	-9.612	-8.279	1.00	2.67
ATOM	1862	CG	PRO	1 750	-7.545	-9.932	-7.664	1.00	2.67
ATOM	1863	CD	PRO	1 750	-6.833	-10.743	-8.759	1.00	2.67
ATOM	1864	N	GLU	1 751	-10.261	-9.636	-11.291	1.00	5.68
ATOM	1865	CA	GLU	1 751	-10.318	-8.882	-12.502	1.00	5.68
ATOM	1866	C	GLU	1 751	-9.848	-7.504	-12.174	1.00	5.68
ATOM	1867	O	GLU	1 751	-9.093	-6.895	-12.931	1.00	5.68
ATOM	1868	CB	GLU	1 751	-11.743	-8.770	-13.073	1.00	5.68
ATOM	1869	CG	GLU	1 751	-12.741	-8.112	-12.116	1.00	5.68

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ATOM	1870	CD	GLU	1	751	-13.010	-9.085	-10.976	1.00	5.68
ATOM	1871	OE1	GLU	1	751	-13.346	-10.263	-11.271	1.00	5.68
ATOM	1872	OE2	GLU	1	751	-12.865	-8.669	-9.796	1.00	5.68
ATOM	1873	N	MET	1	752	-10.275	-6.984	-11.009	1.00	5.28
ATOM	1874	CA	MET	1	752	-9.934	-5.644	-10.636	1.00	5.28
ATOM	1875	C	MET	1	752	-8.448	-5.558	-10.471	1.00	5.28
ATOM	1876	O	MET	1	752	-7.819	-4.609	-10.932	1.00	5.28
ATOM	1877	CB	MET	1	752	-10.589	-5.214	-9.312	1.00	5.28
ATOM	1878	CG	MET	1	752	-10.778	-3.701	-9.185	1.00	5.28
ATOM	1879	SD	MET	1	752	-9.265	-2.716	-9.345	1.00	5.28
ATOM	1880	CE	MET	1	752	-10.099	-1.122	-9.091	1.00	5.28
ATOM	1881	N	LEU	1	753	-7.840	-6.568	-9.818	1.00	0.87
ATOM	1882	CA	LEU	1	753	-6.422	-6.511	-9.613	1.00	0.87
ATOM	1883	C	LEU	1	753	-5.745	-6.551	-10.937	1.00	0.87
ATOM	1884	O	LEU	1	753	-4.771	-5.837	-11.174	1.00	0.87
ATOM	1885	CB	LEU	1	753	-5.856	-7.665	-8.770	1.00	0.87
ATOM	1886	CG	LEU	1	753	-4.331	-7.554	-8.569	1.00	0.87
ATOM	1887	CD1	LEU	1	753	-3.962	-6.286	-7.787	1.00	0.87
ATOM	1888	CD2	LEU	1	753	-3.750	-8.831	-7.940	1.00	0.87
ATOM	1889	N	ALA	1	754	-6.263	-7.386	-11.852	1.00	0.70
ATOM	1890	CA	ALA	1	754	-5.656	-7.499	-13.142	1.00	0.70
ATOM	1891	C	ALA	1	754	-5.733	-6.157	-13.790	1.00	0.70
ATOM	1892	O	ALA	1	754	-4.793	-5.720	-14.451	1.00	0.70
ATOM	1893	CB	ALA	1	754	-6.379	-8.501	-14.058	1.00	0.70
ATOM	1894	N	GLU	1	755	-6.866	-5.460	-13.598	1.00	0.95
ATOM	1895	CA	GLU	1	755	-7.066	-4.196	-14.239	1.00	0.95
ATOM	1896	C	GLU	1	755	-6.048	-3.177	-13.824	1.00	0.95
ATOM	1897	O	GLU	1	755	-5.433	-2.531	-14.670	1.00	0.95
ATOM	1898	CB	GLU	1	755	-8.454	-3.608	-13.929	1.00	0.95
ATOM	1899	CG	GLU	1	755	-8.726	-2.270	-14.618	1.00	0.95
ATOM	1900	CD	GLU	1	755	-10.126	-1.824	-14.224	1.00	0.95
ATOM	1901	OE1	GLU	1	755	-11.063	-2.660	-14.328	1.00	0.95
ATOM	1902	OE2	GLU	1	755	-10.279	-0.644	-13.809	1.00	0.95
ATOM	1903	N	ILE	1	756	-5.818	-3.021	-12.508	1.00	3.83
ATOM	1904	CA	ILE	1	756	-4.918	-2.004	-12.037	1.00	3.83
ATOM	1905	C	ILE	1	756	-3.521	-2.272	-12.504	1.00	3.83
ATOM	1906	O	ILE	1	756	-2.818	-1.368	-12.955	1.00	3.83
ATOM	1907	CB	ILE	1	756	-4.874	-1.937	-10.538	1.00	3.83
ATOM	1908	CG1	ILE	1	756	-6.269	-1.620	-9.974	1.00	3.83
ATOM	1909	CG2	ILE	1	756	-3.801	-0.909	-10.142	1.00	3.83
ATOM	1910	CD1	ILE	1	756	-6.827	-0.277	-10.441	1.00	3.83
ATOM	1911	N	ILE	1	757	-3.091	-3.539	-12.384	1.00	4.18
ATOM	1912	CA	ILE	1	757	-1.774	-3.982	-12.742	1.00	4.18
ATOM	1913	C	ILE	1	757	-1.518	-3.958	-14.217	1.00	4.18
ATOM	1914	O	ILE	1	757	-0.435	-3.571	-14.656	1.00	4.18
ATOM	1915	CB	ILE	1	757	-1.535	-5.393	-12.306	1.00	4.18
ATOM	1916	CG1	ILE	1	757	-1.484	-5.491	-10.772	1.00	4.18
ATOM	1917	CG2	ILE	1	757	-0.288	-5.898	-13.036	1.00	4.18
ATOM	1918	CD1	ILE	1	757	-0.364	-4.662	-10.145	1.00	4.18
ATOM	1919	N	THR	1	758	-2.503	-4.397	-15.023	1.00	5.11
ATOM	1920	CA	THR	1	758	-2.304	-4.465	-16.443	1.00	5.11
ATOM	1921	C	THR	1	758	-2.510	-3.111	-17.031	1.00	5.11
ATOM	1922	O	THR	1	758	-2.949	-2.187	-16.349	1.00	5.11
ATOM	1923	CB	THR	1	758	-3.242	-5.403	-17.143	1.00	5.11
ATOM	1924	OG1	THR	1	758	-2.843	-5.575	-18.496	1.00	5.11
ATOM	1925	CG2	THR	1	758	-4.664	-4.819	-17.077	1.00	5.11
ATOM	1926	N	ASN	1	759	-2.176	-2.957	-18.327	1.00	3.12
ATOM	1927	CA	ASN	1	759	-2.329	-1.679	-18.953	1.00	3.12
ATOM	1928	C	ASN	1	759	-3.541	-1.690	-19.823	1.00	3.12
ATOM	1929	O	ASN	1	759	-3.865	-2.695	-20.451	1.00	3.12
ATOM	1930	CB	ASN	1	759	-1.142	-1.282	-19.849	1.00	3.12

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ATOM	1931	CG	ASN	1	759	0.054	-0.997	-18.952	1.00	3.12
ATOM	1932	OD1	ASN	1	759	-0.082	-0.389	-17.891	1.00	3.12
ATOM	1933	ND2	ASN	1	759	1.261	-1.451	-19.385	1.00	3.12
ATOM	1934	N	GLN	1	760	-4.259	-0.550	-19.855	1.00	5.67
ATOM	1935	CA	GLN	1	760	-5.408	-0.424	-20.700	1.00	5.67
ATOM	1936	C	GLN	1	760	-5.158	0.765	-21.564	1.00	5.67
ATOM	1937	O	GLN	1	760	-4.484	1.710	-21.155	1.00	5.67
ATOM	1938	CB	GLN	1	760	-6.726	-0.152	-19.952	1.00	5.67
ATOM	1939	CG	GLN	1	760	-7.226	-1.330	-19.115	1.00	5.67
ATOM	1940	CD	GLN	1	760	-6.386	-1.415	-17.851	1.00	5.67
ATOM	1941	OE1	GLN	1	760	-5.555	-0.551	-17.573	1.00	5.67
ATOM	1942	NE2	GLN	1	760	-6.616	-2.492	-17.054	1.00	5.67
ATOM	1943	N	ILE	1	761	-5.683	0.737	-22.803	1.00	6.58
ATOM	1944	CA	ILE	1	761	-5.500	1.858	-23.672	1.00	6.58
ATOM	1945	C	ILE	1	761	-6.750	2.723	-23.555	1.00	6.58
ATOM	1946	O	ILE	1	761	-6.596	3.935	-23.246	1.00	6.58
ATOM	1947	CB	ILE	1	761	-5.312	1.476	-25.115	1.00	6.58
ATOM	1948	CG1	ILE	1	761	-6.544	0.739	-25.669	1.00	6.58
ATOM	1949	CG2	ILE	1	761	-4.010	0.667	-25.220	1.00	6.58
ATOM	1950	CD1	ILE	1	761	-6.531	0.593	-27.189	1.00	6.58
ATOM	1951	OXT	ILE	1	761	-7.873	2.190	-23.762	1.00	99.99
TER	1952	ILE	1	761						
HETATM	1953	C1	STR	1		-2.622	-6.967	-0.799	1.00	0.00
HETATM	1954	C2	STR	1		-3.341	-5.965	0.100	1.00	0.05
HETATM	1955	C3	STR	1		-2.352	-5.075	0.821	1.00	0.40
HETATM	1956	C4	STR	1		-1.095	-4.751	0.129	1.00	0.00
HETATM	1957	C5	STR	1		-0.750	-5.273	-1.062	1.00	-0.25
HETATM	1958	C6	STR	1		0.540	-4.815	-1.735	1.00	0.14
HETATM	1959	C7	STR	1		1.328	-6.000	-2.288	1.00	0.00
HETATM	1960	C8	STR	1		0.456	-6.908	-3.164	1.00	0.00
HETATM	1961	C9	STR	1		-0.724	-7.458	-2.322	1.00	0.00
HETATM	1962	C10	STR	1		-1.626	-6.320	-1.778	1.00	0.11
HETATM	1963	C19	STR	1		-2.391	-5.603	-2.902	1.00	0.00
HETATM	1964	C11	STR	1		-1.524	-8.494	-3.148	1.00	0.00
HETATM	1965	C12	STR	1		-0.648	-9.594	-3.770	1.00	0.00
HETATM	1966	C13	STR	1		0.457	-8.988	-4.641	1.00	0.00
HETATM	1967	C14	STR	1		1.275	-8.093	-3.703	1.00	0.00
HETATM	1968	C15	STR	1		2.508	-7.695	-4.513	1.00	0.00
HETATM	1969	C16	STR	1		2.792	-8.947	-5.345	1.00	0.00
HETATM	1970	C17	STR	1		1.625	-9.911	-5.049	1.00	0.05
HETATM	1971	C20	STR	1		1.304	-10.838	-6.220	1.00	0.35
HETATM	1972	C21	STR	1		0.230	-11.885	-6.041	1.00	0.05
HETATM	1973	O104	STR	1		-0.778	-11.710	-7.040	1.00	0.00
HETATM	1974	H104	STR	1		-1.162	-10.845	-6.954	1.00	0.00
HETATM	1975	O20	STR	1		1.927	-10.786	-7.267	1.00	-0.45
HETATM	1976	C18	STR	1		-0.161	-8.233	-5.840	1.00	0.00
HETATM	1977	O100	STR	1		-2.202	-7.806	-4.202	1.00	0.00
HETATM	1978	H100	STR	1		-2.698	-8.429	-4.720	1.00	0.00
HETATM	1979	O3	STR	1		-2.598	-4.635	1.939	1.00	-0.45
HETATM	1980	HE2	HE2	2		6.456	-14.046	-4.976	1.00	99.99
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SUBSTITUTE SHEET (RULE 26)

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **HOMOLOGY MODELS OF THE GLUCOCORTICOID RECEPTOR**

(57) Abstract: A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three-dimensional image, the method comprising: (i) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor; (ii) modifying said x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand; (iii) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (iv) if required modifying the homology model for greater consistency with those binding properties.



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# INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 00/00727

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C07K14/705

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 G06F C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 56812 A (PIKE ASHLEY CHARLES WILLIAM ;BZOWSKI ANDRZEJI MAREK (GB); HUBBAR) 17 December 1998 (1998-12-17) page 3, paragraph 1 page 13, paragraph 3 page 28, paragraph 4 claims 13,53,54,56 ---	1-13, 17-20
X	WO 97 21993 A (UNIV CALIFORNIA) 19 June 1997 (1997-06-19) abstract; claims 10-12,23,29-31,38-45 page 3, paragraph 1 page 10, line 19 - line 27 page 29, line 24 -page 30, line 13 --- -/--	1-13, 17-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

3 August 2000

Date of mailing of the international search report

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# INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 00/00727

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 50658 A (GREENE GEOFFREY L ;AGARD DAVID A (US); ARCH DEV CORP (US); KUSHNER) 7 October 1999 (1999-10-07) abstract; claims 1-71 ---	1-13, 17-20
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A	ANSTEAD G M ET AL: "The estradiol pharmacophore: Ligand structure-estrogen receptor binding affinity relationships and a model for the receptor binding site" STERIODS: STRUCTURE, FUNCTION, AND REGULATION,US,ELSEVIER SCIENCE PUBLISHERS, NEW YORK, NY, vol. 62, no. 3, 1 March 1997 (1997-03-01), pages 268-303, XP004057108 ISSN: 0039-128X abstract ---	1-13, 17-20
A	R C J RIBEIRO ET AL: "Mechanisms of Thyroid Hormone Action: Insights from X-ray Crystallographic and Functional Studies" RECENT PROGRESS IN HORMONE RESEARCH,US,ACADEMIC PRESS, NEW YORK, NY, vol. 53, no. 53, 1998, pages 351-394-394, XP002101079 ISSN: 0079-9963 abstract page 373, paragraph 4 page 377, paragraph 2 - paragraph 3 ---	1-13, 17-20
A	BRZOZOWSKI A ET AL: "Molecular basis of agonism and antagonism in the oestrogen receptor" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, no. 389, 16 October 1997 (1997-10-16), pages 753-758, XP002075907 ISSN: 0028-0836 page 757, left-hand column, paragraph 4 -right-hand column, paragraph 2 ---	1-13, 17-20
A	BOURGUET W ET AL: "Crystal structure of the ligand-binding domain of the human nuclear receptor RXR-alpha" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, no. 375, 1 July 1995 (1995-07-01), pages 377-382, XP002075905 ISSN: 0028-0836 page 379, right-hand column, paragraph 3 -----	1-13, 17-20

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/GB 00/00727

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 14-16  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/SA/ 210

Continuation of Box I.2

Claims Nos.: 14-16

Claims 14-16 refer to a glucocorticoid agonist/antagonist without giving a true technical characterisation. Consequently, the scope of said claims is ambiguous and vague. No meaningful search can be carried out for such claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 00/00727

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